

173999

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Monday, December 12, 2005 2:44 PM
To: Zeman, Mary; STIC-Biotech/ChemLib
Subject: RE: Rush Seq Search 09/924400

Please ~~rush~~. Thanks. Chris

URF8

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Zeman, Mary
Sent: Monday, December 12, 2005 1:32 PM
To: Chan, Christina
Subject: Rush Seq Search 09/924400

This amended application may soon be allowable.
Please search SEQ ID NO: 302, 303 in ALL files including interference
Please do an OLIGO search of SEQ ID NO: 302, 303 in all files. Minimum 10
contiguous nucleotides.
Paper printout please
Thank you, Mary Z

Mary K. Zeman
Primary Examiner, 1631
571-272-0723
Remsen 2D61
MAILBOX: REM 2C70
mary.zeman@uspto.gov

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 12/13/05
Date completed: 12/28/05
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 024
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:05:29 ; Search time 1011.9 Seconds
(without alignments)
11242.903 Million cell updates/sec

Title: US-09-924-400-302

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11752642

Minimum DB seq length: 10

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	2000	100.0	2000	6	AR371071
6	2000	100.0	2000	6	AR400211
7	2000	100.0	2000	6	AR405478
8	2000	100.0	2000	6	AR433319
9	2000	100.0	2000	6	AR563858
10	2000	100.0	2000	6	AR588844
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VERSION	JP 2002520054-A/359.				
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SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 2000)				
AUTHORS	Dillon,D.C., Harlocker,S.L., Yugu,J., Xu,J. and Mitcham,J.L.				
TITLE	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use				
JOURNAL	Patent: JP 2002520054-A 359 09-JUL-2002;				
COMMENT	CORIXA CORP				
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PD	09-JUL-2002				
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23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR					
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09-APR-1999 US 09/288946					
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JIANGCHUN XU, LYNN MITCHAM					
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PC	CI2N5/10,				
PC	CI2P21/08,CI2Q1/68,G01N33/574,G01N33/68//A61P35/00,CI2N15/00,				
PC	A61K37/02,				
PC	CI2N5/00				
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CC	and methods				
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CC	key				
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FT	1..2000				
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ORIGIN

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Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 374 from patent US 6512094.
 ACCESSION AR278479
 VERSION AR278479.1 GI:29712725
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 2000)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
 Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,T.A.W.,
 Hepler,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate
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 JOURNAL Patent: US 6512094-A 374 28-JAN-2003;
 Corixa Corporation; Seattle, WA
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LOCUS AR350943
DEFINITION Sequence 302 from patent US 6586570.
ACCESSION AR350943
VERSION AR350943.1 GI:33752583
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2000)
T. N., Reed, S. G., Smith, J. M., and Misher, L.
TITLES Compositions and methods for the treatment and diagnosis of breast
cancer.
JOURNAL Patent: US 6586570-A 302 01-JUL-2003;
Corixa Corporation; Seattle, WA
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RESULT 4
AR367175 2000 bp DNA linear PAT 12-SEP-2003
LOCUS AR367175
DEFINITION Sequence 374 from patent US 6329505.
ACCESSION AR367175
VERSION AR367175.1 GI:34600150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yudin,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6329505-A 374 11-DEC-2001;
Corixa Corporation; Seattle, WA
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 5
AR371071 2000 bp DNA linear PAT 12-SBP-2003
LOCUS AR371071
DEFINITION Sequence 374 from patent US 6395278.
ACCESSION AR371071
VERSION AR371071.1 GI:34607964
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 2000)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L. and Yudin, J.
TITLE Prostate specific fusion protein compositions
JOURNAL Patent: US 6395278-A 374 28-MAY-2002;
Corixa Corporation; Seattle, WA

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source location/Qualifiers
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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AR405478
LOCUS AR405478 2000 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 374 from patent US 6630305.
ACCESSION AR405478
VERSION AR405478.1 GI:40154315
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fenger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 374 07-OCT-2003;
Corixa Corporation; Seattle, WA;
WOX;

FEATURES
source location/Qualifiers
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AR433319 2000 bp DNA linear PAT 18-DEC-2003
LOCUS AR433319
DEFINITION Sequence 302 from patent US 6656480.
ACCESSION AR433319
VERSION AR433319.1 GI:40196101
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 2000)
Rettner M.W. and Dillon, D.C.
TITLE
Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL
Patent: US 6656480-A 302 02-DEC-2003;
Corixa Corporation; Seattle, WA
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
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RESULT 9
AR563858
LOCUS AR563858 2000 bp DNA linear PART 08-OCT-2004
DEFINITION Sequence 374 from patent US 6759515.
ACCESSION AR563858
VERSION AR563858.1 GI:53978909
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2000)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocke,S.L., Jiang,Y.,
Kaloos,M.D., Fanger,G.R., Retter,M.W., Stoik,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,

Heppler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate cancer
Patent: US 6759515-A 374 06-JUL-2004;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AR588844
LOCUS AR588844 2000 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 374 from patent US 6800746.
ACCESSION AR588844
VERSION AR588844.1 GI:56635741
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6800746-A 374 05-OCT-2004;
Corixa Corporation; Seattle, WA
FEATURES
source 1..2000
Location/Qualifiers
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR605664 2000 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 374 from patent US 6818751.
ACCESSION AR605664
VERSION AR605664.1 GI:56657328
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalogh,M.D., Fanger,G.R., Reister,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6818751-A 374 16-NOV-2004;
FEATURES
source Corixa Corporation; Seattle, WA
Location/Qualifiers
1..2000
/organism="Unknown"
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 12
AR615063
LOCUS AR615063
DEFINITION Sequence 302 from patent US 6828431.
ACCESSION AR615063
VERSION AR615063.1 GI:56671467
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Prudekis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
Retter,M.W., Wang,A., Skeiky,Y.A.W. and Harlocke,S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: US 6828431-A 302 07-DEC-2004;
Corixa Corporation; Seattle, WA
FEATURES
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/organism="unknown"
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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AR642105 2000 bp DNA linear PAT 20-APR-2005
LOCUS AR642105 Sequence 302 from patent US 6861506.
DEFINITION AR642105
ACCESSION AR642105
VERSION AR642105.1 GI:62778253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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REFERENCE 1 (bases 1 to 2000)
AUTHORS Prudakis,T.N., Smith,J.M., Reed,S.G., Misher,L.E., Retter,M.W. and
Dillon,D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast
cancer
JOURNAL Patent: US 6861506-A 302 01-MAR-2005;
Corixa Corporation; Seattle, WA
FEATURES
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS ARE57003
DEFINITION Sequence 374 from patent US 6894146.
ACCESSION ARE57003
VERSION ARE57003.1 GI:67590123
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y., Kalsg M.D., Fanger G.R., Retter M.W., Stoik J.A., Day C.H., Veddyk T.S., Carter D., Li S.X., Wang A., Skelky Y.A.W., Hepler W.T. and Henderson R.A.
COMPOSITIONS and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6894146-A 374 17-MAY-2005;
Corixa Corporation; Seattle, WA
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 REFERENCE 1
 AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
 TITLES Compositions and methods for therapy and diagnosis of prostate cancer
 JOURNAL Patent: WO 0125272-A 374 12-APR-2001;
 CORIXA CORPORATION (US)
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Search completed: December 19, 2005, 15:33:32
Job time : 10119.9 secs

CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 3; Length 2000;
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04-OCT-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #9.

Human; prostate cancer; prostate-specific; diagnosis; vaccine;
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Homo sapiens.

WO200151633-A2.

19-JUL-2001.

16-JAN-2001; 2001WO-US001574.

14-JAN-2000; 2000US-00483672.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;

Wang A, Meagher MJ;

WPI; 2001-425873/45.

New polynucleotide encoding a prostate-specific protein, for diagnosing,

monitoring and treating prostate cancer in a patient and for use in

vaccines.

Claim 1; Page 347-348; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode
prostate-specific proteins (II). (I) and (II) have cytostatic activity,
and can be used in vaccine production and gene therapy. (I), (II),
antibodies to (II), fusion proteins comprising (II), and isolated T cells
prepared using (I) or (II) are used treat cancer in a patient. (I) and
the antibodies are also used in the detection of cancer in a patient. The
cancer that is diagnosed or treated is particularly prostate cancer. (I)
and (II) can be used in vaccines. The antibodies or (I) can be used for
monitoring the progression of cancer in a patient. (I) and (II) can also
be used to improve diagnostic and therapeutic methods for prostate
cancer. They can indicate the level of metastasis as well as the prostate
volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
polynucleotide and amino acid sequences used in the exemplification of
the present invention

Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 4; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTATTCATTCAGTGGGCTGCTCTTCTGTGAAGAAGCATTGGTCTC 60
DB 1 ATGGTGGTGGAGTATTCATTCAGTGGGCTGCTCTTCTGTGAAGAAGCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGTGCAAGGAGAGCGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGTGCAAGGAGAGCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAAGCAAGAGCACTCTGCTATGAAGACATCAGAGCAAG 180

DB 121 AGCAAGTGGGCACTTCTGGAAGCAAGAGCACTCTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGTGCAAGGAGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGCTTGTGAGACCAGACGACTCTGCTATGAAGACCTCAGCAACAAAGATGGCGAG 300
DB 241 GGGCGCTTGTGAGACCAGACGACTCTGCTATGAAGACCTCAGCAACAAAGATGGCGAG 300
QY 301 TGGTGTGCTGACGCTTCCCTGTGCAAGGAGAGCGCAAGGAGTGGCGCTTGG 360
DB 301 TGGTGTGCTGACGCTTCCCTGTGCAAGGAGAGCGCAAGGAGTGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGTCTTCATGAGCCCAAGTACACGTCCGTGGAGAGATCTG 420
DB 361 GGAGACTAGATGACAGTGTCTTCATGAGCCCAAGTACACGTCCGTGGAGAGATCTG 420
QY 421 GACAACTTCAAGAGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAACTTCAAGAGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGGGACATGAGGTGAACAAGAGCAAGCAAAAGAGAGATCTCATGCTCATG 540
DB 481 CTCAGGGGACATGAGGTGAACAAGAGCAAGCAAAAGAGAGATCTCATGCTCATG 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAATAAATCTGCTGAGACAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAATAAATCTGCTGAGACAGATGTCAACTTAAT 600
QY 601 GTCTTTGACAAACAAAAGAGAGACAGCTCTGATTAAGGCGGTACAAATGCCAGAAAGATGA 660
DB 601 GTCTTTGACAAACAAAAGAGAGACAGCTCTGATTAAGGCGGTACAAATGCCAGAAAGATGA 660
QY 661 TGTGGCTTAATGTGTGTGAACATGAGCACTGATCCAAATATTCAGATAGTATGAAT 720
DB 661 TGTGGCTTAATGTGTGTGAACATGAGCACTGATCCAAATATTCAGATAGTATGAAT 720
QY 721 ACCACTGTGCACTAGGCTATCTATATAGTAAGTAATAATTAAGGCCAAACACTGCTCTTA 780
DB 721 ACCACTGTGCACTAGGCTATCTATATAGTAAGTAATAATTAAGGCCAAACACTGCTCTTA 780
QY 781 TATGTGCTGATATGCAATCAAAAAAGAGATGCGCTCACACCACTGTTACTTGTGTGA 840
DB 781 TATGTGCTGATATGCAATCAAAAAAGAGATGCGCTCACACCACTGTTACTTGTGTGA 840
QY 841 CATGAGCAAAAACAGAAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGAAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATATGATGAAAGAGCTGCTCATACTTGTGTAATGTTGTGGATCAGCAATATTA 960
DB 901 CTGGATATGATGAAAGAGCTGCTCATACTTGTGTAATGTTGTGGATCAGCAATATTA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCAAGATCTATCTGGACAGAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCAAGATCTATCTGGACAGAG 1020
QY 1021 GCCAAGAGATAGCTGTTTCTATGATCATCATATTAATTTGGCAGTACTTTCTGATAC 1080
DB 1021 GCCAAGAGATAGCTGTTTCTATGATCATCATATTAATTTGGCAGTACTTTCTGATAC 1080
QY 1081 AAGAGAAAAAGATCTTAATAATCTCTTGTGAAAACAGAAATCCAGAACAGACTTAAG 1140
DB 1081 AAGAGAAAAAGATCTTAATAATCTCTTGTGAAAACAGAAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAAAGAGTCAAAAAGTTCAAAAGCATGAATAATGACGACAGAGAAA 1200
DB 1141 CTGACATCAGAGAAAGAGTCAAAAAGTTCAAAAGCATGAATAATGACGACAGAGAAA 1200
QY 1201 ATGTCTCAAGAAACCGAAATTAATAGATGTGTGATAGAGAGTGAAGAAATGAAG 1260

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Db 1201 ATGTCTCAAGAAACAGAAATAAATAGATGTGTATGAGAGGTGTGAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATATATATGTGGATTACTAGAAAACTGTACTTAATGTGTGACTGTGGC 1320
Db 1261 AAGCATGAAGATATATATGTGGATTACTAGAAAACTGTACTTAATGTGTGACTGTGGC 1320
Qy 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAACCTTGAATAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAACCTTGAATAATCAGCAATTT 1380
Qy 1381 CCTGAAGAGAGAGAGAGAGATTCACAGAAATTTGGAAATTTAGTTCTGTACTTCAGAAAG 1440
Db 1381 CCTGAAGAGAGAGAGAGAGATTCACAGAAATTTGGAAATTTAGTTCTGTACTTCAGAAAG 1440
Qy 1441 AAACAGATGCCAAATTAATCTTCTGAAAAAGCAACCCAGAAACAAAGCTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAAGCAACCCAGAAACAAAGCTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGAGAGAGAGCTTGAAGGAGAGTGAATAATGGCCAGCAGAGCTAGAAAT 1560
Db 1501 TCAGAGAGAGAGAGAGAGAGCTTGAAGGAGAGTGAATAATGGCCAGCAGAGCTAGAAAT 1560
Qy 1561 TTTATGGCTATCGAAGAAATGAAGAGACGAGAAAGTACTATGTGGATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAGACGAGAAAGTACTATGTGGATTTCCAGAAAC 1620
Qy 1621 CTGACTAATAGTGCCTGCTGGCAATGTGATGATGATTAATTCCTCCAGAGAGAGAGC 1680
Db 1621 CTGACTAATAGTGCCTGCTGGCAATGTGATGATGATTAATTCCTCCAGAGAGAGAGC 1680
Qy 1681 AGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 AGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 CAAAAAGATATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 CAAAAAGATATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Qy 1801 ATTCTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 ATTCTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Qy 1861 CTTAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 CTTAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1921 GGCATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GGCATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3
AA167212
ID AA167212 standard; cDNA; 2000 BP.
XX
AC AA167212;
XX
XX 11-FEB-2002 (first entry)
XX
DE B305D isoform C splice variant 2 encoding cDNA.
XX
XX Genetic substructure: DNA microarray analysis; polymerase chain reaction;
XX cancer; B305D; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1971
XX FT /tag= a
```

```
FT /product= "B305D isoform C splice variant"
XX
XX MO200175171-A2.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001; 2001WO-US010631.
XX
XX 03-APR-2000; 2000US-0194241P.
XX
XX 27-JUL-2000; 2000US-0219862P.
XX
XX 18-DEC-2000; 2000US-0256592P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Houghton RI, Dillon DC, Molesch DA, Xu J, Zehentner B, Persing DH;
XX
XX WPI; 2001-626449/72.
XX
XX P-PSDB; AAG65977.
XX
XX Identifying tissue (tumor)-specific polynucleotides overexpressed in
XX
XX tissue of interest, as compared to control tissue, for detecting cancer
XX
XX polymerase chain reaction.
XX
XX Claim 4; Page 94; 127p; English.
XX
XX The invention relates to identifying tissue-specific polynucleotides (P)
XX
XX that involves performing a genetic substructure to identify pool of (P)
XX
XX from tissue of interest (TI), performing DNA microarray analysis to
XX
XX identify first subset of polynucleotides (Sp1) at least 2-fold over
XX
XX expressed in TI, and performing quantitative polymerase chain reaction
XX
XX (PCR) analysis on Sp1 to identify second subset of (P). The method is
XX
XX useful for determining the presence or absence of a cancer cell in a
XX
XX patient, monitoring the progression of cancer in a patient using a
XX
XX biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
XX
XX urine or a tumor biopsy sample. The methods are useful for determining
XX
XX the presence or absence of or monitoring progression of prostate, breast,
XX
XX colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
XX
XX gastric, kidney, bladder, pancreatic or endometrial cancer. The present
XX
XX sequence represents a cDNA encoding a B305D isoform C splice variant
XX
XX
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX
XX
XX Query Match 100.0%; Score 2000; DB 4; Length 2000;
XX
XX Best Local Similarity 100.0%; Pred. No. 0;
XX
XX Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 ATGTGTTGATGAGATTGATTCATGCGGCTGCTCTTGTGAAGAGCATTTGGTCTC 60
XX
XX 1 ATGTGTTGATGAGATTGATTCATGCGGCTGCTCTTGTGAAGAGCATTTGGTCTC 60
XX
XX 61 AAGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGAGCGGCAAG 120
XX
XX 61 AAGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGAGCGGCAAG 120
XX
XX 61 AAGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGAGCGGCAAG 120
XX
XX 121 AAGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
XX
XX 121 AAGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
XX
XX 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAG 240
XX
XX 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAG 240
XX
XX 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAG 240
XX
XX 241 GGCCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
XX
XX 241 GGCCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
XX
XX 241 GGCCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
XX
XX 301 TGTGTGCTGCACTGCTTCCCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
XX
XX 301 TGTGTGCTGCACTGCTTCCCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
XX
XX 361 GGAGACTAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 420
XX
XX 361 GGAGACTAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 420
```

Db	361	GGAGCTACGATGACAGTGGCTTTCATGAGCCAGGTACACGTCCTCGAGGAAGTCTG	420
OY	421	GACAACTTCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
Db	421	GACAACTTCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
OY	481	CTCAGGGGACACTGAGGTGAACAAGAAAGACAAAGCAAAAGAGACTGCTCTACATTGGCC	540
Db	481	CTCAGGGGACACTGAGGTGAACAAGAAAGACAAAGCAAAAGAGACTGCTCTACATTGGCC	540
OY	541	TCTGCGAATGGGAATTCAGAAAGTAGTAAATCTCCGCTGAGCAGACGATGTCACCTTAAT	600
Db	541	TCTGCGAATGGGAATTCAGAAAGTAGTAAATCTCCGCTGAGCAGACGATGTCACCTTAAT	600
OY	601	GTCTTGAACAACAAAAGAGGACAGCTGTGATAAAGGCGGTACATATGCAAGAAAGATGA	660
Db	601	GTCTTGAACAACAAAAGAGGACAGCTGTGATAAAGGCGGTACATATGCAAGAAAGATGA	660
OY	661	TGTGCGTTAATGTGCTGGGAACATGGCACCTGATCCAAATATTCCAGATAGTAGAAAT	720
Db	661	TGTGCGTTAATGTGCTGGGAACATGGCACCTGATCCAAATATTCCAGATAGTAGAAAT	720
OY	721	ACCACTTGCACCTAGCTATCTATATAGTAAGTAAATTAATGAGCCAAAGCACTGCTCTA	780
Db	721	ACCACTTGCACCTAGCTATCTATATAGTAAGTAAATTAATGAGCCAAAGCACTGCTCTA	780
OY	781	TATGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTTTACTTGGTGA	840
Db	781	TATGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTTTACTTGGTGA	840
OY	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATATGCA	900
OY	901	CTGATATATATGAAAGACAGCTCTCATCTGCTGATATGTTGATATGACCAAGTATA	960
Db	901	CTGATATATATGAAAGACAGCTCTCATCTGCTGATATGTTGATATGACCAAGTATA	960
OY	961	GTCAGCCTTCTACTTGAGCAAAAATTTATGATGATCTTCTCAAGATCTTCTGACAGAG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAAATTTATGATGATCTTCTCAAGATCTTCTGACAGAG	1020
OY	1021	GCCAGAGATATGCTGTTCTAGTCATCATATGTAATTTGCGACTTACTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTCTAGTCATCATATGTAATTTGCGACTTACTTCTGACTAC	1080
OY	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAAAGACTTAAG	1140
Db	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAAAGACTTAAG	1140
OY	1141	CTGACATCAGAGGAAGTCAACAAAGTTCAAGCAAGTAAATTAAGCAGCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGTCAACAAAGTTCAAGCAAGTAAATTAAGCAGCAGAGAA	1200
OY	1201	ATGTCCTCAAGAACCAAGAAATTAATTAAGATGGTGTATAGAGGTTGAAGAAATGAAG	1260
Db	1201	ATGTCCTCAAGAACCAAGAAATTAATTAAGATGGTGTATAGAGGTTGAAGAAATGAAG	1260
OY	1261	AAAGCATGAAGTATATATGTTGGGATTACTAGAAAACTGACTAATGTGTCTACCTGGC	1320
Db	1261	AAAGCATGAAGTATATATGTTGGGATTACTAGAAAACTGACTAATGTGTCTACCTGGC	1320
OY	1321	AATGTGTATATGATTAATTCCTCAAAAGAGACACAACTGAAATTAAGCAATTT	1380
Db	1321	AATGTGTATATGATTAATTCCTCAAAAGAGACACAACTGAAATTAAGCAATTT	1380
OY	1381	CCTGCAACGAAGTGAAGAGTATCAGAAATTTGCGAATTAGTTCTGACTACAAAGAA	1440
Db	1381	CCTGCAACGAAGTGAAGAGTATCAGAAATTTGCGAATTAGTTCTGACTACAAAGAA	1440
OY	1441	AAACGATGCCAAATACTCTTCTGAAAACAGCAACCAAGAACAAAGCTTAAAGTCA	1500
Db	1441	AAACGATGCCAAATACTCTTCTGAAAACAGCAACCAAGAACAAAGCTTAAAGTCA	1500

Db	1441	AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGAGTCACAAAGGCTTTGAGGCGCATGTGAAAATGCGCAGCAGACTTGAAAAAT	1560
Db	1501	TCAGAGGAAGAGTCACAAAGGCTTTGAGGCGCATGTGAAAATGCGCAGCAGACTTGAAAAAT	1560
Qy	1561	TTTATGTGCTATCCGAAGAAATGGAAGAACACGGAAAGTACTCATGTGCGGAATTTCCCGAAGAAC	1620
Db	1561	TTTATGTGCTATCCGAAGAAATGGAAGAACACGGAAAGTACTCATGTGCGGAATTTCCCGAAGAAC	1620
Qy	1621	CTGACTATGATGGTGCACCTGCTGGCAATGTGATGATGATTAATTTCTCCAGAAGAGAC	1680
Db	1621	CTGACTATGATGGTGCACCTGCTGGCAATGTGATGATGATTAATTTCTCCAGAAGAGAC	1680
Qy	1681	AGAACACCTGGAAGCCAGCAATTTCTTGACACTGGAATGAGAGTATCAACGTGACGAA	1740
Db	1681	AGAACACCTGGAAGCCAGCAATTTCTTGACACTGGAATGAGAGTATCAACGTGACGAA	1740
Qy	1741	CAAAATGATACTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATATTTACACGATGAG	1800
Db	1741	CAAAATGATACTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATATTTACACGATGAG	1800
Qy	1801	ATTCTGATTCATGAGAAAAGCAGATGAGTGAAGTGTGTAAGAAAATGAATTCGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAGAAAAGCAGATGAGTGAAGTGTGTAAGAAAATGAATTCGAGCTTCT	1860
Qy	1861	CTTAGTGTGTAAGAAAAGAACATCTTTCGATGAAAATATGATCGTTGCGGGAAGAAAT	1920
Db	1861	CTTAGTGTGTAAGAAAAGAACATCTTTCGATGAAAATATGATCGTTGCGGGAAGAAAT	1920
Qy	1921	GCCATGCTAAGACTGGAAGCTTAGACACATGAAACATCAGAGCCAGCTTAAGAAAAA	1980
Db	1921	GCCATGCTAAGACTGGAAGCTTAGACACATGAAACATCAGAGCCAGCTTAAGAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	
RESULT 4			
AA563808			
ID	AA563808	standard; cDNA; 2000 BP.	
XX	AA563808;		
XX			
DT	29-JAN-2002	(first entry)	
XX			
DE	Human prostate cDNA clone B305D splice variant #9.		
XX			
KW	Human; prostate cancer; ss; cytoslatic; immunostimulant; tumour.		
XX			
OS	Homo sapiens.		
XX			
FN	W0200173032-A2.		
XX			
PD	04-OCT-2001.		
XX			
PF	27-MAR-2001; 2001MO-US009919.		
XX			
XX	27-MAR-2000; 2000US-00536857.		
PR	09-MAY-2000; 2000US-00568100.		
PR	12-MAY-2000; 2000US-00570737.		
PR	13-JUN-2000; 2000US-00593793.		
PR	27-JUN-2000; 2000US-00605783.		
PR	09-AUG-2000; 2000US-00636215.		
PR	29-AUG-2000; 2000US-00651236.		
PR	06-SEP-2000; 2000US-00657279.		
PR	02-OCT-2000; 2000US-00679426.		
PR	10-OCT-2000; 2000US-00685166.		
PR	09-NOV-2000; 2000US-00709729.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			

PI Xu J, Dillon DC, Mutcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX
XX WPI: 2001-639232/73.
XX P-PDB: AA069778.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
PS Claim 1; Page 349-350; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polynucleotide of the invention
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGATTGAGGTGATTCATGCGCGCTCTCTTGTGGAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGATTGAGGTGATTCATGCGCGCTCTCTTGTGGAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTGTGGAAGCAGACGACTGTGTAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTGTGGAAGCAGACGACTGTGTAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
QY 241 GGGGCTTCTGAGACACAGACGACTGTGATGAACACTCAGAAAGATGGGCAAG 300
DB 241 GGGGCTTCTGAGACACAGACGACTGTGATGAACACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTCGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
DB 301 TGGTGTCGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
QY 361 GGAAGCTAGATGACAGTGTCTTATGAGCCAGGTACACGCTCCGTGGAAGATCTG 420
DB 361 GGAAGCTAGATGACAGTGTCTTATGAGCCAGGTACACGCTCCGTGGAAGATCTG 420
QY 421 GACAACTCCACAGACCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAACTCCACAGACCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAAAGAGATCTCTTACATCTGGCC 540
DB 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAAAGAGATCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGTCAGACGATGTCATTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGTCAGACGATGTCATTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTTGATTAAGGCGGTACAAATGCCAGGAAGATGA 660
DB 601 GTCTTGAACAACAAAAGAGACAGCTTGATTAAGGCGGTACAAATGCCAGGAAGATGA 660

DB 601 GTCTTGAACAACAAAAGAGACAGCTTGATTAAGGCGGTACAAATGCCAGGAAGATGA 660
QY 661 TGTGGTTAAATGTGTGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGGTTAAATGTGTGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTAGCTATCTATAAGATTAATTAATGAGCCAAAGACCTGCTTA 780
DB 721 ACCACTGTGCACTAGCTATCTATAAGATTAATTAATGAGCCAAAGACCTGCTTA 780
QY 781 TATGTGCTGATATGATCAAAAAACAAGCATGCGCTCACACCACTGTTACTGGTGA 840
DB 781 TATGTGCTGATATGATCAAAAAACAAGCATGCGCTCACACCACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAACAGAAAGTGTGAATTTTAACTCAAGAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAACAGAAAGTGTGAATTTTAACTCAAGAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATATGAAAGACCTGCTCATACTTGTGCTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAAAGACCTGCTCATACTTGTGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTCTATGATCATCATGTAATTTGCGAGTACTTCTGATC 1080
DB 1021 GCCAGAGATATGCTGTTCTATGATCATCATGTAATTTGCGAGTACTTCTGATC 1080
QY 1081 AAGAAAAACAGATCTAAATAATCTTCTGAAAAACAGCAATCCAGAACAAAGCTTAAAG 1140
DB 1081 AAGAAAAACAGATCTAAATAATCTTCTGAAAAACAGCAATCCAGAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGATCACAAGGTTCAAGGCAAGTAAATGCCAGCGAGAA 1200
DB 1141 CTGACATCAGAGAAAGATCACAAGGTTCAAGGCAAGTAAATGCCAGCGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGTGGAATTAATGGAATACTGAAAACTGACTTAATGTGTCTGAC 1320
DB 1261 AAGCATGAAGATTAATGTGGAATTAATGGAATACTGAAAACTGACTTAATGTGTCTGAC 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAAAGACAAACCTGAAAAATGACAAATTT 1380
DB 1321 AATGTGATTAATGATTAATTCCTCAAGAGAAAGACAAACCTGAAAAATGACAAATTT 1380
QY 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGGAATTTGTTCTGACTTCAAGAA 1440
DB 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGGAATTTGTTCTGACTTCAAGAA 1440
QY 1441 AAAAGATGCAAAATATCTCTTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCAAAATATCTCTTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
QY 1501 TCAAGAGAAAGATCACAAGGCTTGAAGGCAAGTAAATGCGCAGCAGAGCTGAAAT 1560
DB 1501 TCAAGAGAAAGATCACAAGGCTTGAAGGCAAGTAAATGCGCAGCAGAGCTGAAAT 1560
QY 1561 TTTATGCTATGAGAAATTAAGAAAGCAGGAAGTACATGAGTGGATTTCCAGAAAC 1620
DB 1561 TTTATGCTATGAGAAATTAAGAAAGCAGGAAGTACATGAGTGGATTTCCAGAAAC 1620
QY 1621 CTGACTTAATGTGCACTGCTGCAATGTGATGATGATTAATTTCTTCAAGAAAGAC 1680
DB 1621 CTGACTTAATGTGCACTGCTGCAATGTGATGATGATTAATTTCTTCAAGAAAGAC 1680
QY 1681 AGAACACTGAAGCCAGCAATTTCTTGACACTGAAATGAAGATATCACAGTACGA 1740
DB 1681 AGAACACTGAAGCCAGCAATTTCTTGACACTGAAATGAAGATATCACAGTACGA 1740

Qy	1741	CAAAATGATCTCCGAGAACATTTTGTGTAAGAACAAGAACTGGAATTTACAGATGAG	1800
Db	1741	CAAAATGATCTCCGAGAACATTTTGTGTAAGAACAAGAACTGGAATTTACAGATGAG	1800
Qy	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGTGTGAAAAATGAATTCAGACTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGTGTGAAAAATGAATTCAGACTTCT	1860
Qy	1861	CTTGATGTTAAGAAAGAAAGACATCTTTCATGAAAATATAGCTTCCGGGAAAGAAAT	1920
Db	1861	CTTGATGTTAAGAAAGAAAGACATCTTTCATGAAAATATAGCTTCCGGGAAAGAAAT	1920
Qy	1921	GCATGCTAGACCTGAGACTAGACAAATGAAAACATCTAGAGCCAGCTTAAAAA	1980
Db	1921	GCATGCTAGACCTGAGACTAGACAAATGAAAACATCTAGAGCCAGCTTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	

RESULT 5
AAH02780
ID AAH02780 standard; cDNA; 2000 BP.

DT 14-JUN-2001 (first entry)

DE Prostate tumour antigen determined cDNA splice variant of B305D #9.

KW Human, prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.

OS Homo sapiens.

PN WO200125272-A2.

PD 12-APR-2001.

PF 04-OCT-2000; 2000WO-US027464.

PR 04-OCT-1999; 99US-0157455P.

PA (CORI-) CORIXA CORP.

PI Xu J, Skeiky YAW, Reed SG, Cheever MA;

DR WPI; 2001-245062/25.

XX

PT treatment and dia

PS Claim 50; Page 232; 276pp; English.

CC The present invention describes an isolated polypeptide (I) comprising at
CC least an immunogenic portion of a prostate tumour antigen protein or its
CC variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a polynucleotide
CC that encodes a prostate specific protein are useful for detecting the
CC presence or absence of a cancer or monitoring the progression the
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
CC exemplification of the present invention

SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2000;	DB 4;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ATGAGGTGATGAGGTGATGATTCATGACGGGCGTCCCTCTCTGTGAAGAACATTTGGTCTC	60
Db	1	ATGGTGGTGAAGGTGATTCATGATCCGGCTGACCCTCTCTGTGAAGAACATTTGGTCTC	60
QY	61	AGAGCAAGATATGGGCAAGTGGTGTGCTGCTTCTCCCTGTGCAAGGAGAGCCGCAAG	120
Db	61	AGAGCAAGATATGGGCAAGTGGTGTGCTGCTTCTCCCTGTGCAAGGAGAGCCGCAAG	120
QY	121	AGCAAGCTGGGCACTTCTGGAGACACAGAGACTCTGTATGAAGACATCTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGGAGACACAGAGACTCTGTATGAAGACATCTCAGAGCAAG	180
QY	181	ATGGGCAAGTGGTGTGCTGCTTCCCTGTGCAAGGGGAGTGGCAAGCAAGCATG	240
Db	181	ATGGGCAAGTGGTGTGCTGCTTCCCTGTGCAAGGGGAGTGGCAAGCAAGCATG	240
QY	241	GGCGCTTCTGGAGACACAGACTCTGTATGAAGACACTCAGAGAACAGATGGGCAAG	300
Db	241	GGCGCTTCTGGAGACACAGACTCTGTATGAAGACACTCAGAGAACAGATGGGCAAG	300
QY	301	TGGTGTGCTGCCACTGCTTCCCTGTGTGAGGGGGAGCCGCAAGACAGTGTGGGCTTGG	360
Db	301	TGGTGTGCTGCCACTGCTTCCCTGTGTGAGGGGGAGCCGCAAGACAGTGTGGGCTTGG	360
QY	361	GGAGACTACGATGACATGTGCTTCACTGAGAGCCGAGTACACAGTCCGTGGAGAAATCTG	420
Db	361	GGAGACTACGATGACATGTGCTTCACTGAGAGCCGAGTACACAGTCCGTGGAGAAATCTG	420
QY	421	GACAAAGCTCCACAGAGCTGCTGTGGGGGTAAAGTCCCAAGAAAGATCTTATCTGATG	480
Db	421	GACAAAGCTCCACAGAGCTGCTGTGGGGGTAAAGTCCCAAGAAAGATCTTATCTGATG	480
QY	481	CTCAGGGGACACTGACGTGAACAAGAAAGCAAGCAAAAGAGGACTGCTTACATCTGGCC	540
Db	481	CTCAGGGGACACTGACGTGAACAAGAAAGCAAGCAAAAGAGGACTGCTTACATCTGGCC	540
QY	541	TCTGCAATGGGAATTCAGAAAGTATGAAAACTCCGTGTGACACAGCAGTGTCACTTAAAT	600
Db	541	TCTGCAATGGGAATTCAGAAAGTATGAAAACTCCGTGTGACACAGCAGTGTCACTTAAAT	600
QY	601	GTCTTGAACAACAAAAAGAGACAGCTCTGTATTAAGGCCGTGACATGCCAGAAAGATGAA	660
Db	601	GTCTTGAACAACAAAAAGAGACAGCTCTGTATTAAGGCCGTGACATGCCAGAAAGATGAA	660
QY	661	TGTGCGTTAATGTGTGCGGAACATGGACATGATCCAAATTTCCAGATGAGTATGAAAT	720
Db	661	TGTGCGTTAATGTGTGCGGAACATGACATGATCCAAATTTCCAGATGAGTATGAAAT	720
QY	721	ACCACTGTGACATACGCTATCTATATGAAGATTAATTAATGACCAAGCATGCTCTTA	780
Db	721	ACCACTGTGACATACGCTATCTATATGAAGATTAATTAATGACCAAGCATGCTCTTA	780
QY	781	TATGTGTCTGATATTCGAATCAAAAAACAAGCATGGCCCTCACACACATGTTATCTTGATGA	840
Db	781	TATGTGTCTGATATTCGAATCAAAAAACAAGCATGGCCCTCACACACATGTTATCTTGATGA	840
QY	841	CATAGAGAAAAACAGCAAGTCTGTAAATTTTAAATCAAGAAAAAGGAATTTAAATGCA	900
Db	841	CATAGAGAAAAACAGCAAGTCTGTAAATTTTAAATCAAGAAAAAGGAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGGACTGCTCTCATACTTGTGATGTGTGATCAAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGGACTGCTCTCATACTTGTGATGTGTGATCAAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACACAGC	1020
Db	961	GTCAGCCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACACAGC	1020
QY	1021	GCCAGAGATATGCTGTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGATAC	1080

Db 301 TGGTGTGCGCATGCTTCCCTCTGCGAGGGGAGCGGCAAGAGCGAGGCGGCTTGG 360
Qy 361 GGAGATTAAGATACAGTGTCTTCAATGAGCCAGGATCCAGCTCCGTGAGAAATCTG 420
Db 361 GGAGATTAAGATACAGTGTCTTCAATGAGCCAGGATCCAGCTCCGTGAGAAATCTG 420
Qy 421 GACAACTCCACAGAGCTGCTGTGGGGGTAAAGTCCCGAGAAAGATCTACGTCAG 480
Db 421 GACAACTCCACAGAGCTGCTGTGGGGGTAAAGTCCCGAGAAAGATCTACGTCAG 480
Qy 481 CTCAGGAGACCTGACGCTGAAACAAGAAAGACAAAGAGAGAGCTCTCAATCTGGC 540
Db 481 CTCAGGAGACCTGACGCTGAAACAAGAAAGAGAGAGAGCTCTCTCAATCTGGC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGAACAGAGATGTCATTAA 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGAACAGAGATGTCATTAA 600
Qy 601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGA 660
Db 601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGACATACCTCTATCTAATGAAGATAAATTAAGCCAAAGCATGCTCTTA 780
Db 721 ACCACTCTGACATACCTCTATCTAATGAAGATAAATTAAGCCAAAGCATGCTCTTA 780
Qy 781 TATGCGTGAATTCGAATCAAAAACAGCATGCGCTCACACCTGTTACTTGGTGA 840
Db 781 TATGCGTGAATTCGAATCAAAAACAGCATGCGCTCACACCTGTTACTTGGTGA 840
Qy 841 CATGACAAAAACAGCAAGCTGTAATTTTATCAAGAAAAACGAATTTAAATGA 900
Db 841 CATGACAAAAACAGCAAGCTGTAATTTTATCAAGAAAAACGAATTTAAATGA 900
Qy 901 CTGGATGATATGGAAGAGCTGCTCATACCTGCTGATATGTTGGATCAGCAATATA 960
Db 901 CTGGATGATATGGAAGAGCTGCTCATACCTGCTGATATGTTGGATCAGCAATATA 960
Qy 961 GTCAAGCTTCTACTTGAAGAAAAATTTGATGATCTTCTCAAGATCTTATCTGACGAG 1020
Db 961 GTCAAGCTTCTACTTGAAGAAAAATTTGATGATCTTCTCAAGATCTTATCTGACGAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCAAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCAAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAATCTCTTGAAGAACAGCAATCCAGAACAGATTAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAATCTCTTGAAGAACAGCAATCCAGAACAGATTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAAGGAGTGAATTTGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAAGGAGTGAATTTGCCAGCCAGAGAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAAGATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAAGATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGTTGAGATTAAGAAACCTGATCTAATGCTGCTGAC 1320
Db 1261 AAGCATGAAGATTAATATGTTGAGATTAAGAAACCTGATCTAATGCTGCTGAC 1320
Qy 1321 AATGATGAATTAATTAATTTCTCAAGAGAGAGAGAACCTGAAATCAGCAATTT 1380
Db 1321 AATGATGAATTAATTAATTTCTCAAGAGAGAGAGAACCTGAAATCAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTATCAGAAATTTGGAATTTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTATCAGAAATTTGGAATTTAGTTCTGACTACAAAGAA 1440

Db 1381 CCTGACAAAGAAAGTATCAGAAATTTGGAATTTAGTTCTGACTACAAAGAA 1440
Qy 1441 AAAAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAACAGATTTAAAGTGA 1500
Db 1441 AAAAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAACAGATTTAAAGTGA 1500
Qy 1501 TCAGAGAAAGATGCAAAAGGCTTGAAGGAGGAGTGAATAAGGCGAGCAGAGTGA 1560
Db 1501 TCAGAGAAAGATGCAAAAGGCTTGAAGGAGGAGTGAATAAGGCGAGCAGAGTGA 1560
Qy 1561 TTTATGCTATCGAAGAAATTAAGAAAGACAGAAAGTACTCATGTGGAATTCAGAA 1620
Db 1561 TTTATGCTATCGAAGAAATTAAGAAAGACAGAAAGTACTCATGTGGAATTCAGAA 1620
Qy 1621 CTGACTAATGTGCGCATGCTGCGCAATGGTATGATGATTAATTTCTCAAGAA 1680
Db 1621 CTGACTAATGTGCGCATGCTGCGCAATGGTATGATGATTAATTTCTCAAGAA 1680
Qy 1681 AGAACACCTGAAGAGAGCAATTTCTGCACTGAGAAATGAAGATATCAGATGAG 1740
Db 1681 AGAACACCTGAAGAGAGCAATTTCTGCACTGAGAAATGAAGATATCAGATGAG 1740
Qy 1741 CAAAAATGATCTCAGAAAGATTTTGTGAAGAACAGAACTGGAATTTACAGATGAG 1800
Db 1741 CAAAAATGATCTCAGAAAGATTTTGTGAAGAACAGAACTGGAATTTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAGAGATGAGATGGTTGAAAAATGAATTTCTGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGAGATGAGATGGTTGAAAAATGAATTTCTGAGCTTCT 1860
Qy 1861 CTTAGTTGTAAGAAAGAAAGAAACATCTTGCATGAAAAATGATGCTGGGAGAA 1920
Db 1861 CTTAGTTGTAAGAAAGAAAGAAACATCTTGCATGAAAAATGATGCTGGGAGAA 1920
Qy 1921 GCCATGCTAAGCTGAGAGCTAGACAAATGAACATCAGAGCAGCTAATTAATTA 1980
Db 1921 GCCATGCTAAGCTGAGAGCTAGACAAATGAACATCAGAGCAGCTAATTAATTA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 7
ID ACAS9616
ID ACAS9616 standard; cDNA; 2000 BP.
XX
AC ACAS9616;
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #359.
XX
KW Prostate cancer; vaccine; gene therapy; cytosolic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSM; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUC/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
 DR MPI; 2001-245062/25.
 XX P-PSDB; ABU71669.
 PT
 PT Prostate specific protein and its encoding polymucleotide, useful for the
 treatment and diagnosis of prostate cancer.
 XX
 PS Example 11; SEQ ID NO 374; 85bp; English.
 XX
 CC The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 35 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This sequence represents a prostate cancer
 CC therapy associated cDNA. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docid=US20020192763
 CC
 XX
 SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2000; DB 5; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGTGTTGAGGTGATTCATGCGGCTGCTCTTTGTGTAAGAACCATTTGCTTC 60
 DB 1 ATGTGTGTTGAGGTGATTCATGCGGCTGCTCTTTGTGTAAGAACCATTTGCTTC 60
 QY 61 AGAAGCAAGATGGGCAAGTGTGCTGCTTCCCTGTGCAAGGAGAGACGGCAG 120
 DB 61 AGAAGCAAGATGGGCAAGTGTGCTGCTTCCCTGTGCAAGGAGAGACGGCAG 120
 QY 121 AGCAACGTGGGCACTTTGAGACACAGCACTCTGTATGAAGACACTCAGAGCAAG 180
 DB 121 AGCAACGTGGGCACTTTGAGACACAGCACTCTGTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTGCAAGGAGAGTGGCAAGCAACGTG 240
 DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTGCAAGGAGAGTGGCAAGCAACGTG 240
 QY 241 GGGGCTTTGGAGACCAAGCACTGTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
 DB 241 GGGGCTTTGGAGACCAAGCACTGTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300

QY 301 TGGTCTGGCACTGCTTCCCTGTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
 DB 301 TGGTCTGGCACTGCTTCCCTGTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
 QY 361 GGAAGCTAGATGACAGTGCCTTCAATGAGGCCAGGTACACGTCCTGTGGAAGATCTTG 420
 DB 361 GGAAGCTAGATGACAGTGCCTTCAATGAGGCCAGGTACACGTCCTGTGGAAGATCTTG 420
 QY 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTACGTCAG 480
 DB 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTACGTCAG 480
 QY 481 CTCAGGACACTGACGTGAACAAGAGACCAAGCAAAAGAGACTGCTTACATCTGGCC 540
 DB 481 CTCAGGACACTGACGTGAACAAGAGACCAAGCAAAAGAGACTGCTTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTGCAAGTATGTAATACTCTGCTGTCGACAGACGATGTCACTTAAT 600
 DB 541 TCTGCCAATGGGAATTGCAAGTATGTAATACTCTGCTGTCGACAGACGATGTCACTTAAT 600
 QY 601 GTCCCTGCAACAAGAAAGAGACAGCTCTGATTAAGCCGTCACATGCCAGGAAGTGA 660
 DB 601 GTCCCTGCAACAAGAAAGAGACAGCTCTGATTAAGCCGTCACATGCCAGGAAGTGA 660
 QY 661 TGTGCGTTAATGTTGCTGGAAACATGACCTGATCCAAATATTCAGATAGTATGGAAAT 720
 DB 661 TGTGCGTTAATGTTGCTGGAAACATGACCTGATCCAAATATTCAGATAGTATGGAAAT 720
 QY 721 ACCACTCTGACCTACGCTATCTATATGAAGATTAATTAAGCCCAAGACATGCTCTTA 780
 DB 721 ACCACTCTGACCTACGCTATCTATATGAAGATTAATTAAGCCCAAGACATGCTCTTA 780
 QY 781 TATGTGTCGATATGGAATCAAAAACAAAGCATGCGCTCAACCATGTTACTTGGTGA 840
 DB 781 TATGTGTCGATATGGAATCAAAAACAAAGCATGCGCTCAACCATGTTACTTGGTGA 840
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 DB 841 CATGACCAAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAAGCGAATTTAATGCA 900
 QY 901 CTGATATGATATGAAGAGCTGCTCATCTTCTGTATGTTGTGGATCAGCAAGTATA 960
 DB 901 CTGATATGATATGAAGAGCTGCTCATCTTCTGTATGTTGTGGATCAGCAAGTATA 960
 QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCCAGATCTATCTGACAGAG 1020
 DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCCAGATCTATCTGACAGAG 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
 DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
 QY 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACTTAAAG 1140
 DB 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACTTAAAG 1140
 QY 1141 CTGACATCAGAGAAAGTCAAAAAGCTTCAAAAGCATGGAATAATGCCAGCAAGAAA 1200
 DB 1141 CTGACATCAGAGAAAGTCAAAAAGCTTCAAAAGCATGGAATAATGCCAGCAAGAAA 1200
 QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
 DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAATATATGAGGAATTAATGAGAACTGTAATATGATGCTGCTGAC 1320
 DB 1261 AAGCATGAAAGTAATATATGAGGAATTAATGAGAACTGTAATATGATGCTGCTGAC 1320
 QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAAAGAGCAACCTGCAAAATCAGCAATTT 1380
 DB 1321 AATGTGATATATGATTAATTTCTCAAGAGAAAGAGCAACCTGCAAAATCAGCAATTT 1380
 QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440

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Db 1381 CCGACACACGAAAGTGAAGATATCAAGATTTTGGCAATTAAGTTTGTGCTACAAAGAA 1440
Qy 1441 AAACAGATGCCAAATACTCTTCTGAAACAGCAACCAGAACAGACTTAAGCTTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTTCTGAAACAGCAACCAGAACAGACTTAAGCTTGACA 1500
Qy 1501 TCAGAGGAAGATCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCGAGCTTGAAAT 1560
Db 1501 TCAGAGGAAGATCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCGAGCTTGAAAT 1560
Qy 1561 TTTATGGCTATCGAAGAAATGAAGACAGCAAGTATCTCATGTCGGAATCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGACAGCAAGTATCTCATGTCGGAATCCAGAAAC 1620
Qy 1621 CTGACTAATGATGCGCACTGCTGGCAATGTGATGATGATTAATCTCCAGAGAGAGC 1680
Db 1621 CTGACTAATGATGCGCACTGCTGGCAATGTGATGATGATTAATCTCCAGAGAGAGC 1680
Qy 1681 AGAACAACCTGAAGCCGCAATTTCTGACACTGAGAAATGAAGATTCACAGTGACGA 1740
Db 1681 AGAACAACCTGAAGCCGCAATTTCTGACACTGAGAAATGAAGATTCACAGTGACGA 1740
Qy 1741 CAAAATGATCTACGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
Db 1741 CAAAATGATCTACGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAGCAAGATGAAGTGGTTGAAATAATGAATTCGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGCAAGATGAAGTGGTTGAAATAATGAATTCGAGCTTCT 1860
Qy 1861 CTTAGTTGTAGAAAGAAAGACATTTGCTGAGAAATGTACGTTGCCGAAAGAAAT 1920
Db 1861 CTTAGTTGTAGAAAGAAAGACATTTGCTGAGAAATGTACGTTGCCGAAAGAAAT 1920
Qy 1921 GCCATGCTAGACTGAGGCTGAGACACAAATGAAATCATGAGCCAGCTTAAGAAAAA 1980
Db 1921 GCCATGCTAGACTGAGGCTGAGACACAAATGAAATCATGAGCCAGCTTAAGAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
ABL95179
ID ABL95179 standard; cDNA; 2000 BP.
AC ABL95179;
XX
XX 19-JUL-2002 (first entry)
DT
XX
XX Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
XX Human; Cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-00759143.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 10-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
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PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
XX (XUJ/) XU J.
XX (DIL/) DILON D C.
XX (MIT/) MITCHAM J L.
XX (HAR/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer.
XX
XX Claim 1; SEQ ID NO 374; 87bp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX CC their encoded proteins. These can be used in the diagnosis and treatment
XX CC of cancers, particularly prostate cancer. The present sequence is a cDNA
XX CC described in the invention
XX
XX SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2000; DB 6; Length 2000;
XX Best Local Similarity 100.0%; Pred No. 0;
XX Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
Db 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
Qy 61 AGAGCAAGATGGGCAAGTGGTCTGCGGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTCTGCGGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Qy 241 GGGGCTTCTGAGACCAACGACACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300
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Db      241 GGGGCTTTGGAGACCAAGGAGCACTCTGCTATGAAGCACTCAGAAACAAGATGGGCAAG 300
Qy      301 TGGTGTGCGCACTGCTTCCCTCTGTCAGGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
Db      301 TGGTGTGCGCACTGCTTCCCTCTGTCAGGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
Qy      361 GGAGACTAGTAGAGTGGCTTCATGAGGCCAGGATCCAGCTCCGTGGAGAAAGATCTG 420
Db      361 GGAGACTAGTAGAGTGGCTTCATGAGGCCAGGATCCAGCTCCGTGGAGAAAGATCTG 420
Qy      421 GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTAG 480
Db      421 GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTAG 480
Qy      481 CTCAGGGACCTACGCTGAAACAAGAAAGACACAAAGAAAGAGCTGCTTACATCTGGCC 540
Db      481 CTCAGGGACCTACGCTGAAACAAGAAAGACACAAAGAAAGAGCTGCTTACATCTGGCC 540
Qy      541 TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGAGCAGACGATGCACTTAAT 600
Db      541 TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGAGCAGACGATGCACTTAAT 600
Qy      601 GTCTTGAACAACAAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGAAAGATGA 660
Db      601 GTCTTGAACAACAAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGAAAGATGA 660
Qy      661 TGTGCGTTAATGTTGCTGGAACATGCGCATGATCCAAATTTCCATGATAGTATGGAAT 720
Db      661 TGTGCGTTAATGTTGCTGGAACATGCGCATGATCCAAATTTCCATGATAGTATGGAAT 720
Qy      721 ACCACTGTGCACTACGCTATCTATTAATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
Db      721 ACCACTGTGCACTACGCTATCTATTAATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
Qy      781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCAACACACTGTTACTTGTGTGA 840
Db      781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCAACACACTGTTACTTGTGTGA 840
Qy      841 CATGACCAAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAAGCAATTTAAATGCA 900
Db      841 CATGACCAAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAAGCAATTTAAATGCA 900
Qy      901 CTGGATAGATATGGAAGGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGTATA 960
Db      901 CTGGATAGATATGGAAGGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGTATA 960
Qy      961 GTGAGCTTCTACTTGAAGCAAAATATTGATGTAATCTTCTCAAGATCTATCTGAGACAG 1020
Db      961 GTGAGCTTCTACTTGAAGCAAAATATTGATGTAATCTTCTCAAGATCTATCTGAGACAG 1020
Qy      1021 GCCAGAGAGTATGCTGTTTCTACTCATCATCATATGTTTGGCAAGTAACTTTCTGACTAC 1080
Db      1021 GCCAGAGAGTATGCTGTTTCTACTCATCATCATATGTTTGGCAAGTAACTTTCTGACTAC 1080
Qy      1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAAACAGCAATCAGAAACAAGACTTAAG 1140
Db      1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAAACAGCAATCAGAAACAAGACTTAAG 1140
Qy      1141 CTGACATCAGAGGAGAGTCAAAAGTTCAAAAGGCAAGTGAATAATAGCCAGCCAGAGAAA 1200
Db      1141 CTGACATCAGAGGAGAGTCAAAAGTTCAAAAGGCAAGTGAATAATAGCCAGCCAGAGAAA 1200
Qy      1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTTGATGAGAGGTTGAAGAAAGAAAG 1260
Db      1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTTGATGAGAGGTTGAAGAAAGAAAG 1260
Qy      1261 AAGCATGAAGATATAATGTTGAGTTACTAGAAAACTGACTATGGTGCATGCTGGC 1320
Db      1261 AAGCATGAAGATATAATGTTGAGTTACTAGAAAACTGACTATGGTGCATGCTGGC 1320
Qy      1321 AATGTGATTAATGATTTAATTTCTCAAGAGAGAGCAAGACACTGAAAAATCAGCAATTT 1380

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Db      1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAACACTGTAATTCAGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAAATTGATTCTGACTACAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAAATTGATTCTGACTACAAAGAA 1440
Qy      1441 AAAAGATGCAAAATATCTCTTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
Db      1441 AAAAGATGCAAAATATCTCTTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGAGTCAAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCAGAGCTAGAAAT 1560
Db      1501 TCAGAGAAAGAGTCAAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCAGAGCTAGAAAT 1560
Qy      1561 TTTATGGCTATGGAAGAAATGAAGAAAGCAGGAAGTACTCATGTGGATTTCCAGAAAG 1620
Db      1561 TTTATGGCTATGGAAGAAATGAAGAAAGCAGGAAGTACTCATGTGGATTTCCAGAAAG 1620
Qy      1621 CTGACTAATGTGGCCACTGCTGCAATGATGATGATTAATTCCTCAAGAGAAAGAC 1680
Db      1621 CTGACTAATGTGGCCACTGCTGCAATGATGATGATTAATTCCTCAAGAGAAAGAC 1680
Qy      1681 AGAACACTGAAGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCACAGTACGAA 1740
Db      1681 AGAACACTGAAGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCACAGTACGAA 1740
Qy      1741 CAAATGATATCTCAAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
Db      1741 CAAATGATATCTCAAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGTAAGAAATATGAAATCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGTAAGAAATATGAAATCTGAGCTTTCT 1860
Qy      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATAATAGTATGCTGCGGAGAAAGATT 1920
Db      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATAATAGTATGCTGCGGAGAAAGATT 1920
Qy      1921 GCCATGCTTAAGCTGAGAGCTAAGACAAATGAAGCATCAGAGCCAGCTTAAGAAAAA 1980
Db      1921 GCCATGCTTAAGCTGAGAGCTAAGACAAATGAAGCATCAGAGCCAGCTTAAGAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 9
AAS9858
ID AAS9858 standard; cDNA; 2000 BP.
XX
AC AAS9858;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11g1 splice variant B11C-8.
XX
KW Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN MO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WC-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00692925.
PR 16-MAR-2001; 2001US-00810936.
XX

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(CORI-) CORIXA CORP.

PA Prudakis TM, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MM,
 PI Mang A, Skeiky YM, Harlocker SL, Day CH;
 XX MPI; 2002-089919/12.
 DR P-PSDB; AAU74378.

XX New breast tumor proteins and polynucleotides encoding them, useful for
 PT treating and/or preventing cancer, particularly breast cancer, and for
 PT eliciting humoral and/or cellular immune response.

XX Claim 1; Page 224; 245pp; English.

XX The invention relates to novel breast tumor polynucleotides and
 CC polypeptides. The polypeptides and polynucleotides are useful in
 CC pharmaceutical compositions for treating and/or preventing cancer,
 CC particularly breast cancer, and for eliciting an immune response,
 CC particularly humoral and/or cellular immune response. The polynucleotides
 CC may be used as probes or primers for nucleic acid hybridization, in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC tumor polypeptides and proteins, and in recombinant DNA molecules to
 CC direct expression of a polypeptide in host cells. AAS9570-AAS9988
 CC represent novel human breast cancer protein coding sequences and PCR
 CC primers of the invention

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 6; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTATTCATGCGCGCTCTTCTGTGAAGACCATTTGGTCTC 60
 Db 1 ATGGTGGTTGAGGTTATTCATGCGCGCTCTTCTGTGAAGACCATTTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGAGGAGAGCGGCAAG 120
 Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGAGGAGAGCGGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGAGACACGACACTCTGTATGAAACACTCAGAGCAAG 180
 Db 121 AGCAAGTGGGCACTTCTGAGACACGACACTCTGTATGAAACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGTGG 240
 Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGTGG 240
 QY 241 GGGCGCTTCTGAGACACGACACTCTGTATGAAACACTCAGAGCAAGTGGCAAG 300
 Db 241 GGGCGCTTCTGAGACACGACACTCTGTATGAAACACTCAGAGCAAGTGGCAAG 300
 QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
 Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
 QY 361 GGAAGACTAGATGACAGTGCCTTCTGATGAGCCCAAGTACCACTCGTGAAGATCTG 420
 Db 361 GGAAGACTAGATGACAGTGCCTTCTGATGAGCCCAAGTACCACTCGTGAAGATCTG 420
 QY 421 GACAAGCTCCACAGAGCTGCTGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAG 480
 Db 421 GACAAGCTCCACAGAGCTGCTGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAG 480
 QY 481 CTCAGGGAACATGACCTGTAACAAGAGCAAGCAAAAGAGACTCTCTACATCTGGCC 540
 Db 481 CTCAGGGAACATGACCTGTAACAAGAGCAAGCAAAAGAGACTCTCTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTCTGAGACAGAGATGTCAACTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTCTGAGACAGAGATGTCAACTTAAT 600
 QY 601 GTCCTTGAACAACAAAAGAGACAGCTCTGATTAAGCGGTACAATGCCAGGAAGTGA 660

Db 601 GTCCTTGAACAACAAAAGAGACAGCTCTGATTAAGCGGTACAATGCCAGGAAGTGA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGAGCACTGATTCGAATATTCAGATGATGAAT 720
 Db 661 TGTGCGTTAATGTTGCTGGAACATGAGCACTGATTCGAATATTCAGATGATGAAT 720
 QY 721 ACCACTGCACTAGCTATCTATTAAGAAATTAATGAGCAACCACTGCTCTTA 780
 Db 721 ACCACTGCACTAGCTATCTATTAAGAAATTAATGAGCAACCACTGCTCTTA 780
 QY 781 TATGTCGTGATATCGAATCAAAAAACAGACATGCGCTCACACCTGTTACTGGTGA 840
 Db 781 TATGTCGTGATATCGAATCAAAAAACAGACATGCGCTCACACCTGTTACTGGTGA 840
 QY 841 CATGACAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGAAATTTAAATGCA 900
 Db 841 CATGACAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGAAATTTAAATGCA 900
 QY 901 CTGATATGATGAAAGACCTGCTCATCTTGTGCTATGTTGTGATCAAGATATA 960
 Db 901 CTGATATGATGAAAGACCTGCTCATCTTGTGCTATGTTGTGATCAAGATATA 960
 QY 961 GTCAGCTTCTACTTGAGCAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
 Db 961 GTCAGCTTCTACTTGAGCAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
 Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
 QY 1081 AAAAGAAAAACAGATGTTAAAAATCTTCTGAAAAACAGAAATCCAGAACTTAAAG 1140
 Db 1081 AAAAGAAAAACAGATGTTAAAAATCTTCTGAAAAACAGAAATCCAGAACTTAAAG 1140
 QY 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGCAGTGAATAATGCGACAGAGAA 1200
 Db 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGCAGTGAATAATGCGACAGAGAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAAGATGATGATGAGAGTTGAAAGAAATGAAG 1260
 Db 1201 ATGTCTCAAGAACAGAAATTAATAAGATGATGATGAGAGTTGAAAGAAATGAAG 1260
 QY 1261 AAGCATGAAGTAAATATGTTGGATTACTGAGAAAACTGACATTAATGCTGCTGCG 1320
 Db 1261 AAGCATGAAGTAAATATGTTGGATTACTGAGAAAACTGACATTAATGCTGCTGCG 1320
 QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGACAGAACTGAAATACAGCAATT 1380
 Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGACAGAACTGAAATACAGCAATT 1380
 QY 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTTACAAAGAA 1440
 Db 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTTACAAAGAA 1440
 QY 1441 AAACAGATGCCAAAATTAATCTTCTGAAAAACAGAAACCCAGAACTTAAAGCTGACA 1500
 Db 1441 AAACAGATGCCAAAATTAATCTTCTGAAAAACAGAAACCCAGAACTTAAAGCTGACA 1500
 QY 1501 TCAAGGAAGATCAAAAGGCTTGAAGGCAATGAAAAAGGCAAGCTAAGAAAT 1560
 Db 1501 TCAAGGAAGATCAAAAGGCTTGAAGGCAATGAAAAAGGCAAGCTAAGAAAT 1560
 QY 1561 TTTATGCTATCGAAGAAATGAAGAGCAGGAATCTCATGTGGAATTCAGAAAGAC 1620
 Db 1561 TTTATGCTATCGAAGAAATGAAGAGCAGGAATCTCATGTGGAATTCAGAAAGAC 1620
 QY 1621 CTGACTAATGTGCACTGCTGCAATGTTGATGATTAATTTCTCAAGAAAGAC 1680
 Db 1621 CTGACTAATGTGCACTGCTGCAATGTTGATGATTAATTTCTCAAGAAAGAC 1680
 QY 1681 AGAACCTGAAAGCAGCAATTTCTGACACTGGAATGAAGATACAGTACGAA 1740

Db 1681 AAGAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCACAGTGAAGAA 1740
Qy 1741 CAAAATGATACACAGCAATTTTGTGAAGAAACAGAACACTGGAATATTACACATGAG 1800
Db 1741 CAAAATGATACACAGCAATTTTGTGAAGAAACAGAACACTGGAATATTACACATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAGAGAGATGAGTGTGAAATTTGAACTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGAGAGATGAGTGTGAAATTTGAACTTCT 1860
Qy 1861 CTTAGTGTGAAGAAAGAGAGATGAGTGTGAAATTTGAACTTCT 1920
Db 1861 CTTAGTGTGAAGAAAGAGAGATGAGTGTGAAATTTGAACTTCT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10

ACC95343
ID ACC95343 standard; cDNA; 2000 BP.

AC 95343;
XX

DT 28-AUG-2003 (first entry)
XX

DE Prostate tumour specific cDNA sequence SEQ ID 374.
XX

KM Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX
KW immune response; prostate cancer; ss.

OS Homo sapiens.
XX

PN WO200289747-A2.
XX

PD 14-NOV-2002.
XX

PF 09-MAY-2002; 2002WO-US014753.
XX

PR 09-MAY-2001; 2001US-00852911.
XX

PR 29-JUN-2001; 2001US-00895814.
XX

PR 10-DEC-2001; 2001US-00012896.
XX

PA (CORI-) CORIXA CORP.
XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX

PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Veddyck TS;
XX

PI Carter D, Li SX, Wang A, Skeiky YAW, Hepier WT, Hurral J;
XX

PI McNeill PD, Houghton RL, Vinals Y De Baesolc, Roy TM, Watanabe Y;
XX

PI Deng T;
XX

DR MPI; 2003-167130/16.
XX

PT New prostate-specific proteins and genes, useful in gene therapy,
XX

PT particularly for stimulating an immune response in a patient, or treating
XX

PT prostate cancer in a patient, as well as for diagnosing prostate cancer
XX

CC in a patient.
XX

PS Example 11; Page 415-416; 691pp; English.
XX

CC The present invention relates to novel prostate-specific proteins (PSP)
XX

CC and their coding sequences. The PSPs and their coding sequences are
XX

CC useful for stimulating an immune response in a patient, or for treating
XX

CC prostate cancer in a patient and for determining, detecting or diagnosing
XX

CC the presence of a cancer in a patient. The present sequence was used to
XX

CC illustrate the invention
XX

CC Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX

Query Match 100.0%; Score 2000; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTGAGGTGATTCATGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGTGTGTGAGGTGATTCATGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AAGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AAGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Qy 121 ACGAAGTGGGCACTTTGGAAGACCAAGCACTCTGATGAAGACATCAGAGCAAG 180
Db 121 ACGAAGTGGGCACTTTGGAAGACCAAGCACTCTGATGAAGACATCAGAGCAAG 180
Qy 181 ATGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 181 ATGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Qy 241 GGGGCTTCTGAGACCAAGCACTCTGATGAAGACATCAGAGCAAGATGGGCAAG 300
Db 241 GGGGCTTCTGAGACCAAGCACTCTGATGAAGACATCAGAGCAAGATGGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Qy 361 GGAAGCACTGATGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
Db 361 GGAAGCACTGATGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
Qy 421 GACCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 421 GACCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Qy 481 CTCAAGGACACTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 CTCAAGGACACTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGCAAGAGATGCTCAATTA 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGCAAGAGATGCTCAATTA 600
Qy 601 GTCTTGAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 601 GTCTTGAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTGA 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTGA 720
Qy 721 ACCACTCTGCACTAGCTATATTAATGAAGTAAATTAATGAGGAGGAGGAGG 780
Db 721 ACCACTCTGCACTAGCTATATTAATGAAGTAAATTAATGAGGAGGAGGAGG 780
Qy 781 TATGTGCTGATATGATATCAAAAAAAGAGATGGCTCAACCATGTTACTGGTGA 840
Db 781 TATGTGCTGATATGATATCAAAAAAAGAGATGGCTCAACCATGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAAGAGATGGTGAATTTTAAATCAAGAAAAAGCAATTTAATGCA 900
Db 841 CATGAGCAAAAAAGAGATGGTGAATTTTAAATCAAGAAAAAGCAATTTAATGCA 900
Qy 901 CTGATGATATGAG 960
Db 901 CTGATGATATGAG 960
Qy 961 GTGAGCTTCTACTTGAAGAAAAATTTGATATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTACTTGAAGAAAAATTTGATATCTTCAAGATCTATCTGACAGAG 1020

QY	1021	GGCACAAGATGATGCGTTTCTAGATCATCATATGAAATTTCCAGATTACTTTTGCATAC	1080
Db	1021	GCACAAGATGATGCGTTTCTAGATCATCATATGAAATTTCCAGATTACTTTTGCATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGATATCCAGAACAGACTTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGATATCCAGAACAGACTTTAAAG	1140
QY	1141	CTGACATCAGAGAAAGATGCACAAAGTTCAAAGGCACTGAAAAATAGCCACAGAGAA	1200
Db	1141	CTGACATCAGAGAAAGATGCACAAAGTTCAAAGGCACTGAAAAATAGCCACAGAGAA	1200
QY	1201	ATGCTTCAAGAACCCAGAAATTAATTAAGATGTGCTATAGAGGCTTGAAGAAATGAAG	1260
Db	1201	ATGCTTCAAGAACCCAGAAATTAATTAAGATGTGCTATAGAGGCTTGAAGAAATGAAG	1260
QY	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAAACCTGAATATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAAACCTGAATATGTGTCACTGTGGC	1320
QY	1321	AATGTGTAAATGATTAATTTCTTCAAGAAAGACAGAACACCTGAAAAATCAACAATTT	1380
Db	1321	AATGTGTAAATGATTAATTTCTTCAAGAAAGACAGAACACCTGAAAAATCAACAATTT	1380
QY	1381	CCTGACAAACGAAAGTGAAGATATCAAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAAGTGAAGATATCAAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACGATGCCAAAATACTCTTTCTGAAAACAGCAACCCAGAACAAAGCTTAAACCTGACA	1500
Db	1441	AAACGATGCCAAAATACTCTTTCTGAAAACAGCAACCCAGAACAAAGCTTAAACCTGACA	1500
QY	1501	TCAGAGAAAGTGCACAAAGGCTTGAAGGCGAGTGAATTTGSCCAGCCAGACTGAAAT	1560
Db	1501	TCAGAGAAAGTGCACAAAGGCTTGAAGGCGAGTGAATTTGSCCAGCCAGACTGAAAT	1560
QY	1561	TTTATGCTATCGAAGAAATGAAAGACGGAAGTACTCATGTTCGATTTCCAGAAAAC	1620
Db	1561	TTTATGCTATCGAAGAAATGAAAGACGGAAGTACTCATGTTCGATTTCCAGAAAAC	1620
QY	1621	CTGACTAATGTGTGCCACTGCTGGCAATGCTGATGATTAATTTCTCCAGAGAAAGC	1680
Db	1621	CTGACTAATGTGTGCCACTGCTGGCAATGCTGATGATTAATTTCTCCAGAGAAAGC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGGAATGAAGAGTATCAACATGAGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGGAATGAAGAGTATCAACATGAGAA	1740
QY	1741	CAAAATGATCTCAGAAACCAATTTTGTGAAGACAGAACACTGGAAATTTACAGATGAG	1800
Db	1741	CAAAATGATCTCAGAAACCAATTTTGTGAAGACAGAACACTGGAAATTTACAGATGAG	1800
QY	1801	ATTCTGATTCATGAAGAAAGACAGATAGAAGTGGTTGAAAAATGAATTTCTGAGCTTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGACAGATAGAAGTGGTTGAAAAATGAATTTCTGAGCTTTCT	1860
QY	1861	CTTAGTGTAAAGAAAGAAAGACACTCTTGATGAAAAATAGTAGTTGCGGGAAGAAAT	1920
Db	1861	CTTAGTGTAAAGAAAGAAAGACACTCTTGATGAAAAATAGTAGTTGCGGGAAGAAAT	1920
QY	1921	GCCATGCTAAGACTGGAAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAAGAAAAA	1980
Db	1921	GCCATGCTAAGACTGGAAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAAGAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

AC ADAl1381;
XX
XX 06-NOV-2003 (first entry)
XX
DE Human breast cancer specific cDNA B1C-8.
XX
XX ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.
XX OS Homo sapiens.
XX PN US2002165371-A1.
XX PD 07-NOV-2002.
XX PF 07-AUG-2001; 2001US-00924400.
XX PR 11-JAN-1996; 96US-00585392.
PR 10-JAN-1997; 97WO-US000485.
PR 09-APR-1997; 97US-00838762.
PR 11-DEC-1997; 97US-00991789.
PR 17-APR-1998; 98US-0062451.
PR 09-APR-1999; 98US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.
PR 24-MAY-2000; 2000US-00577505.
PR 26-JUN-2000; 2000US-00590583.
PR 28-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX (FRUD)/ FRUDAKIS T N.
PA (REED)/ REED S G.
PA (SMIT)/ SMITH J M.
PA (MISH)/ MISHER L E.
PA (DILL)/ DILLON D C.
PA (RETT)/ RETTER M W.
PA (WANG)/ WANG A.
PA (SKEI)/ SKEIKY Y A W.
PA (HARL)/ HARLOCKER S L.
PA (DAYC)/ DAY C H.
PA (LISX)/ LI S X.
PA (DENG)/ DENG T.
XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
PI Wang A, Skelky YAW, Harlocker SL, Day CH, Li SX, Deng T;
DR MPI, 2003-247262/24.
XX P-PsDB; ADAl1384.
XX
PT New breast tumor proteins nucleic acids encoding such proteins, useful in
PT diagnosing, preventing and/or treating diseases such as cancer,
PT particularly breast cancer, and as markers for detecting the presence of
PT a cancer.
XX
PS Claim 1; Page 140; 190pp; English.

CC contacting T cells with at least one component selected from (a), (ii)
CC and antigen-presenting cells that express (ii), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (ii), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosis,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a breast cancer specific cDNA of the
CC invention.

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGACCATTTGCTTC 60
DB 1 ATGTGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGACCATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTCCCTGCTGCAAGGAGACGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTCCCTGCTGCAAGGAGACGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACACTGTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTGTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGTG 240
DB 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGTG 240
QY 241 GGGGCTTCTGAGACACAGACACTGTGCTATGAAGACACTCAGAGCAAGGAGTGGCAAG 300
DB 241 GGGGCTTCTGAGACACAGACACTGTGCTATGAAGACACTCAGAGCAAGGAGTGGCAAG 300
QY 301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
DB 301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
QY 361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGGAAGAGATCTG 420
DB 361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGGAAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCGAGAAAGGATCTCATGTCAG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCGAGAAAGGATCTCATGTCAG 480
QY 481 CTCAGAGGACATGACGCTGAAACAAGAGACCAAGCAAAAGAGACTCTCTTCAATCTGGCC 540
DB 481 CTCAGAGGACATGACGCTGAAACAAGAGACCAAGCAAAAGAGACTCTCTTCAATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGCAGACGATGTCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGCAGACGATGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTGTAATAAGCCGTAAAGCCAGAGCAAGATGGA 660
DB 601 GTCTTGAACAACAAAAGAGACAGCTGTAATAAGCCGTAAAGCCAGAGCAAGATGGA 660
QY 661 TGTGCGTTAATGTTGTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGACATACGCTATCTAATAAGATAAATTAATGAGCAAGCACTGCTTCTTA 780
DB 721 ACCACTCTGACATACGCTATCTAATAAGATAAATTAATGAGCAAGCAAGCACTGCTTCTTA 780

QY 781 TATGTGCTGATATGGAATCAAAAAACAAGACATGGCTCACACCACTGTACTGTGTTGA 840
DB 781 TATGTGCTGATATGGAATCAAAAAACAAGACATGGCTCACACCACTGTACTGTGTTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATGAAAGACCTGCTCATCTTGTGTAATGTTGTGATCAGCAAGTAA 960
DB 901 CTGATATGATGAAAGACCTGCTCATCTTGTGTAATGTTGTGATCAGCAAGTAA 960
QY 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
DB 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGCAGTAAATATGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGCAGTAAATATGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGTATAGAGAGTTGAAGAAATGAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGTATAGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAAGTAAATATGTGGATTACTGAAAACTGATTAATGTGTCTACTGTGGC 1320
DB 1261 AAGCATGAAAGTAAATATGTGGATTACTGAAAACTGATTAATGTGTCTACTGTGGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAATACAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAATACAGCAATTT 1380
QY 1381 CCTGCAACGAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTTCAAGAA 1440
DB 1381 CCTGCAACGAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTTCAAGAA 1440
QY 1441 AAAACAGTGCCTAAATATCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
DB 1441 AAAACAGTGCCTAAATATCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATCAAAAAGGCTTGAGGAGTGAAGAAATGGCCAGCAGAGCTAGAAAT 1560
DB 1501 TCAGAGAAAGATCAAAAAGGCTTGAGGAGTGAAGAAATGGCCAGCAGAGCTAGAAAT 1560
QY 1561 TTTATGCTATGGAAGAAATGAAGACACGAAAGTACTCATGTGGAATTTCCAGAAAAAC 1620
DB 1561 TTTATGCTATGGAAGAAATGAAGACACGAAAGTACTCATGTGGAATTTCCAGAAAAAC 1620
QY 1621 CTGACTAATGTTGTCACCTGCTGCAATGTTGATGATTAATTTCTTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTTGTCACCTGCTGCAATGTTGATGATTAATTTCTTCAAGAAAGAC 1680
QY 1681 AGAACAACCTGAAAGCAGCAATTTTCTGCACTGGAAGAAAGAGTATCAGAGTGCAGAA 1740
DB 1681 AGAACAACCTGAAAGCAGCAATTTTCTGCACTGGAAGAAAGAGTATCAGAGTGCAGAA 1740
QY 1741 CAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
DB 1741 CAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGTGTTGAAAAATGAATTTCTGACTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGTGTTGAAAAATGAATTTCTGACTTTCT 1860

QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATAAGTTCGTTGGGGAAGAAAT 1920
DB 1861 CTTAGTGTGTGAAGAAAGAAAGACATCTTGATGAAATAAGTTCGTTGGGGAAGAAAT 1920
QY 1921 GCCATGCTAGAGCTGAGCTAGACACAAATGAAAATCATGAGAGCCAGCTTAAAAA 1980
DB 1921 GCCATGCTAGAGCTGAGCTAGACACAAATGAAAATCATGAGAGCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 12
ADCL5354
ID ADCL5354 standard; DNA; 2000 BP.
XX
AC ADCL5354;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human breast tumour protein DNA, SEQ ID 302.
XX
KM Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KM de.
OS Homo sapiens.
XX
PN MO2003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002MO-US024917.
XX
PR 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
PA (CORI-) CORIXA CORP.
PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
DR MPI; 2003-342398/32.
XX
PT New polynucleotide, useful for preparing a composition for diagnosing,
PT treating or preventing cancer.
XX
PS Example 1; SEQ ID NO 302; 308bp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which stimulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best local Similarity 100.0%; Pred No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGTGGCAAGTGGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120

DB 61 AGGAGCAAGTGGCAAGTGGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTCTGAGACACAGACACTGCTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
DB 241 GGGGCTTCTGAGACACAGACACTGCTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCTGAGGGGAGGGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCTGAGGGGAGGGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGGCTTCAATGAGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
DB 361 GGAAGCTACGATGACAGTGGCTTCAATGAGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAG 480
DB 421 GACAAGCTCCACAGAGCTGCTGCTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAG 480
QY 481 CTCAGGGAACATGACCTGGAACAAGAGCAAGCAAGAGAGTCTCTTACATCTGGCC 540
DB 481 CTCAGGGAACATGACCTGGAACAAGAGCAAGCAAGAGAGTCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAAACTCTGCTGAGACAGAGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAAACTCTGCTGAGACAGAGTCACTTAAT 600
QY 601 GTCCCTTGAACAACAAAAGAGACAGCTGATTAAGCCGTCACAAAGCCAGAAAGTGA 660
DB 601 GTCCCTTGAACAACAAAAGAGACAGCTGATTAAGCCGTCACAAAGCCAGAAAGTGA 660
QY 661 TGTGCTTATGTTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTATGTTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTTGCACCTACGCTATCTAATATGAAGATTAATGAGCCAGACACTGCTTA 780
DB 721 ACCACTTGCACCTACGCTATCTAATATGAAGATTAATGAGCCAGACACTGCTTA 780
QY 781 TATGTCGTGATATGGAATCAAAAACAGCATGGCTCAACACTGTTACTTGGTGA 840
DB 781 TATGTCGTGATATGGAATCAAAAACAGCATGGCTCAACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATATGAAGAAAGCGAATTTAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATATGAAGAAAGCGAATTTAATGCA 900
QY 901 CTGATATGATGAGAAAGACTGCTCATATCTGCTATGTTGGTGGATCAGCAATAT 960
DB 901 CTGATATGATGAGAAAGACTGCTCATATCTGCTATGTTGGTGGATCAGCAATAT 960
QY 961 GTGAGCTTCTACTTGAAGAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTTGAAGAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCAATCATATGTAATTTGCGAGTTACTTTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCAATCATATGTAATTTGCGAGTTACTTTGACTAC 1080
QY 1081 AAGAGAAAACAGATGTAATAATCTTCTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
DB 1081 AAGAGAAAACAGATGTAATAATCTTCTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAGGATGAAATATCCAGCAAGGAAA 1200

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Db      1141 CTGACATCAGAGAGAGATCACAAAAGTTCAAAAGCAGTGAATAAGCCAGCAGAGAAA 1200
Qy      1201 ATGTCTCAAGAACACAGAAATTAATAAGATGTGATAGAGAGGTGAAGAAGAAATGAAG 1260
Db      1201 ATGTCTCAAGAACACAGAAATTAATAAGATGTGATAGAGAGGTGAAGAAGAAATGAAG 1260
Qy      1261 AAGCATGAAAGTAATAATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGCGC 1320
Db      1261 AAGCATGAAAGTAATAATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGCGC 1320
Qy      1321 AATGTGATTAATGATTAATTTCTCTCAAGAGAGACGAAACACTGTAATAATGCAATTT 1380
Db      1321 AATGTGATTAATGATTAATTTCTCTCAAGAGAGACGAAACACTGTAATAATGCAATTT 1380
Qy      1381 CCTGACACGAAAGTGAAGATGATCAAGAAATTTGGCAATTAATTTCTGACTCAAGAAA 1440
Db      1381 CCTGACACGAAAGTGAAGATGATCAAGAAATTTGGCAATTAATTTCTGACTCAAGAAA 1440
Qy      1441 AAACAGATGCGCAAAATACTCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCGCAAAATACTCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAGAGAGATCACAAAAGCTTTGAGGCGCATGTAATAATGGCCAGCCAGACTGAGAAAT 1560
Db      1501 TCAGAGAGAGAGATCACAAAAGCTTTGAGGCGCATGTAATAATGGCCAGCCAGACTGAGAAAT 1560
Qy      1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGGATTTCCAGAAAC 1620
Db      1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGGATTTCCAGAAAC 1620
Qy      1621 CTGACTAATGTGTCACATGTCGCAATGTGTGATGATGATTAATTTCTCCAGAGAGAGC 1680
Db      1621 CTGACTAATGTGTCACATGTCGCAATGTGTGATGATGATTAATTTCTCCAGAGAGAGC 1680
Qy      1681 AGAACAACCTGAAAAGCCAGCAATTTCTGACACTGAAATGAAGATATCACTAGTCGAA 1740
Db      1681 AGAACAACCTGAAAAGCCAGCAATTTCTGACACTGAAATGAAGATATCACTAGTCGAA 1740
Qy      1741 CAAATATGATCTAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTTACCGATGAG 1800
Db      1741 CAAATATGATCTAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTTACCGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAAAAAGCAGATAGAAAGTGTGAAAAATGAAATCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAGAAAAAGCAGATAGAAAGTGTGAAAAATGAAATCTGAGCTTTCT 1860
Qy      1861 CTTAGTTTGAAGAAAGAAAGCATCTTGTGATGAAATATGTAAGTGTGCGGGAAGAAAT 1920
Db      1861 CTTAGTTTGAAGAAAGAAAGCATCTTGTGATGAAATATGTAAGTGTGCGGGAAGAAAT 1920
Qy      1921 GCCATGCTTAAGACTGAGAGCTAGACATGAAATCATCAGAGCCAGCTAAAAAATTA 1980
Db      1921 GCCATGCTTAAGACTGAGAGCTAGACATGAAATCATCAGAGCCAGCTAAAAAATTA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 13
ADBI3824
ID      ADBI3824 standard; cDNA; 2000 BP.
XX
AC      ADBI3824;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Human prostate specific cDNA B305 splice variant #9.
XX
KW      Human; ss; prostate specific cDNA; cytosolic; immunostimulant;
KW      gene therapy; cell therapy; vaccine; T-cell epitope;
KW      class I major histocompatibility complex allele; MHC; prostate cancer;
KW      tumour; antigen presenting cell.

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XX      XX      Homo sapiens.
OS      OS      US2003185830-A1.
XX      XX      02-OCT-2003.
XX      XX      12-NOV-2002; 2002US-00294025.
XX      XX      25-FEB-1997; 97US-00806099.
XX      XX      01-AUG-1997; 97US-00904804.
XX      XX      09-FEB-1998; 98US-00020956.
XX      XX      25-FEB-1998; 98US-00030607.
XX      XX      14-JUL-1998; 98US-00115453.
XX      XX      23-SEP-1998; 98US-00159812.
XX      XX      15-JAN-1999; 99US-00232149.
XX      XX      09-APR-1999; 99US-00288946.
XX      XX      13-JUL-1999; 99US-00352616.
XX      XX      12-NOV-1999; 99US-00439313.
XX      XX      18-NOV-1999; 99US-00443686.
XX      XX      14-JAN-2000; 2000US-00483672.
XX      XX      27-MAR-2000; 2000US-00536857.
XX      XX      09-MAY-2000; 2000US-00568100.
XX      XX      12-MAY-2000; 2000US-00570737.
XX      XX      13-JUN-2000; 2000US-00593793.
XX      XX      27-JUN-2000; 2000US-00605783.
XX      XX      09-AUG-2000; 2000US-00636215.
XX      XX      29-AUG-2000; 2000US-00651235.
XX      XX      06-SEP-2000; 2000US-00657279.
XX      XX      02-OCT-2000; 2000US-00679426.
XX      XX      10-OCT-2000; 2000US-00685166.
XX      XX      09-NOV-2000; 2000US-00709729.
XX      XX      12-JAN-2001; 2001US-00759143.
XX      XX      09-FEB-2001; 2001US-00780669.
XX      XX      09-MAY-2001; 2001US-00852911.
XX      XX      29-JUN-2001; 2001US-00895814.
XX      XX      10-DEC-2001; 2001US-0012896.
XX      XX      09-MAY-2002; 2002US-00144678.

(COR-) CORIXA CORP.
PI      PI      Xu J, Stoik JA, Kalos MD;
XX      XX      WPI; 2003-756193/71.
XX      XX      P-PsDB; ADBI3829.
XX      XX      New isolated polypeptide for use in a vaccine for stimulating an immune
XX      XX      response, or for treating or diagnosis cancer, preferably prostate
XX      XX      cancer.
XX      XX      Example 11; Page; 101pp; English.
XX      XX      The invention relates to an isolated polypeptide comprising no more than
XX      XX      11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
XX      XX      peptides comprise a fragment ADBI3563 of that contain naturally processed
XX      XX      T-cell epitopes for 3 class I major histocompatibility complex (MHC)
XX      XX      alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
XX      XX      cDNA, one of 648 disclosed as new. Also included are nucleic acids
XX      XX      encoding the proteins and peptides, expression vectors, a host cell
XX      XX      transformed with the vector, an isolated antibody (or antigen binding
XX      XX      fragment) that specifically binds to the protein or peptide, detecting
XX      XX      the presence of a cancer in a patient (comprising contacting a patient
XX      XX      sample with a binding agent that binds to the peptides or a polypeptide
XX      XX      appearing as ADBI3558, detecting the amount of polypeptide that binds to
XX      XX      the agent and comparing the amount of polypeptide to a predetermined cut-
XX      XX      off value to determine the presence of cancer), a fusion protein
XX      XX      comprising the peptides or proteins, stimulating or expanding T cells
XX      XX      specific for a tumour protein comprising contacting T cells with the
XX      XX      peptides or the isolated T cell population, treating prostate cancer in a
XX      XX      patient comprising administering a composition comprising the peptides,
XX      XX      nucleic acids, antibodies or compounds, determining the presence of a
XX      XX      cancer in a patient and treating prostate cancer in a patient comprising
XX      XX      incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

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CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptide (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known CDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific CDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPO at
CC seqdata.uspo.gov/sequence.html?docid=20030185830.

XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATGCGCGCTGCTCTTGTGGAAGACCATTTGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATGCGCGCTGCTCTTGTGGAAGACCATTTGTCTC 60

QY 61 AGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120

QY 121 AGCAGTGGGCACTTGTGAGACCAAGCACTGCTATGAAAGACATCAGAGAGAG 180
DB 121 AGCAGTGGGCACTTGTGAGACCAAGCACTGCTATGAAAGACATCAGAGAGAG 180

QY 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTG 240
DB 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTG 240

QY 241 GGGGCTTGTGAGACCAAGCACTGCTATGAAAGACATCAGAGAGAG 300
DB 241 GGGGCTTGTGAGACCAAGCACTGCTATGAAAGACATCAGAGAGAG 300

QY 301 TGGTGGGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
DB 301 TGGTGGGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360

QY 361 GGAGCACTAGATGACAGTGTCTTCAATGAGCCAGAGTACCACTGCTGGAAGAGATCTG 420
DB 361 GGAGCACTAGATGACAGTGTCTTCAATGAGCCAGAGTACCACTGCTGGAAGAGATCTG 420

QY 421 GACAGCTTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAAGAGATCTCATGCTAG 480
DB 421 GACAGCTTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAAGAGATCTCATGCTAG 480

QY 481 CTCAGGAGACCTGACGTGAAACAAGAGAGACAAAGAGAGCTGCTCTACATCTGAGCC 540
DB 481 CTCAGGAGACCTGACGTGAAACAAGAGAGACAAAGAGAGCTGCTCTACATCTGAGCC 540

QY 541 TCTGCAATGGAATTCAGAAATGTAATAAATCTGCTGGAAGAGATGTAAT 600
DB 541 TCTGCAATGGAATTCAGAAATGTAATAAATCTGCTGGAAGAGATGTAAT 600

QY 601 GTCTTGAACAACAAAAGAGAGAGAGCTGTGATTAAGGCGCTACATGCGAAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGAGAGCTGTGATTAAGGCGCTACATGCGAAGATGAA 660

QY 661 TGTGCGTTAATGTTGCGAACAATGCAATGCAATCCAAATTTCCAAATGATGTAAT 720
DB 661 TGTGCGTTAATGTTGCGAACAATGCAATGCAATCCAAATTTCCAAATGATGTAAT 720

QY 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAAGGCAAGAGATGCTCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGCGCAAGAGATGCTCTTA 780

QY 781 TATGTCCTGATATGCAATTAACAAAACAGCATGCGCTCACACCATGTTACTTGTGTA 840
DB 781 TATGTCCTGATATGCAATTAACAAAACAGCATGCGCTCACACCATGTTACTTGTGTA 840

QY 841 CATGACCAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAAGCAATTTAATATGA 900
DB 841 CATGACCAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAAGCAATTTAATATGA 900

QY 901 CTGATATGATATGAAAGAGCTGCTCATATCTTGTGAAACAGCAATTCAGATGATA 960
DB 901 CTGATATGATATGAAAGAGCTGCTCATATCTTGTGAAACAGCAATTCAGATGATA 960

QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATGCAAGAGC 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATGCAAGAGC 1020

QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080

QY 1081 AAGAAAAACAGATGCTAAATAATCTCTGTAACAGCAATTCAGAACAGACTTAAAG 1140
DB 1081 AAGAAAAACAGATGCTAAATAATCTCTGTAACAGCAATTCAGAACAGACTTAAAG 1140

QY 1141 CTGACATCAGAGAGAGATGCAAAAGTTCAAGGCAAGTAATAATGCCAGCAAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGATGCAAAAGTTCAAGGCAAGTAATAATGCCAGCAAGAGAA 1200

QY 1201 ATGTCTCAAGAAACCAAAATTAATAGATGTGTGATGAGAGGTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAAACCAAAATTAATAGATGTGTGATGAGAGGTGAAGAAATGAAG 1260

QY 1261 AAGCATGAAGATATATATGTGGATTTACTAGAAAACCTGACTATGCTGTGCTG 1320
DB 1261 AAGCATGAAGATATATATGTGGATTTACTAGAAAACCTGACTATGCTGTGCTG 1320

QY 1321 AATGTGATATGATTAATTTCTCAAGAGAGAGCAAAACCTGAAATACGCAATTT 1380
DB 1321 AATGTGATATGATTAATTTCTCAAGAGAGAGCAAAACCTGAAATACGCAATTT 1380

QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTTCTGACTACAAAGAA 1440

QY 1441 AAAAGATGCCAAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
DB 1441 AAAAGATGCCAAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500

QY 1501 TCAAGAGAAAGATCACAAAGGCTTGAAGGCAAGTAAATGGCCAGAGCTTAAAGAT 1560
DB 1501 TCAAGAGAAAGATCACAAAGGCTTGAAGGCAAGTAAATGGCCAGAGCTTAAAGAT 1560

QY 1561 TTTATGCTATGGAAGAAATGAAGAGACGAAAGTACTATGTCGATTCCTCAAGAAAC 1620
DB 1561 TTTATGCTATGGAAGAAATGAAGAGACGAAAGTACTATGTCGATTCCTCAAGAAAC 1620

QY 1621 CTGACTTAATGTGTCACCTGCTGCAATGATGATGATTAATTTCTCAAGAAAGAGC 1680
DB 1621 CTGACTTAATGTGTCACCTGCTGCAATGATGATGATTAATTTCTCAAGAAAGAGC 1680

QY 1681 AGAACCTGAAAGCCAGAAATTTCTGACACTGAGAAATGAAGATATCAACTGACGA 1740
DB 1681 AGAACCTGAAAGCCAGAAATTTCTGACACTGAGAAATGAAGATATCAACTGACGA 1740

QY 1741 CAAATGATATCTCAGAAAGCAATTTTGTGAAGAACGAACTGGAATATTAACAGATGAG 1800
DB 1741 CAAATGATATCTCAGAAAGCAATTTTGTGAAGAACGAACTGGAATATTAACAGATGAG 1800

QY 1801 ATTCTGATTCATGAAGAAAGAGATGAGATGATGATGATGATGATGATGATGATGAT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATGAGATGATGATGATGATGATGATGATGATGAT 1860

QY 1861 CTTAGTGTGAAGAAAAAGACATCTTGATGAAAAATAGTCTTGCGGAGAAATT 1920
DB 1861 CTTAGTGTGAAGAAAAAGACATCTTGATGAAAAATAGTCTTGCGGAGAAATT 1920
QY 1921 GCCATGCTTAAGACTGAGCTGACACACATGAAACATGAGCCAGCTTAATAAAAAA 1980
DB 1921 GCCATGCTTAAGACTGAGCTGACACACATGAAACATGAGCCAGCTTAATAAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000
RESULT 14
ID ADG26240 standard; cDNA; 2000 BP.
AC ADG26240;
DT 26-FEB-2004 (first entry)
XX Human prostate-specific CDNA #359.
DE Human prostate-specific CDNA #359.
KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;
XX cytoskeletal.
OS Homo sapiens.
XX US2003157089-A1.
XX 21-AUG-2003.
XX 09-MAY-2002; 2002US-00144678.
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
PI Carier D, Li SX, Wang A, Skelky YAW, Hepner WT, Hurral J;
PI McNeill PD, Houghton RL, Vinals Y De Baasolac, Roy TM, Matanabe Y,
PI Meagher MJ, Deng T;
XX
DR MPI; 2003-777973/73.
DR P-PDB; ADG26245.

XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
PS Example 11; SEQ ID NO 374; 99pp; English.
XX
CC The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2000 BP, 698 A, 388 C, 489 G, 425 T; 0 U; 0 Other;
Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best local similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAACCAATTGGTCTC 60
DB 1 ATGTGTGTTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAACCAATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCGGTGCTCCCTGCTGCAAGGAGACGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCGGTGCTCCCTGCTGCAAGGAGACGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
QY 241 GGGGCTTCTGAGACCAAGCACTCTGTATGAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGACCAAGCACTCTGTATGAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
DB 301 TGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGCCTTCATGAGAGCCAGGTACAGTCCGTGAGAAAGTCTG 420
DB 361 GGAAGCTACGATGACAGTGCCTTCATGAGAGCCAGGTACAGTCCGTGAGAAAGTCTG 420
QY 421 GAAAGCTCCAGAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCGCAGT 480
DB 421 GAAAGCTCCAGAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCGCAGT 480
QY 481 CTCAGGACACTGACGTGGAAGAGCAAGCAAGCAAGCAAGCAAGTCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGGAAGAGCAAGCAAGCAAGCAAGCAAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGAAATTCAGAGTAAACTCTGCTGGAACAGAGATGCACTTAAT 600
DB 541 TCTGCCAATGGAAATTCAGAGTAAACTCTGCTGGAACAGAGATGCACTTAAT 600
QY 601 GTCTTGAAGAAAGAGGAGCAAGCTGTATGAAGGCGGTCAATGCCAGGAAGTGA 660
DB 601 GTCTTGAAGAAAGAGGAGCAAGCTGTATGAAGGCGGTCAATGCCAGGAAGTGA 660
QY 661 TGTGCTTAATGTGTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTGTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720

Db 661 TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATAGAAAT 720
Qy 721 ACCACTGTCACAAACCTATCTATTAATGAAGATTAATGCGCAAGACCTGCTTCT 780
Db 722 ACCACTGTCACAAACCTATCTATTAATGAAGATTAATGCGCAAGACCTGCTTCT 780
Qy 781 TATGTGCTGATATCAATCAAAAAAACAAGCATGGCTCACAACAGTCTACTTGGAT 840
Db 781 TATGTGCTGATATCAATCAAAAAAACAAGCATGGCTCACAACAGTCTACTTGGAT 840
Qy 841 CATGACCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAAGCAATTTAAATGCA 900
Db 841 CATGACCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATGATATGGAAGAGACTGCTCATATCTTCTGATATGTTGATGATCAGCAAT 960
Db 901 CTGATATGATATGGAAGAGACTGCTCATATCTTCTGATATGTTGATGATCAGCAAT 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGCAGC 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGCAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATATTTGCGATTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATATTTGCGATTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGTCTAAAAATCTCTTCTGAAAAACAGCAATCAGAACAGACTTAA 1140
Db 1081 AAAAGAAAAACAGTCTAAAAATCTCTTCTGAAAAACAGCAATCAGAACAGACTTAA 1140
Qy 1141 CTGACATCAGAGAAAGTCAAAAGTTTCAAGAGAGTAAATGTCAGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAAAGTCAAAAGTTTCAAGAGAGTAAATGTCAGCCAGCAGAGAAA 1200
Qy 1201 ATGCTCAAGAAACAGAAATTAATAAGATGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAAACAGAAATTAATAAGATGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATGATGAGATTAATAAGAACTGATATGATGATGATGATG 1320
Db 1261 AAGCATGAAAGTAAATGATGAGATTAATAAGAACTGATATGATGATGATGATG 1320
Qy 1321 AATGATGATTAATGATTAATTTCTCAAGAGAAAGCAACCTGAAATTCGCAATTT 1380
Db 1321 AATGATGATTAATGATTAATTTCTCAAGAGAAAGCAACCTGAAATTCGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTGCAATTTGCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTGCAATTTGCTGACTCAAGAA 1440
Qy 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGAACCCAGAACAGACTTAAAGCTGAC 1500
Db 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGAACCCAGAACAGACTTAAAGCTGAC 1500
Qy 1501 TCAGAGGAAGATCAAAAGCTTGAAGGCAAGTAAATGCGCAGCAGACTGAGAAAT 1560
Db 1501 TCAGAGGAAGATCAAAAGCTTGAAGGCAAGTAAATGCGCAGCAGACTGAGAAAT 1560
Qy 1561 TTTATGCTATCGAAGAAATGAAGAGACGGAAGTACTCATGCGAATTTCCAGAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAAGAGACGGAAGTACTCATGCGAATTTCCAGAAAC 1620
Qy 1621 CTGACTAATGATGCACTGCTGCAATGATGATTAATTTCTCCAGAAAGAG 1680
Db 1621 CTGACTAATGATGCACTGCTGCAATGATGATTAATTTCTCCAGAAAGAG 1680
Qy 1681 AGAAGACCTGGAAGCCAGCAATTTCTGACATGGAATGAAGATCACTGACGAA 1740
Db 1681 AGAAGACCTGGAAGCCAGCAATTTCTGACATGGAATGAAGATCACTGACGAA 1740
Qy 1741 CAAATATGATCTAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
Db 1741 CAAATATGATCTAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800

Qy 1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGTGTGTTAAAAATGAAATTTCTGACTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGTGTGTTAAAAATGAAATTTCTGACTTCT 1860
Qy 1861 CTGATGTTGAGAAAGAAAGACATCTTGCATGAAATATGATGCTTGGCGGGAAGAAAT 1920
Db 1861 CTGATGTTGAGAAAGAAAGACATCTTGCATGAAATATGATGCTTGGCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGGCTAGACCAATGAAACATCAGAGCCAGCTTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGGCTAGACCAATGAAACATCAGAGCCAGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 15
AAA06599
ID AAA06599 standard; cDNA; 2000 BP.
AC AAA06599;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:374.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KM immunogenic; cytostatic; vaccine; ss.
OS Homo sapiens.
XX
PN WO200004149-A2.
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
XX
PR 14-JUL-1998; 98US-00116134.
PR 23-SRP-1998; 98US-00159812.
PR 23-SRP-1998; 98US-00159822.
PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PS comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 50; Page 222-223; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (pp). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptide can be used to generate antibodies or anti-
CC idiotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AA082000 to AA082020 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 2000 BP; 698 A; 387 C; 489 G; 426 T; 0 U; 0 Other;

Db 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGTGCAAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCTTCTGGAGACCAAGCACTGCTGTAATGAAGCACTGAGAAACAAGATGGGCAAG 300
Db 241 GGGCTTCTGGAGACCAAGCACTGCTGTAATGAAGCACTGAGAAACAAGATGGGCAAG 300
Qy 301 TGGTGTGCGCACTGCTTCCCTGTGCAAGGGGAGGCGGCAAGCAAGATGGGCGCTTGG 360
Db 301 TGGTGTGCGCACTGCTTCCCTGTGCAAGGGGAGGCGGCAAGCAAGATGGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCCAAGATCAAGTCCCTGTGAGAAAGTCTG 420
Db 361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCCAAGATCAAGTCCCTGTGAGAAAGTCTG 420
Qy 421 GACAAGCTCCAGAGAGTGTGCTGAGTGAAGTCCCAAGAAAGATCTCATGCTGATG 480
Db 421 GACAAGCTCCAGAGAGTGTGCTGAGTGAAGTCCCAAGAAAGATCTCATGCTGATG 480
Qy 481 CTGAGGAGACATGACGCTGAACAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGACC 540
Db 481 CTGAGGAGACATGACGCTGAACAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGACC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTGAATCTCTGCTGCAAGAGATGCTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTGAATCTCTGCTGCAAGAGATGCTCACTTAAT 600
Qy 601 GTCTTGAACAACAAAAAGAGAGAGCTGTATGAAGGCGGTACATGCGCAAGAGATGA 660
Db 601 GTCTTGAACAACAAAAAGAGAGAGCTGTATGAAGGCGGTACATGCGCAAGAGATGA 660
Qy 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTGTGACATGACGTATCTATTAATGAAGATTAATGAGCAAGATGCTCTTA 780
Db 721 ACCACTGTGACATGACGTATCTATTAATGAAGATTAATGAGCAAGATGCTCTTA 780
Qy 781 TATGTGTGATATTCGATCAAAAAACAAGATGAGCTGCAACCACTGTTACTTGGTGA 840
Db 781 TATGTGTGATATTCGATCAAAAAACAAGATGAGCTGCAACCACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAAAGCAAGCTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAAGCAAGCTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATGATATGGAAGAGATGCTCTCATCTTGTGATATTTGCAAGTAACTTTCTGACTAC 960
Db 901 CTGGATGATATGGAAGAGATGCTCTCATCTTGTGATATTTGCAAGTAACTTTCTGACTAC 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Qy 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAGAAAAACAATGCTAAAAATCTCTTCTGAAAAAGCAATCAAGACAAAGCTTTAAAG 1140
Db 1081 AAGAAAAACAATGCTAAAAATCTCTTCTGAAAAAGCAATCAAGACAAAGCTTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGATGACAAAGGTTCAAAAGGAGTGAATTTGCCAGGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGATGACAAAGGTTCAAAAGGAGTGAATTTGCCAGGAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAAATTAATGAAGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATGAAGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATGTTGGATTAATGAAAACTGACTAATGTGTCACTGCTGGC 1320
Db 1261 AAGCATGAAGATTAATGTTGGATTAATGAAAACTGACTAATGTGTCACTGCTGGC 1320

Qy 1321 AATGTGATTAATGATTAATTTCTCAAGAAAGAGAGACCACTGAAAAATGACAAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAAAGAGAGACCACTGAAAAATGACAAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
Qy 1441 AAAACAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAAACAGACTTTAAAGCTGACA 1500
Db 1441 AAAACAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAAACAGACTTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGAGTCAAAAGGCTTTGAGGAGAGTGAATTTGGCAGGACAGAGCTAGAAAT 1560
Db 1501 TCAGAGAAAGAGTCAAAAGGCTTTGAGGAGAGTGAATTTGGCAGGACAGAGCTAGAAAT 1560
Qy 1561 TTTATGCTATGCAAGAAATGAAGAGCAAGAAAGTCTCATGTGCAATTTCCAGAAAC 1620
Db 1561 TTTATGCTATGCAAGAAATGAAGAGCAAGAAAGTCTCATGTGCAATTTCCAGAAAC 1620
Qy 1621 CTGACTAATGTGTGCACTGCTGCAATGATGATTAATTTCTTCAAGAAAGAGC 1680
Db 1621 CTGACTAATGTGTGCACTGCTGCAATGATGATTAATTTCTTCAAGAAAGAGC 1680
Qy 1681 AGAACACCTGAAAGGAGCAATTTCTGCACTGAGAAAGAAAGATGACAGTGAAGAA 1740
Db 1681 AGAACACCTGAAAGGAGCAATTTCTGCACTGAGAAAGAAAGATGACAGTGAAGAA 1740
Qy 1741 CAAATGATATCTCAGAAAGCAATTTGTGGAAGAACAGAACTGGAATTAACAGATGAG 1800
Db 1741 CAAATGATATCTCAGAAAGCAATTTGTGGAAGAACAGAACTGGAATTAACAGATGAG 1800
Qy 1801 ATTTGATTTCAAGAAAGAAAGAGATGAAGGTGTTGAAAAATGATTTCTGAGCTTTCT 1860
Db 1801 ATTTGATTTCAAGAAAGAAAGAGATGAAGGTGTTGAAAAATGATTTCTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAAATGATACGTGCGGAGAAATTT 1920
Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAAATGATACGTGCGGAGAAATTT 1920
Qy 1921 GCCATGCTTAAGCTGAGAGCTAGACCAATGAACATCAGAGGCAAGTAAAAA 1980
Db 1921 GCCATGCTTAAGCTGAGAGCTAGACCAATGAACATCAGAGGCAAGTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-352-616A-374
Sequence 374, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Wang, Yugu
APPLICANT: Xu, Jianshun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGAATTCATATGCGGCTGCTCTTCTGTGGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGGTGAAGTGAATTCATATGCGGCTGCTCTTCTGTGGAAGAGCCATTGGTCTC 60

QY 61 AGAGCAAGATGGGCAAGTGGTGTCTGCTTCCCTGTCTGCAAGGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGGTGTCTGCTTCCCTGTCTGCAAGGAGAGCGGCAAG 120

QY 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCACTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCACTGTATGAAGCACTCAGAGCAAG 180

QY 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGTCTGCAAGGAGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGTCTGCAAGGAGAGTGGCAAGCAAGT 240

QY 241 GGGGCTTCTGAGACAAGCAAGCACTGTCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTCTGAGACAAGCAAGCACTGTCTATGAAGCACTCAGAGCAAGATGGGCAAG 300

QY 301 TGGTGTGCACTGCTTCCCTGTCTGCAAGGAGAGGCAAGGATGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGTCTGCAAGGAGAGGCAAGGATGGGCGCTTGG 360

QY 361 GGAGCACTAGATGACAGTGTCTTATGAGCCCAAGGTACCAAGTCCGTGAGAGAGTCTG 420
DB 361 GGAGCACTAGATGACAGTGTCTTATGAGCCCAAGGTACCAAGTCCGTGAGAGAGTCTG 420

QY 421 GACAGACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCTAG 480
DB 421 GACAGACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCTAG 480

QY 481 CTCAGGAGCACTGAGCGTGAACAAGAGCAAGCAAGAAAGGAGCTGTCTACATCTGGCC 540
DB 481 CTCAGGAGCACTGAGCGTGAACAAGAGCAAGCAAGAAAGGAGCTGTCTACATCTGGCC 540

QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGAGCAAGAGATGCACTTAAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGAGCAAGAGATGCACTTAAAT 600

QY 601 GTCTTGAACAACAAAAGAGAGCAGCTGTATTAAGCGGTAAAGTCCCAAGAAAGATGA 660
DB 601 GTCTTGAACAACAAAAGAGAGCAGCTGTATTAAGCGGTAAAGTCCCAAGAAAGATGA 660

QY 661 TGTGGCTTAATGTGTGGAACAATGGCACTGATCCAAATTTCCAGATGATGGAAT 720
DB 661 TGTGGCTTAATGTGTGGAACAATGGCACTGATCCAAATTTCCAGATGATGGAAT 720

QY 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTA 780

QY 781 TATGTGTGATATGCAATCAAAAACAAAGATGAGCTTCAACACTGTATCTTGTGTGA 840
DB 781 TATGTGTGATATGCAATCAAAAACAAAGATGAGCTTCAACACTGTATCTTGTGTGA 840

QY 841 CATTGACAAAACAGCAAGTCCGTAATTTTAAATGAAGAAAACCGAATTTAAATGCA 900
DB 841 CATTGACAAAACAGCAAGTCCGTAATTTTAAATGAAGAAAACCGAATTTAAATGCA 900

QY 901 CTGATAGATATGAAGAGCTGCTCATATCTGTATGTGTGATGAGCAAGATATA 960
DB 901 CTGATAGATATGAAGAGCTGCTCATATCTGTATGTGTGATGAGCAAGATATA 960

QY 961 GTGAGCTTCTTACTTGAAGAAAATTAATTAATCTTCTCAAGATCTATCTGAGACAG 1020
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QY 1021 GCCAGAGATATGCTTTCTATCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

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QY 1081 AAAAGAAAACAGATGCTAAATCTCTTGTGAACAAGCAATCCAGAACAGACTTAAAG 1140
DB 1081 AAAAGAAAACAGATGCTAAATCTCTTGTGAACAAGCAATCCAGAACAGACTTAAAG 1140

QY 1141 CTGACATCAGAGAGAGTCAACAAGTTCAAAAGCAGTGAATAATGCCAGCCAGAGAA 1200
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QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGGATGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGGATGATGAGAGGTTGAAGAAATGAAG 1260

QY 1261 AAGCATGAAGATTAATATGAGATTAATCTAGAAAACCTGATTAATGTGTCTGCTGGC 1320
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QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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RESULT 3
US-09-289-198-302
; Sequence 302, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:

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1  APPLICANT: Frudakis, Tony N.
2  APPLICANT: Smith, John M.
3  APPLICANT: Reed, Steven G.
4  APPLICANT: Misher, Lynda
5  TITLE OF INVENTION: COMPOSITIONS AND METH
6  TITLE OF INVENTION: TREATMENT AND DIAGNOS
7  FILE REFERENCE: 210121.419C5
8  CURRENT APPLICATION NUMBER: US/09/289,198
9  CURRENT FILING DATE: 1999-04-09
10 EARLIER APPLICATION NUMBER: US 09/062,451
11 EARLIER FILING DATE: 1998-04-17
12 EARLIER APPLICATION NUMBER: US 08/991,789
13 EARLIER FILING DATE: 1997-12-11
14 EARLIER APPLICATION NUMBER: US 08/838,762
15 EARLIER FILING DATE: 1997-04-09
16 EARLIER APPLICATION NUMBER: PCT/US97/0048
17 EARLIER FILING DATE: 1997-01-10
18 EARLIER APPLICATION NUMBER: US 08/700,014
19 EARLIER FILING DATE: 1996-08-20
20 EARLIER APPLICATION NUMBER: US 08/585,392
21 EARLIER FILING DATE: 1996-01-01
22 NUMBER OF SEQ ID NOS: 312
23 SOFTWARE: FastSeq for Windows Version 3.0
24 SEQ ID NO 302
25 LENGTH: 2000
26 TYPE: DNA
27 ORGANISM: Homo sapien
28 US-09-289-198-302

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Query Match	100.0%	Score 2000;	DB 3;	Length 2000;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2000; Conservative	0;	Mismatches	0;	Gaps 0

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Db	61	AGAGCAAGATGGGCAAGTGTGTCTGCGCTTGCTTCCCTGTGCAGAGGAGCGGCAAG	120
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QY	181	ATGGCAAGTGTGTGCGCGCACTGCTTCCCTGTGTCAGGGGGGAGTGGCAAGCAAGT	240
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QY	241	GGCGCTTCTGAGAGCCACGACGACTCTGTCTATGAAACACTCAGAAACAAGTGGGCAAG	300
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Db	361	GGAGACTAGATGACAGTGGCTTTCATGAGAGCCACGGTACCACGTCCTGTGAAGAAATCTG	420
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QY	601	GTCTTTGACAAACAAAAGAGACAGCTCTGTATTAAGGCCGTACAAATGCCAGAAAGATGAA	660
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Db	961	GTCAAGCCTTCTACTTGGACAAAATATTGATATCTTCTCAAGATCTATCTGGACAGACG	1020
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QY	1141	CTGACATCAGAGAAAGTCACAAAAGTTCAAAGCGCTGAAAATATAGCCAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGAAAGTCACAAAAGTTCAAAGCGCTGAAAATATAGCCAGCCAGAGAAA	1200
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Db	1261	AAGCATGAAAGTAAATATATGTGGATTAATAAGAAACCTGACTATGTGTCTACCTGTGC	1320
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Db	1381	CCTGACAAACGAAAGTGAAGAGTATCACAGATTTGGAAATTAAGTTTCTGACTCAAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAAAGACTTTAAAGCTGACA	1500
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Db	1501	TCAGAGGAAGAGTCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTTGAAAT	1560
QY	1561	TTTATGTGCTATTCGAAGAAATGAANAACACGAAAGTACTCATGTCCGATTTCCAGAAAC	1620
Db	1561	TTTATGTGCTATTCGAAGAAATGAANAACACGAAAGTACTCATGTCCGATTTCCAGAAAC	1620
QY	1621	CTGACTAATGGTGGCACTGCTGGCAATGTGTATGATGGAATTAATTTCTCCAGAGAAAGC	1680
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Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-636-215-374
Sequence 374, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636, 215
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-636-215-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 6
US-09-429-755-302
; Sequence 302, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Prudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Mismatches 0; Indels 0; Gaps 0;

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Db 541 TCTGCCAATGGGAAATTCAGAGATGTAATAAATCTGCTGGACAGAGATGTAACCTTAAT 600
Qy 601 GTCTCTTGACCAACAAAAGAGAGACAGCTGTATTAAGCCGTACCAATGCCAGGAAGATGAA 660
Db 601 GTCTCTTGACCAACAAAAGAGAGACAGCTGTATTAAGCCGTACCAATGCCAGGAAGATGAA 660
Qy 661 TGTGCTTAAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCTTAAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACACTGTTACTTGTGTA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACACTGTTACTTGTGTA 840
Qy 841 CATGAGCAAAAAACAGAAAGTCGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGAAAGTCGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATGATATGGAAGAGACTGCTCATATCTGCTGTAATGTTGTGATCAGCAATATA 960
Db 901 CTGATATGATATGGAAGAGACTGCTCATATCTGCTGTAATGTTGTGATCAGCAATATA 960
Qy 961 GTCAAGCTTCTACTTGAAGCAAAATATTGATGTAATCTTCTCAAGATCTATCTGGACAGAG 1020
Db 961 GTCAAGCTTCTACTTGAAGCAAAATATTGATGTAATCTTCTCAAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATTAATGCTGTTCTGATCATCATATGTAATTTGCCAGTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATTAATGCTGTTCTGATCATCATATGTAATTTGCCAGTACTTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCAGAAACAAGCTTAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCAGAAACAAGCTTAAG 1140
Qy 1141 CTGACATCAAGAGAGAGTCACAAAAGTTCAAAAGCAGTGAATAATGACGACAGAGAA 1200
Db 1141 CTGACATCAAGAGAGAGTCACAAAAGTTCAAAAGCAGTGAATAATGACGACAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAAATTAATAGATGATGATGAGAGGTTGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATAGATGATGATGAGAGGTTGAAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATATGTTGGATTACTAGAAAACTGACTPATGTTGCTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATATGTTGGATTACTAGAAAACTGACTPATGTTGCTGCTGGC 1320
Qy 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGCAATTTGTTCTGATCAAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGCAATTTGTTCTGATCAAAAGAA 1440
Qy 1441 AAAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500
Db 1441 AAAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500
Qy 1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCAAGTGAATGCGCAGGCTAGAGAAAT 1560
Db 1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCAAGTGAATGCGCAGGCTAGAGAAAT 1560
Qy 1561 TTTATGCTATGCAAGAAATGAAGAGCAAGAGATGATGATGCTGATTTCCAGAAAAAC 1620
Db 1561 TTTATGCTATGCAAGAAATGAAGAGCAAGAGATGATGATGCTGATTTCCAGAAAAAC 1620

Qy 1621 CTGACTAATGNGGCCACTGCTGGCAATGATGATGATTAATTTCTTCCAAAGAGAGC 1680
Db 1621 CTGACTAATGNGGCCACTGCTGGCAATGATGATGATTAATTTCTTCCAAAGAGAGC 1680
Qy 1681 AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAAATGAAGATATCACAGTACGA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAAATGAAGATATCACAGTACGA 1740
Qy 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAG 1800
Db 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAG 1800
Qy 1801 ATTCTGATTCATGAAAGAAAGAGATAGAAAGTGTGAAAAATATGAAATCTGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAAAGAAAGAGATAGAAAGTGTGAAAAATATGAAATCTGAGCTTCT 1860
Qy 1861 CTTAGTTGTAGAAAAAGAAAGACATCTTGATGAAATATGATGCTTGGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAGAAAAAGAAAGACATCTTGATGAAATATGATGCTTGGGGAAGAAAT 1920
Qy 1921 GCCATGCTTAAGCTGAGCTAGACATGAAACATCAGAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTTAAGCTGAGCTAGACATGAAACATCAGAGCCAGCTAAAAAAGAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-679-426-374
Sequence 374, Application US/09679426
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yael A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq For Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
Db 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60

OY	61	AGGAGCAAGAATGGGCAAGTGGCTGGCCGTTGCTTCCCCTGTGGAGGGAGACAGCGGCAAG	120
Db	61	AGGACCAAGATGGGCAAGTGGCTGGCCGTTGCTTCCCCTGTGGAGGGAGACAGCGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTTGAGAACCAACGACGACTCTGCTATGAAACACTCAGAGGCAAG	180
Db	121	AGCAACGTGGGCACTTCTTGAGAACCAACGACGACTCTGCTATGAAACACTCAGAGGCAAG	180
OY	181	ATGGCGAAGTGGTGGCCGCACTGCTTCCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	240
Db	181	ATGGCGAAGTGGTGGCCGCACTGCTTCCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	240
OY	241	GGCGCTTCTGGAGACACGACGACTCTGCTATGAAACACTCAGAACTAGAGTGGCAAG	300
Db	241	GGCGCTTCTGGAGACACGACGACTCTGCTATGAAACACTCAGAACTAGAGTGGCAAG	300
OY	301	TGTTGCTGCACTGCTTCCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360
Db	301	TGTTGCTGCACTGCTTCCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360
OY	361	GGAGACTACGATGACAGTGGCTTCAATGAGCCAGGTACCAAGTCCGTGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGGCTTCAATGAGCCAGGTACCAAGTCCGTGAGAAAGATCTG	420
OY	421	GACAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAGAAAGAGATCTCATGTCAATG	480
Db	421	GACAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAGAAAGAGATCTCATGTCAATG	480
OY	481	CTCAGGGACACTGACGTGTAACAAGAGGCAAGCAAAAGAGGACTGCTCATCTGGCC	540
Db	481	CTCAGGGACACTGACGTGTAACAAGAGGCAAGCAAAAGAGGACTGCTCATCTGGCC	540
OY	541	TCTGCGCAATGGGAATTCAGAAAGTACTAAACCTCTGCTGACAGACGATCTCAACTTAAAT	600
Db	541	TCTGCGCAATGGGAATTCAGAAAGTACTAAACCTCTGCTGACAGACGATCTCAACTTAAAT	600
OY	601	GTCCTTGAACAACAAAAGAGCAGCTCTGATAAAGGCCGTACATGCAAGAAAGATGAA	660
Db	601	GTCCTTGAACAACAAAAGAGCAGCTCTGATAAAGGCCGTACATGCAAGAAAGATGAA	660
OY	661	TGTGCGTAAATGTTCTGTAACAATGGCACTGATCCAAATATTTCCAGATAGATAGGAAT	720
Db	661	TGTGCGTAAATGTTCTGTAACAATGGCACTGATCCAAATATTTCCAGATAGATAGGAAT	720
OY	721	ACCACTGCACTACGCTATCTATATGAAGTAAATTAATGAGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGCACTACGCTATCTATATGAAGTAAATTAATGAGCCAAAGCACTGCTCTTA	780
OY	781	TATGTGCTGATATGGAATCAAAAAACAAGATGGCTCACACCACTGTACTTGGTGTGA	840
Db	781	TATGTGCTGATATGGAATCAAAAAACAAGATGGCTCACACCACTGTACTTGGTGTGA	840
OY	841	CATAGGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Db	841	CATAGGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGAGCTGCTCTACTCTTGTGATGTTGGAATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGAGCTGCTCTACTCTTGTGATGTTGGAATCAGCAAGTATA	960
OY	961	GTCAGCTCTTACTTGAACAAATATATGATGTATCTTCAAGATCTATCTGGAACAAGC	1020
Db	961	GTCAGCTCTTACTTGAACAAATATATGATGTATCTTCAAGATCTATCTGGAACAAGC	1020
OY	1021	GCCAGAGATATGCGTTTCTAATCATATCATATGTAATTTGGCCAGTTACTTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCGTTTCTAATCATATCATATGTAATTTGGCCAGTTACTTTCTGACTAC	1080
OY	1081	AAAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
OY	1141	CTGACATCAGAGAAAGTCAACAAAGTTCAAGGCACTGAAATAATGCCACGACAGAGAA	1200

Db	1141	CTGACATCAGAGGAAGTGCACAAAGGTTCAAAAGCAGTGAATAATACCCAGCCAGAGAAA	1200
Qy	1201	ATGATCTCAAGAAACAGAAAATTAATTAAGATATGATATGAGAGGTTGAAGAAGAAATGAG	1260
Db	1201	ATGCTCAGAGAACCAAGAAATTAATTAAGATATGATATGAGAGGTTGAAGAAGAAATGAG	1260
Qy	1261	AAGCATGAAGATTAATTAATGATGGATTAATCTGAGAAAACCTGACTAATGGTGTCACTGTGC	1320
Db	1261	AAGCATGAAGATTAATTAATGATGGATTAATCTGAGAAAACCTGACTAATGGTGTCACTGTGC	1320
Qy	1321	AATGGTGAATATGATTAATTAATTCCTCAAGAGACAGAACCACTGAAAATCAGCAATTT	1380
Db	1321	AATGGTGAATATGATTAATTAATTCCTCAAGAGACAGAACCACTGAAAATCAGCAATTT	1380
Qy	1381	CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGGCAATTTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGGCAATTTAGTTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAGACTGACA	1500
Db	1441	AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAGACTGACA	1500
Qy	1501	TCACAGGAAGAGTACAAAGGCTTGAGGCGATGTAATAATGGCCAGCCAGACTTGAAAT	1560
Db	1501	TCACAGGAAGAGTACAAAGGCTTGAGGCGATGTAATAATGGCCAGCCAGACTTGAAAT	1560
Qy	1561	TTTATGGCTATCGAAGAAATGAAGAACACAGGAAGTCTCATGTGGATTCCTCCAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAACACAGGAAGTCTCATGTGGATTCCTCCAGAAAC	1620
Qy	1621	CTGACTAATGATGCGCACTGCTGGCAATGATGATGATGATTAATTCCTCCAGAAAGAGC	1680
Db	1621	CTGACTAATGATGCGCACTGCTGGCAATGATGATGATGATTAATTCCTCCAGAAAGAGC	1680
Qy	1681	AGAACACCTGTAAGGCCAGCAATTTCTGACACTGAGATGAAGATATCAACATGACGAA	1740
Db	1681	AGAACACCTGTAAGGCCAGCAATTTCTGACACTGAGATGAAGATATCAACATGACGAA	1740
Qy	1741	CAAAATATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG	1800
Db	1741	CAAAATATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG	1800
Qy	1801	ATTCTGATTCATGTAAGAAAGCAGATGAAGTGGTTGAAAAATGAAATTCGAGCTTCT	1860
Db	1801	ATTCTGATTCATGTAAGAAAGCAGATGAAGTGGTTGAAAAATGAAATTCGAGCTTCT	1860
Qy	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGATGAATAATATGTAATTCGAGCTTCT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGATGAATAATATGTAATTCGAGCTTCT	1920
Qy	1921	GCCATGCTAAGACTGAGGCTGAGACAAATGAATCATCAGAGCCAGCTTAATTAATTAATTAAT	1980
Db	1921	GCCATGCTAAGACTGAGGCTGAGACAAATGAATCATCAGAGCCAGCTTAATTAATTAATTAAT	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

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/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Derrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yaelir A.W.
/ APPLICANT: Hedler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C23
/ CURRENT APPLICATION NUMBER: US/09/759,143
/ NUMBER OF SEQ ID NOS: 934
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-09-759-143-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGTGTTGAGGTGATTCATGCGGGCTCTTGTGTGAAGAAGCATTTGGTCTC 60
DB      1  ATGGTGTTGAGGTGATTCATGCGGGCTCTTGTGTGAAGAAGCATTTGGTCTC 60
QY      61  AGGAGCAAGATGGGCAAGTGGTCTGCCGTTGCTTCCCTGTGCAAGGAGAGCGGCAAG 120
DB      61  AGGAGCAAGATGGGCAAGTGGTCTGCCGTTGCTTCCCTGTGCAAGGAGAGCGGCAAG 120
QY      121  AGCAAGTGGGCACTTCTGGAACAAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
DB      121  AGCAAGTGGGCACTTCTGGAACAAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
QY      181  ATGGGCAAGTGGGCGGCACTGCTTCCCTGTGCAAGGAGGAGTGGCAAGCAAGCTG 240
DB      181  ATGGGCAAGTGGGCGGCACTGCTTCCCTGTGCAAGGAGGAGTGGCAAGCAAGCTG 240
QY      241  GGGGCTTCTGAGACCAAGCAAGCTCTGTATGAAGACACTCAGAAACAAGTGGCAAG 300
DB      241  GGGGCTTCTGAGACCAAGCAAGCTCTGTATGAAGACACTCAGAAACAAGTGGCAAG 300
QY      301  TGGTGTGCGCACTGCTTCCCTGTGCAAGGAGGAGGCGCAAGAGTGGCGCTTGG 360
DB      301  TGGTGTGCGCACTGCTTCCCTGTGCAAGGAGGAGGCGCAAGAGTGGCGCTTGG 360
QY      361  GGAGACTAGATGACAGTGGCTTCAATGAGGCCAAGGTACCAAGTCCGTGGAGAAATCTG 420
DB      361  GGAGACTAGATGACAGTGGCTTCAATGAGGCCAAGGTACCAAGTCCGTGGAGAAATCTG 420
QY      421  GACAACTCCACAGAGCTGCTGTGTGAGGATTAAGTCCCGCAAGAAAGATCTCATGTCATG 480
DB      421  GACAACTCCACAGAGCTGCTGTGTGAGGATTAAGTCCCGCAAGAAAGATCTCATGTCATG 480
QY      481  CTAAGGACACTGACGTGAACAAGAGACAAAGAAAGAGAGCTGCTTCAATCTGGCC 540
DB      481  CTAAGGACACTGACGTGAACAAGAGAGCAACAAAGAAAGAGAGCTGCTTCAATCTGGCC 540
QY      541  TCTGCCAATGGGAATTCAAGAGTAAATCTCTGTGGAAGAGATGTCAACTTAAT 600
DB      541  TCTGCCAATGGGAATTCAAGAGTAAATCTCTGTGGAAGAGATGTCAACTTAAT 600
QY      601  GTCTTTGACAAACAAAAGAGAGAGCTGTGATAAGGCCGTACATGCGCAAGAGATGA 660
DB      601  GTCTTTGACAAACAAAAGAGAGAGCTGTGATAAGGCCGTACATGCGCAAGAGATGA 660
QY      661  TGTGCTTAATGTGCTGGAACATGGCATGTCAATATTCAGATGATGGAAT 720
DB      661  TGTGCTTAATGTGCTGGAACATGGCATGTCAATATTCAGATGATGGAAT 720
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QY      721  ACCACTGCACTAGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTCTTA 780
DB      721  ACCACTGCACTAGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTCTTA 780
QY      781  TATGTGTGATATGAAATCAAAAAACAAGATGGCTCACACACTGTACTTGGTGTGA 840
DB      781  TATGTGTGATATGAAATCAAAAAACAAGATGGCTCACACACTGTACTTGGTGTGA 840
QY      841  CATGAGCAAAAAACAGAGTGTGAATTTTATCAAGAAAAAAGCGAATTTAATGCA 900
DB      841  CATGAGCAAAAAACAGAGTGTGAATTTTATCAAGAAAAAAGCGAATTTAATGCA 900
QY      901  CTGATATGATGAAAGGAGCTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960
DB      901  CTGATATGATGAAAGGAGCTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960
QY      961  GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
DB      961  GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
QY      1021  GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB      1021  GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY      1081  AAGAAAAACAGATGCTAAATAATCTCTGAAAAACAGCAATCCAGAACTTAAAG 1140
DB      1081  AAGAAAAACAGATGCTAAATAATCTCTGAAAAACAGCAATCCAGAACTTAAAG 1140
QY      1141  CTGACATCAGAGAAAGAGTCAAAAAGTTCAAAAGCATGAAATATGCGCCAGAGAA 1200
DB      1141  CTGACATCAGAGAAAGAGTCAAAAAGTTCAAAAGCATGAAATATGCGCCAGAGAA 1200
QY      1201  ATGTCTCAAGAAACAGAAATTAATGAAGTGGTATGAGAGGTTGAAGAAATGAAG 1260
DB      1201  ATGTCTCAAGAAACAGAAATTAATGAAGTGGTATGAGAGGTTGAAGAAATGAAG 1260
QY      1261  AAGCATGAAAGTAAATATGTTGGGATTAATAGAAAACTGACTAATGTTGCACTGCTG 1320
DB      1261  AAGCATGAAAGTAAATATGTTGGGATTAATAGAAAACTGACTAATGTTGCACTGCTG 1320
QY      1321  AATGTGATATGATTAATTAATCTTCAAGAAAGAGAGCAACCTGAAATAGCAATTT 1380
DB      1321  AATGTGATATGATTAATTAATCTTCAAGAAAGAGAGCAACCTGAAATAGCAATTT 1380
QY      1381  CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
DB      1381  CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
QY      1441  AAACAGATGCCAAATATCTCTCTGAAAAACAGAAACCCAGAAACAAGACTTAAAGCTGACA 1500
DB      1441  AAACAGATGCCAAATATCTCTCTGAAAAACAGAAACCCAGAAACAAGACTTAAAGCTGACA 1500
QY      1501  TCAGAGAAAGTCAAAAAGCTTGAAGGCAAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
DB      1501  TCAGAGAAAGTCAAAAAGCTTGAAGGCAAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
QY      1561  TTTATGCTATGAAAGAAATGAAGAGCCGAAATGTAATGTGGATTTCCCAAGAAAC 1620
DB      1561  TTTATGCTATGAAAGAAATGAAGAGCCGAAATGTAATGTGGATTTCCCAAGAAAC 1620
QY      1621  CTGACTAATAGTGCCACTGCTGCAATGTTGATGATTAATCTCTCAAGAAAGAGC 1680
DB      1621  CTGACTAATAGTGCCACTGCTGCAATGTTGATGATTAATCTCTCAAGAAAGAGC 1680
QY      1681  AGAAACCTGAAGCCAGCAATTTCTCTGCACTGAGAAATGAAGATGATCAGATGCGAA 1740
DB      1681  AGAAACCTGAAGCCAGCAATTTCTCTGCACTGAGAAATGAAGATGATCAGATGCGAA 1740
QY      1741  CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
DB      1741  CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
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QY	1801	ATTCGATCATGAAGAAAGACAGATAGAGTGTGAAGAAATGAATTCGAGCTTCT	1860
Db	1801	ATTCTGATTCCATGAAGAAAGACAGATAGAGTGTGAAGAAATGAATTCGAGCTTCT	1860
QY	1861	CTTAGCTTGAAGAAAGAAAGACATCTTCGATGAAGAAATAGTACGTTGCGGAGAAATT	1920
Db	1861	CTTAGCTTGAAGAAAGAAAGACATCTTCGATGAAGAAATAGTACGTTGCGGAGAAATT	1920
QY	1921	GCCATGCTTAAGACTGAGCTAGACACAATGAACATCAAGGCACTAAAAA	1980
Db	1921	GCCATGCTTAAGACTGAGCTAGACACAATGAACATCAAGGCACTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	
RESULT 9			
	US-09-651-236-374		
	/ Sequence 374, Application US/09651236		
	/ Patent No. 6818751		
	/ GENERAL INFORMATION:		
	/ APPLICANT: Xu, Jiangchun		
	/ APPLICANT: Dillon, Davin C.		
	/ APPLICANT: Mitcham, Jennifer L.		
	/ APPLICANT: Harlocker, Susan L.		
	/ APPLICANT: Jiang, Yugu		
	/ APPLICANT: Henderson, Robert A.		
	/ APPLICANT: Kalos, Michael D.		
	/ APPLICANT: Panger, Gary R.		
	/ APPLICANT: Retter, Marc W.		
	/ APPLICANT: Stolk, John A.		
	/ APPLICANT: Day, Craig H.		
	/ APPLICANT: Vedwick, Thomas S.		
	/ APPLICANT: Carter, Darriick		
	/ APPLICANT: Li, Samuel		
	/ APPLICANT: Wang, Aijun		
	/ APPLICANT: Skelky, Yasir A.W.		
	/ APPLICANT: Hepler, William		
	/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND		
	/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER		
	/ FILE REFERENCE: 210121.42718C18		
	/ CURRENT FILING DATE: US/09/651,236		
	/ NUMBER OF SEQ ID NOS: 865		
	/ SOFTWARE: FastSeq for Windows Version 3.0		
	/ SEQ ID NO 374		
	/ LENGTH: 2000		
	/ TYPE: DNA		
	/ ORGANISM: Homo sapien		
	US-09-651-236-374		
Query Match			
	Best local Similarity	100.0%;	Score 2000; DB 3; Length 2000;
	Matches 2000; Conservative	100.0%; Pred. No. 0;	
		Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGGTGTTGAGTGGATTCCATGCGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC	60
Db	1	ATGGGTGTTGAGTGGATTCCATGCGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC	60
QY	61	AGAGCAAGATGAGGCAAGTGTGCTGCGCTTCCCTGCTGTCAGGAGAGCGGCAAG	120
Db	61	AGAGCAAGATGAGGCAAGTGTGCTGCGCTTCCCTGCTGTCAGGAGAGCGGCAAG	120
QY	121	AGCAACGTGGGCACTTCTGAGAGCCAGACACTGTGCTATGAAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGAGAGCCAGACACTGTGCTATGAAGACACTCAGAGCAAG	180
QY	181	ATGGCAAGTGTGTCGCGCACTGCTTCCCTGCTGTCAGGAGGAGTGGCAAGCAACGTG	240
Db	181	ATGGCAAGTGTGTCGCGCACTGCTTCCCTGCTGTCAGGAGGAGTGGCAAGCAACGTG	240
QY	241	GCGGCTTTCGAGACCAAGCACTCTGCTATGAAGACACTCAGGAACAAGTGGCAAG	300

Db	241	GGCGCTTTGGAGACCAAGACGACTCTGCTATGAAACATTCAGGAACAAATGGGCAAG	300
QY	301	TGATGTGECGCACTGCTTCCCTCGCTGCAAGGGGAGCGGCAAGACAAAGTGGGCGCTTGG	360
Db	301	TGATGTGECGCACTGCTTCCCTCGCTGCAAGGGGAGCGGCAAGACAAAGTGGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGGCTTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGGCTTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAAGATCTG	420
QY	421	GACAAAGCTCCACAAAGCTGCTGGTGGGGTTAACTCCCGAAGAAAGATTCATGCTATG	480
Db	421	GACAAAGCTCCACAAAGCTGCTGGTGGGGTTAACTCCCGAAGAAAGATTCATGCTATG	480
QY	481	CTCAGGGGCACTGACGTGACCAAAAGGACAAAGGAGAAAGAGAGACTGCTCTCATCTGGCC	540
Db	481	CTCAGGGGCACTGACGTGACCAAAAGGACAAAGGAGAAAGAGAGACTGCTCTCATCTGGCC	540
QY	541	TCTGCGCAATGGGAATTCCAGAGTAGTAAATCTCTCGCTGACAGACGATGTCAACTTAAT	600
Db	541	TCTGCGCAATGGGAATTCCAGAGTAGTAAATCTCTCGCTGACAGACGATGTCAACTTAAT	600
QY	601	GTCCTTGACACAAAAAAGAGACAGCTCTGATTAAGGCCGTACAAATGCCAGAAAGATGAA	660
Db	601	GTCCTTGACACAAAAAAGAGACAGCTCTGATTAAGGCCGTACAAATGCCAGAAAGATGAA	660
QY	661	TGTGGGTTAATGTTGGCTGAGAACATGGGCACTGATCCAAATATTTCCAGATGAGTATGAAAT	720
Db	661	TGTGGGTTAATGTTGGCTGAGAACATGGGCACTGATCCAAATATTTCCAGATGAGTATGAAAT	720
QY	721	ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
QY	781	TATGTGTGCTGATATTCGAATCAAAAAACAAGATGGGCTCACACCACTGTTACTTGGTGTA	840
Db	781	TATGTGTGCTGATATTCGAATCAAAAAACAAGATGGGCTCACACCACTGTTACTTGGTGTA	840
QY	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAAGGAAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAAGGAAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGGACTGCTCTCATACTTCTGATAGTTGATGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGGACTGCTCTCATACTTCTGATAGTTGATGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAACAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGACG	1020
Db	961	GTCAGCCTTCTACTTGAACAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGACG	1020
QY	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTGCACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTGCACTAC	1080
QY	1081	AAAAAAGAAACAGATGCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAAAGCTTAAAG	1140
Db	1081	AAAAAAGAAACAGATGCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAAAGCTTAAAG	1140
QY	1141	CTGACATTCAGAGAAAGTCCAAAGGTTCCAAAGGCGAGTGAAAAATAGCCACAGAGAAA	1200
Db	1141	CTGACATTCAGAGAAAGTCCAAAGGTTCCAAAGGCGAGTGAAAAATAGCCACAGAGAAA	1200
QY	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTGATGAGAGGTTGAAGAAAGAAATGAG	1260
Db	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTGATGAGAGGTTGAAGAAAGAAATGAG	1260
QY	1261	AAGCATGAAAGTAAATATGTTGGGATTACTAGAAAAACCTGACTATATGCTGTCACCTGCTGC	1320
Db	1261	AAGCATGAAAGTAAATATGTTGGGATTACTAGAAAAACCTGACTATATGCTGTCACCTGCTGC	1320
QY	1321	AATGTGATTAATGATTAATTTCTTCAAGAGAACGCAACCTGAAAAATCAGCAATTT	1380

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Db      1321 AATGTGATTAATGATTAATTCCTCAAGAGAGACGAAACCTGAAATACGACATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATACAGAAATTTGGAAATGATTTCTGACTACAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATACAGAAATTTGGAAATGATTTCTGACTACAAAGAA 1440
Qy      1441 AAAAGATGCGCAAAATATCTTTCTGAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500
Db      1441 AAAAGATGCGCAAAATATCTTTCTGAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGAGTCAGAAAGGCTTGAGGCGAGTGAATAATGGCCAGACAGCTAGTAAAT 1560
Db      1501 TCAGAGAAAGAGTCAGAAAGGCTTGAGGCGAGTGAATAATGGCCAGACAGCTAGTAAAT 1560
Qy      1561 TTTATGCTATCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGGATTTCCAGAAAC 1620
Db      1561 TTTATGCTATCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGGATTTCCAGAAAC 1620
Qy      1621 CTGACTTAATGTCGCCACTGCTGGCAAATGTTGATGATGATTAATTCCTCAAGAAAGAC 1680
Db      1621 CTGACTTAATGTCGCCACTGCTGGCAAATGTTGATGATGATTAATTCCTCAAGAAAGAC 1680
Qy      1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGCAG 1740
Db      1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGCAG 1740
Qy      1741 CAAATATGATCTAGAAAGCAATTTTGTGAAGAAAGCAAGCACTGGAATATTAACAGTAG 1800
Db      1741 CAAATATGATCTAGAAAGCAATTTTGTGAAGAAAGCAAGCACTGGAATATTAACAGTAG 1800
Qy      1801 ATTCTGATTCATGAGAAAGAGAGATAGAAATGTTGAAATAATGAATTTCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAGAAAGAGAGATAGAAATGTTGAAATAATGAATTTCTGAGCTTTCT 1860
Qy      1861 CTTAGCTTTGAAGAAAGAAAGCATCTTGTGATGAAATATGTAAGTGGGAGAAATTT 1920
Db      1861 CTTAGCTTTGAAGAAAGAAAGCATCTTGTGATGAAATATGTAAGTGGGAGAAATTT 1920
Qy      1921 GCCATGCTAGAGCTGAGCTAGACACATGAAATCATCAGAGCCAGCTTAAAAA 1980
Db      1921 GCCATGCTAGAGCTGAGCTAGACACATGAAATCATCAGAGCCAGCTTAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-09-699-295-302
; Sequence 302, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
; APPLICANT: Prudakie, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelley, Yaelir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-302

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Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGTGTGTTGAGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCAATTTGCTC 60
Db      1 ATGTGTGTTGAGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCAATTTGCTC 60
Qy      61 AGAGCAAGATGGGAAGTGGTGGCGGTTGCTCCCTGCTGAGAGGAGCGGCAAG 120
Db      61 AGAGCAAGATGGGAAGTGGTGGCGGTTGCTCCCTGCTGAGAGGAGCGGCAAG 120
Qy      121 AGCAAGTGGGCACTTCTGAGAACAGACGACTGTGATGAAAGACACTCAGAGCAAG 180
Db      121 AGCAAGTGGGCACTTCTGAGAACAGACGACTGTGATGAAAGACACTCAGAGCAAG 180
Qy      181 ATGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAG 240
Db      181 ATGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAG 240
Qy      241 GGGCGCTTCTGAGACAGACGACTGTGATGAAAGACACTGAGAAACAGATGGGCAAG 300
Db      241 GGGCGCTTCTGAGACAGACGACTGTGATGAAAGACACTGAGAAACAGATGGGCAAG 300
Qy      301 TGGTCTGCGCACTGCTTCCCTGCTGAGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Db      301 TGGTCTGCGCACTGCTTCCCTGCTGAGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Qy      361 GGAAGCTAGATGACAGTGCCTTCATGAGAGCCAGATACACGCTCCGTGAGAGATCTG 420
Db      361 GGAAGCTAGATGACAGTGCCTTCATGAGAGCCAGATACACGCTCCGTGAGAGATCTG 420
Qy      421 GACAAGCTCCACAGAGCTGCGCTGGTGGGTAAAGTCCCAAGAAAGATCTCAATGTCAG 480
Db      421 GACAAGCTCCACAGAGCTGCGCTGGTGGGTAAAGTCCCAAGAAAGATCTCAATGTCAG 480
Qy      481 CTCAGAGCACTGAGCTGAGCAAGAGAGCAAGCAAGAAAGAGAGCTGCTACATCTGCGC 540
Db      481 CTCAGAGCACTGAGCTGAGCAAGAGAGCAAGCAAGAAAGAGAGCTGCTACATCTGCGC 540
Qy      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGATGTCACATTAAT 600
Db      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGATGTCACATTAAT 600
Qy      601 GTGCTTGAACAAGAAAGAGCAGCTGATTAAGCCGCTCAATGCCAGAGATGAA 660
Db      601 GTGCTTGAACAAGAAAGAGCAGCTGATTAAGCCGCTCAATGCCAGAGATGAA 660
Qy      661 TGTGCTTAATGTTCTGGAACAATGCACTGATCCAAATATTCAGATGAGATGGAAT 720
Db      661 TGTGCTTAATGTTCTGGAACAATGCACTGATCCAAATATTCAGATGAGATGGAAT 720
Qy      721 ACCACTGACCTACGCTATCTATATAGAAATTAATGAGCCAGAACTGCTCTTA 780
Db      721 ACCACTGACCTACGCTATCTATATAGAAATTAATGAGCCAGAACTGCTCTTA 780
Qy      781 TATGTGCTGATATGAAATCAAAAAAGCATGCTTCACACACTGTTACTTGTGTGA 840
Db      781 TATGTGCTGATATGAAATCAAAAAAGCATGCTTCACACACTGTTACTTGTGTGA 840
Qy      841 CATGAGCAAAAAAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db      841 CATGAGCAAAAAAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy      901 CTGATATGATATGAGAGCTGCTCATTAATGTTGATGATGATGATGATGATGATGAT 960
Db      901 CTGATATGATATGAGAGCTGCTCATTAATGTTGATGATGATGATGATGATGATGAT 960
Qy      961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020
Db      961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020

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QY	1021	GCACAGAGTAAAGCTTTCTTACATCATATGTAATTTGCGATTACTTTGACATAC	1088
Db	1021	GCACAGAGTAAAGCTTTCTTACATCATATGTAATTTGCGATTACTTTGACATAC	1088
QY	1081	AAAGAAAAACGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG	1148
Db	1081	AAAGAAAAACGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG	1148
QY	1141	CTGACATCAGAGAGAGAGTCACAAAAGGTTCAAAAGCAGTGAATAATGACCCAGAGAA	1200
Db	1141	CTGACATCAGAGAGAGAGTCACAAAAGGTTCAAAAGCAGTGAATAATGACCCAGAGAA	1200
QY	1201	ATGTCCTCAAGAACCGAAATTAATAAGATGGTGTATAGAGCTTTGAAGAAATGAG	1266
Db	1201	ATGTCCTCAAGAACCGAAATTAATAAGATGGTGTATAGAGCTTTGAAGAAATGAG	1266
QY	1261	AAGCATGAAAGTAAATATGTTGGGATTTACTGAAAACTGTAATGTTGTCAGTCTGGC	1320
Db	1261	AAGCATGAAAGTAAATATGTTGGGATTTACTGAAAACTGTAATGTTGTCAGTCTGGC	1320
QY	1321	AATGGTGAATATGATTAATTCCTCAAAAGAAAGCAGAACACCTGAAATCAGCAATTT	1380
Db	1321	AATGGTGAATATGATTAATTCCTCAAAAGAAAGCAGAACACCTGAAATCAGCAATTT	1380
QY	1381	CCTGACAAACGAAAGTAAAGATATCAGAAATTTGCCGAATTAGTTCTTGACTACAAAGA	1440
Db	1381	CCTGACAAACGAAAGTAAAGATATCAGAAATTTGCCGAATTAGTTCTTGACTACAAAGA	1440
QY	1441	AAACGATAGCCAAATATCTCTTCTGAAAAACGCAACCCAGAACAAAGACTTAAGGTGCA	1500
Db	1441	AAACGATAGCCAAATATCTCTTCTGAAAAACGCAACCCAGAACAAAGACTTAAGGTGCA	1500
QY	1501	TCAGAGAAAGTCACAAAAGCTTGAGGCACTGTAATAATGGCCAGCCAGACTGAAAT	1560
Db	1501	TCAGAGAAAGTCACAAAAGCTTGAGGCACTGTAATAATGGCCAGCCAGACTGAAAT	1560
QY	1561	TTTATGCTATTCGAAGAATGAAAGACCGAGACTCATGTCGATTTCCAGAAAC	1620
Db	1561	TTTATGCTATTCGAAGAATGAAAGACCGAGACTCATGTCGATTTCCAGAAAC	1620
QY	1621	CTGATTAATGTTGGCCACTGCTGGCAATGGTATGATGATTAATTTCCCTCAAGAAAGAC	1680
Db	1621	CTGATTAATGTTGGCCACTGCTGGCAATGGTATGATGATTAATTTCCCTCAAGAAAGAC	1680
QY	1681	AGAACCTCTGAAAGCCAGCAATTTCTCTGACACTGGAATGAAGATACACAGTGAACAA	1740
Db	1681	AGAACCTCTGAAAGCCAGCAATTTCTCTGACACTGGAATGAAGATACACAGTGAACAA	1740
QY	1741	CAAAATGATCTCAGAACCAATTTTGTGAAGAACAGAACCTGGAAATTTACAGATAG	1800
Db	1741	CAAAATGATCTCAGAACCAATTTTGTGAAGAACAGAACCTGGAAATTTACAGATAG	1800
QY	1801	AATTCGATTCATGAAGAAAGCAGATGAAGATGATGATTAATTTCTTCTGAGCTTCT	1866
Db	1801	AATTCGATTCATGAAGAAAGCAGATGAAGATGATGATTAATTTCTTCTGAGCTTCT	1866
QY	1861	CTTAAAGTGAAGAAAGAAAGACATCTTCTGATGAATAATAGCTTGGGAAAGAAAT	1920
Db	1861	CTTAAAGTGAAGAAAGAAAGACATCTTCTGATGAATAATAGCTTGGGAAAGAAAT	1920
QY	1921	GCCATGCTAAGAGCTGAGACTGAGACACATATGAACATCAGAGCCAGCTTAAAAA	1980
Db	1921	GCCATGCTAAGAGCTGAGACTGAGACACATATGAACATCAGAGCCAGCTTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

QY	DB	Query Match	Beet Local Similarity	Score 2000	DB 3	length 2000
QY	Db	1	100.0%	100.0%	0	0
QY	Db	1	100.0%	100.0%	0	0
QY	Db	61	100.0%	100.0%	0	0
QY	Db	61	100.0%	100.0%	0	0
QY	Db	121	100.0%	100.0%	0	0
QY	Db	121	100.0%	100.0%	0	0
QY	Db	181	100.0%	100.0%	0	0
QY	Db	181	100.0%	100.0%	0	0
QY	Db	241	100.0%	100.0%	0	0
QY	Db	241	100.0%	100.0%	0	0
QY	Db	301	100.0%	100.0%	0	0
QY	Db	301	100.0%	100.0%	0	0
QY	Db	361	100.0%	100.0%	0	0
QY	Db	361	100.0%	100.0%	0	0
QY	Db	421	100.0%	100.0%	0	0
QY	Db	421	100.0%	100.0%	0	0
QY	Db	481	100.0%	100.0%	0	0
QY	Db	481	100.0%	100.0%	0	0
QY	Db	541	100.0%	100.0%	0	0
QY	Db	541	100.0%	100.0%	0	0
QY	Db	601	100.0%	100.0%	0	0
QY	Db	601	100.0%	100.0%	0	0
QY	Db	661	100.0%	100.0%	0	0
QY	Db	661	100.0%	100.0%	0	0
QY	Db	721	100.0%	100.0%	0	0


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Db      721 ACCACTGTGCACTACGTATCTATATGAAAGTAATTAATGCGCAAGACAGCTGCTCTTA 780
Qy      781 TATGTGCTGATATTCGATCAATCAAAAAACAGCATGCGCTCACACACTGTTACTTGGTGA 840
Db      781 TATGTGCTGATATTCGATCAATCAAAAAACAGCATGCGCTCACACACTGTTACTTGGTGA 840
Qy      841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
Db      841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
Qy      901 CTGATAGATATGAAAGGAGCTGCTCATCTGATGATGTTGGATCAGCAAGTATA 960
Db      901 CTGATAGATATGAAAGGAGCTGCTCATCTGATGATGTTGGATCAGCAAGTATA 960
Qy      961 GTGAGCTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTATGCGACAGCG 1020
Db      961 GTGAGCTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTATGCGACAGCG 1020
Qy      1021 GCCAGAGATAGCTGTTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Db      1021 GCCAGAGATAGCTGTTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Qy      1081 AAAAGAAAAACAGATGCTAAATAATCTCTTGAATAACAGCAATCCAGAACAGACTTAAAG 1140
Db      1081 AAAAGAAAAACAGATGCTAAATAATCTCTTGAATAACAGCAATCCAGAACAGACTTAAAG 1140
Qy      1141 CTGACATCAGAGAAAGTCACAAAAGTTTCAAAAGGAGTGAATAATGCGCCAGAGAAA 1200
Db      1141 CTGACATCAGAGAAAGTCACAAAAGTTTCAAAAGGAGTGAATAATGCGCCAGAGAAA 1200
Qy      1201 ATGCTCAAGAAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db      1201 ATGCTCAAGAAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy      1261 AAGCATGAAAGTATATATGTTGAGATTACTAGAAAACCTGACTATGTTGCTGCTGCG 1320
Db      1261 AAGCATGAAAGTATATATGTTGAGATTACTAGAAAACCTGACTATGTTGCTGCTGCG 1320
Qy      1321 AATGATGATTAATGATTAATCTCTCAAGAAAGAGCAACCTGAAATTCAGCAATTT 1380
Db      1321 AATGATGATTAATGATTAATCTCTCAAGAAAGAGCAACCTGAAATTCAGCAATTT 1380
Qy      1381 CCTGACAAACGAAAGTGAAGATATCAGAAATTTGGAATTTAGTTCTGACTGCAAGAA 1440
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Qy      1441 AAAAGATGCAAAATATCTCTTGAATAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db      1441 AAAAGATGCAAAATATCTCTTGAATAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGAGTGAAGAAATGCGACGACAGCTGAAGAA 1560
Db      1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGAGTGAAGAAATGCGACGACAGCTGAAGAA 1560
Qy      1561 TTTATGCTATCGAAGAAATGAAGAGCAAGAGTACTCATGTGCGATTTCCAGAAAAC 1620
Db      1561 TTTATGCTATCGAAGAAATGAAGAGCAAGAGTACTCATGTGCGATTTCCAGAAAAC 1620
Qy      1621 CTGACTAATGATGCACTGCTGCAATGATGATGATGATTAATCTCTCAAGAAAGAG 1680
Db      1621 CTGACTAATGATGCACTGCTGCAATGATGATGATGATTAATCTCTCAAGAAAGAG 1680
Qy      1681 AGAAGACCTGAAAGCCAGCAATTTCTGAGACATGAGAAATGAAGATTCAGAGTGAAG 1740
Db      1681 AGAAGACCTGAAAGCCAGCAATTTCTGAGACATGAGAAATGAAGATTCAGAGTGAAG 1740
Qy      1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGACAGAACTGGAATATTCAGAGTGAAG 1800
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Db      1801 ATTCTGATTCATGAGAAAGAGATGAAAGTGTGGAATTTGAATTTCTGAGCTTCT 1860
Qy      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATGTTGCGGAGAAATTT 1920
Db      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATGTTGCGGAGAAATTT 1920
Qy      1921 GCCATGCTAAGCTGAGAGTACACAAATGAACATCAGAGGCACTTAATTAATTAATTA 1980
Db      1921 GCCATGCTAAGCTGAGAGTACACAAATGAACATCAGAGGCACTTAATTAATTAATTA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 12
US-09-657-279-374
; Sequence 374, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-657-279-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGATGATGAGAGTGAATTCATGCGAGGCTGCTCTTCTGTAAGAGCAATTTGGTCTC 60
Db      1 ATGATGATGAGAGTGAATTCATGCGAGGCTGCTCTTCTGTAAGAGCAATTTGGTCTC 60
Qy      61 AGAGCAAGATGAGGCAAGTGTGCTGCGCTTCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db      61 AGAGCAAGATGAGGCAAGTGTGCTGCGCTTCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGCTATGAAGACATCTCAGAGCAAG 180
Db      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGCTATGAAGACATCTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGAGCAAGCTG 240
Db      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGAGCAAGCTG 240
Qy      241 GCGGCTTCTGAGAGCAAGCACTCTGCTATGAAGACATCTCAGAGCAAGATGGCAAG 300
Db      241 GCGGCTTCTGAGAGCAAGCACTCTGCTATGAAGACATCTCAGAGCAAGATGGCAAG 300

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QY 301 TGGTGTGCGCATGCTTCCCTCTGCGAGGGGGAGCGGCAAGAGAGTGGGGCTTGG 360
 DB 301 TGGTGTGCGCATGCTTCCCTCTGCGAGGGGGAGCGGCAAGAGAGTGGGGCTTGG 360
 QY 361 GGAGACTAGTAGACAGTGGCTTTCATGAGAGCCAGGTCCAGCTCCGTGGAGAGATCTG 420
 DB 361 GGAGACTAGTAGACAGTGGCTTTCATGAGAGCCAGGTCCAGCTCCGTGGAGAGATCTG 420
 QY 421 GACAACTCCACAGACTGCTTGGTGGGGTAAAGTCCCGCAAGAAAGATCTCATGCTCAG 480
 DB 421 GACAACTCCACAGACTGCTTGGTGGGGTAAAGTCCCGCAAGAAAGATCTCATGCTCAG 480
 QY 481 CTCAGGGACACTGACGCTGAACAAGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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 QY 601 GTCTCTTGAACAACAAAAG 660
 DB 601 GTCTCTTGAACAACAAAAG 660
 QY 661 TGTGGCTTAAATGTTGCTGGAGACATGGCACTGATCCAAATTTTCAGAGTGAATGGAAT 720
 DB 661 TGTGGCTTAAATGTTGCTGGAGACATGGCACTGATCCAAATTTTCAGAGTGAATGGAAT 720
 QY 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATTAATGAGCAAGAGAGAGAGAGAG 780
 DB 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATTAATGAGCAAGAGAGAGAGAGAG 780
 QY 781 TATGTGCTGATATTCGAATCAAAAAACAGCATGGCTCCACACACTGTTACTTGGTGA 840
 DB 781 TATGTGCTGATATTCGAATCAAAAAACAGCATGGCTCCACACACTGTTACTTGGTGA 840
 QY 841 CATGAGCAAAAAAG 900
 DB 841 CATGAGCAAAAAAG 900
 QY 901 CTGATAGATATGAT 960
 DB 901 CTGATAGATATGAT 960
 QY 961 GTGAGCTTCTAATTGAG 1020
 DB 961 GTGAGCTTCTAATTGAG 1020
 QY 1021 GGCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
 DB 1021 GGCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
 QY 1081 AAG 1140
 DB 1081 AAG 1140
 QY 1141 CTGACATCAG 1200
 DB 1141 CTGACATCAG 1200
 QY 1201 ATGTCTCAAG 1260
 DB 1201 ATGTCTCAAG 1260
 QY 1261 AAGCATGAAGATTAATGATGGGATTAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1261 AAGCATGAAGATTAATGATGGGATTAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380
 DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380

QY 1381 CTGACAAAGAAAGTAGAGATATCAGAGATTTGGAGTAAATTTCTGACTACAAAGAA 1440
 DB 1381 CTGACAAAGAAAGTAGAGATATCAGAGATTTGGAGTAAATTTCTGACTACAAAGAA 1440
 QY 1441 AAAAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
 DB 1441 AAAAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGAGAGAGATCAGAAAGGCTTGAAGGCGATGAAAAATGCGCAGCAGAGCTAGAAAT 1560
 DB 1501 TCAGAGAGAGAGATCAGAAAGGCTTGAAGGCGATGAAAAATGCGCAGCAGAGCTAGAAAT 1560
 QY 1561 TTTATGGCTATGAG 1620
 DB 1561 TTTATGGCTATGAG 1620
 QY 1621 CTGACTAATGATGGCCACTGCTGCAATGATGATGATTAATTTCTCCAAAGAGAGAG 1680
 DB 1621 CTGACTAATGATGGCCACTGCTGCAATGATGATGATTAATTTCTCCAAAGAGAGAGAG 1680
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 DB 1681 AGAACACTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAGATATACAGAGTGA 1740
 QY 1741 CAAAATGATATCTCAG 1800
 DB 1741 CAAAATGATATCTCAG 1800
 QY 1801 ATTGATATCAGAGAGAGAGAGAGAGATGAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 1860
 DB 1801 ATTGATATCAGAGAGAGAGAGAGAGATGAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 1860
 QY 1861 CTTAGTTGTAAGAGAGAGAGAGAGAGATCTTGATGAATATGATCGTTGCGGAGAGAAAT 1920
 DB 1861 CTTAGTTGTAAGAGAGAGAGAGAGAGATCTTGATGAATATGATCGTTGCGGAGAGAAAT 1920
 QY 1921 GCCATGCTAAGCTGAGAGTGAACAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 DB 1921 GCCATGCTAAGCTGAGAGTGAACAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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 US-10-012-896-374
 ; Sequence 374, Application US/10012896
 ; Patent No. 6943236
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitchell, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Mantanabe, Yoshihiro

```
/ APPLICANT: Meagher, Madeleine Joy
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ CURRENT REFERENCE: 210121.427C27
/ CURRENT APPLICATION NUMBER: US/10/012,896
/ NUMBER OF SEQ ID NOS: 1011
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-012-896-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAGCAATTTGGTCTC 60
QY      61 AGGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGCAAG 120
DB      61 AGGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGCAAG 120
QY      121 AGCAACGTGGGCACTTCTGAGAGCAAGCACTCTGTAATGAGCACTCAAGAGCAAG 180
DB      121 AGCAACGTGGGCACTTCTGAGAGCAAGCACTCTGTAATGAGCACTCAAGAGCAAG 180
QY      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
DB      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
QY      241 GGGGCTTCTGAGAGCAAGCACTCTGTAATGAGCACTCAAGAGCAAGTGGCAAG 300
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QY      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
DB      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
QY      361 GGAAGCACTGAGTGAAGTGTGCTGCTGAGAGCCAGGTAACAGCTCCGTGAGAGAGTCTG 420
DB      361 GGAAGCACTGAGTGAAGTGTGCTGCTGAGAGCCAGGTAACAGCTCCGTGAGAGAGTCTG 420
QY      421 GACAAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB      421 GACAAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY      481 CTCAGGAGCACTGAGCTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB      481 CTCAGGAGCACTGAGCTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY      541 TCTGCAATGAGGATTCAGAGAGTAAATCTCTGCTGAGCAAGAGTCACTTAAT 600
DB      541 TCTGCAATGAGGATTCAGAGAGTAAATCTCTGCTGAGCAAGAGTCACTTAAT 600
QY      601 GTCTCTTGAACAACAAAGAGAGCACTTGTATTAAGCGGTACATGCAAGAGAGTGA 660
DB      601 GTCTCTTGAACAACAAAGAGAGCACTTGTATTAAGCGGTACATGCAAGAGAGTGA 660
QY      661 TGTGGCTTATGTTGTGAGCACTGAGCACTGCAATTAATTCGAATGAGTGAAT 720
DB      661 TGTGGCTTATGTTGTGAGCACTGAGCACTGCAATTAATTCGAATGAGTGAAT 720
QY      721 ACCACTCTGCACTACCTATCTTAATGAAGATTAATTAAGGCAAGCACTGCTTA 780
DB      721 ACCACTCTGCACTACCTATCTTAATGAAGATTAATTAAGGCAAGCACTGCTTA 780
QY      781 TATGTGCTGATATTCGAATCAACAAAGAGAGTGGCTTCAACCACTGTTACTTGGTGA 840
DB      781 TATGTGCTGATATTCGAATCAACAAAGAGAGTGGCTTCAACCACTGTTACTTGGTGA 840
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DB      841 CATGAGCAAAAAACAGAGTGTGAAATTTTATCAAGAAAAAGCAATTTAATGCA 900
QY      901 CTGATAGATATGAGAGCTGCTCTCATCTGCTGATGTTGGATCAGCAAGTATA 960
DB      901 CTGATAGATATGAGAGCTGCTCTCATCTGCTGATGTTGGATCAGCAAGTATA 960
QY      961 GTCACTCTTCTCATCTGAGCAAAATTAATGATATCTTCAAGATCTATCTGCAAGAG 1020
DB      961 GTCACTCTTCTCATCTGAGCAAAATTAATGATATCTTCAAGATCTATCTGCAAGAG 1020
QY      1021 GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCAAGTACTTCTGCACTAC 1080
DB      1021 GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCAAGTACTTCTGCACTAC 1080
QY      1081 AAGAAAAACAGATCTAAAAATCTCTTGAAGAACAGCAATCCAGAACAGCTTAAG 1140
DB      1081 AAGAAAAACAGATCTAAAAATCTCTTGAAGAACAGCAATCCAGAACAGCTTAAG 1140
QY      1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTAAATAGCCAGCAAGAAA 1200
DB      1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTAAATAGCCAGCAAGAAA 1200
QY      1201 ATGTCTCAAGAACCAAGAAATTAATAGAGTGTGATAGAGAGGTTGAAGAAATGAAG 1260
DB      1201 ATGTCTCAAGAACCAAGAAATTAATAGAGTGTGATAGAGAGGTTGAAGAAATGAAG 1260
QY      1261 AAGCATGAAGATTAATGAGAGATTAATGAGAGATTAATGAGAGATTAATGAGAGAT 1320
DB      1261 AAGCATGAAGATTAATGAGAGATTAATGAGAGATTAATGAGAGATTAATGAGAGAT 1320
QY      1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAAGCACTGAAATATGCAATTT 1380
DB      1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAAGCACTGAAATATGCAATTT 1380
QY      1381 CCTGCAACAGAAAGGAGAGATATCAAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
DB      1381 CCTGCAACAGAAAGGAGAGATATCAAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
QY      1441 AAGCATGAGCAAAATTAATCTTCTGAGAAACAGCAACCAAGCAAGCACTTAAGCTGACA 1500
DB      1441 AAGCATGAGCAAAATTAATCTTCTGAGAAACAGCAACCAAGCAAGCACTTAAGCTGACA 1500
QY      1501 TCAAGAGAGAGATCAAAAGGCTTGAAGGCACTGAAATGAGCAAGCAAGCTTAAGAT 1560
DB      1501 TCAAGAGAGAGATCAAAAGGCTTGAAGGCACTGAAATGAGCAAGCAAGCTTAAGAT 1560
QY      1561 TTTATGAGTATGAGAAATGAAGAGCAAGAGATCAATGAGGATTTCCAGAAAG 1620
DB      1561 TTTATGAGTATGAGAAATGAAGAGCAAGAGATCAATGAGGATTTCCAGAAAG 1620
QY      1621 CTGACTAATGAGTGAAGTGTGAGTGAATGAATTAATTTCTTCAAGAGAGAG 1680
DB      1621 CTGACTAATGAGTGAAGTGTGAGTGAATGAATTAATTTCTTCAAGAGAGAG 1680
QY      1681 AGAACAACCTGAAAGCCAGCAATTTCTGCACTGAGAAAGAGAGATCAAGTGAAG 1740
DB      1681 AGAACAACCTGAAAGCCAGCAATTTCTGCACTGAGAAAGAGAGATCAAGTGAAG 1740
QY      1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATTAACAGATGAG 1800
DB      1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATTAACAGATGAG 1800
QY      1801 ATTCTGATTCATGAGAAAGAGATAGAGTGTGTAAGAAATTAATCTGAGCTTCT 1860
DB      1801 ATTCTGATTCATGAGAAAGAGATAGAGTGTGTAAGAAATTAATCTGAGCTTCT 1860
QY      1861 CTTAGTGTGAAGAAAGAAAGCAATCTTGCATGAATATGATCGTTGGGGAAGAAAT 1920
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QY      1921 GCCATGCTAAGACTGGAGCTAGACACAAATGAAAATCATCAGACGCAATAAAAA 1980
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Db      1981 AAAAAAAAAAAAAAAAAA 2000

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; Sequence 375, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reiter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: PhredSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-375

Query Match      77.5%; Score 1551; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGSGTTGAGGTTGATTCATGCGGCGCTCTTCTGTGAAGACATTTGGTTC 60
QY      61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTCCCGTGTGCAAGGAGCGGCAAG 120
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Db      61 AGGAGCAAGTGGGCAAGTGTGCTGCGGTTGCTCCCGTGTGCAAGGAGCGGCAAG 120
QY      121 AGCAAGTGGGCACTTCTGAGACACAGACACTTGTATGAAGACACTCAGAGCAAG 180
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Db      121 AGCAAGTGGGCACTTCTGAGACACAGACACTTGTATGAAGACACTCAGAGCAAG 180
QY      181 ATGGGCAAGTGTGCGGCGCACTGCTTCCCTGTGTGCAAGGAGGAGTGGCAAGCGT 240
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Db      181 ATGGGCAAGTGTGCGGCGCACTGCTTCCCTGTGTGCAAGGAGGAGTGGCAAGCGT 240
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Db      301 TGGTGTGCGCACTGCTTCCCTGTGTGCAAGGAGGAGCGGCAAGGAGGAGGCGCTTGG 360
QY      361 GGAAGCTAGAGTACAGTGTGCTTCAATGAGGCCAGAGTACAGTCCGTGGAAGAGTCTG 420
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Db      361 GGAAGCTAGAGTACAGTGTGCTTCAATGAGGCCAGAGTACAGTCCGTGGAAGAGTCTG 420
QY      421 GACAAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
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Db      481 CTCAGGACACTGACGCTGAACAAGAAAGACAAAGCAAGCAAGCACTGCTTACATCTGGCC 540
QY      541 TGTGCAATGGGAAATTCAGAAAGTAAACTCTGTGTGAGACAGAGATGTCACTTAAT 600
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Db      541 TGTGCAATGGGAAATTCAGAAAGTAAACTCTGTGTGAGACAGAGATGTCACTTAAT 600
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Db      601 GTCTTGAACAACAAAAGAGACAGCTGTGATAAGCCGTACAAATGCCAGAAAGATGA 660
QY      661 TGTGCTTAATGTTGCTGGAACATGCGACTGATCCAAATATTCAGATGATGGAAT 720
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Db      661 TGTGCTTAATGTTGCTGGAACATGCGACTGATCCAAATATTCAGATGATGGAAT 720
QY      721 ACCACTGTCACCTAGCTATCTATATGAAGATTAATTAAGCCAAAGCACTGCTTA 780
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QY      781 TATGCTGATGATGCAATCAAAAACAGATGCGCTCACACACTGTTACTTGTGTA 840
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Db      781 TATGCTGATGATGCAATCAAAAACAGATGCGCTCACACACTGTTACTTGTGTA 840
QY      841 CATGACAAAACAGCAAGTCTGAAATTTTATATGAAGAAAGCGAATTTAATGCA 900
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Db      841 CATGACAAAACAGCAAGTCTGAAATTTTATATGAAGAAAGCGAATTTAATGCA 900
QY      901 CTGAGATGATGGAAGGACCTGCTCATCTTGCTGATGTTGTGATGAGCAAGTATTA 960
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Db      901 CTGAGATGATGGAAGGACCTGCTCATCTTGCTGATGTTGTGATGAGCAAGTATTA 960
QY      961 GTGAGCTTCTACTTGGAGCAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
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Db      961 GTGAGCTTCTACTTGGAGCAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
QY      1021 GCCAGAGATATGCTGTTTCTAGTCAATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
      |||
Db      1021 GCCAGAGATATGCTGTTTCTAGTCAATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
QY      1081 AAAAAAAAAAAGATGTAATAATCTCTGAAACAGCAATCCAAACAAGCTTAAG 1140
      |||
Db      1081 AAAAAAAAAAAGATGTAATAATCTCTGAAACAGCAATCCAAACAAGCTTAAG 1140
QY      1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAGTGAATAATGCCAGCCAGAGAA 1200
      |||
Db      1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAGTGAATAATGCCAGCCAGAGAA 1200
QY      1201 ATGCTCAAGAACAGAAATTAATAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
      |||
Db      1201 ATGCTCAAGAACAGAAATTAATAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
QY      1261 AAGCATGAAGATTAATGAGATTAATCTGAAACCTGATTAATGCTGCTGCG 1320
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Db      1261 AAGCATGAAGATTAATGAGATTAATCTGAAACCTGATTAATGCTGCTGCG 1320
QY      1321 AATGTGATTAATGATTAATCTCCTCAAGAGAGAGCAACCTGAAATCGCAATTT 1380
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Db      1321 AATGTGATTAATGATTAATCTCCTCAAGAGAGAGCAACCTGAAATCGCAATTT 1380
QY      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTAATGTTCTGATCAAGAA 1440
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QY      1441 AAAAGATGCGCAAAATATCTCTGAAACACCAACCCGAACAGACTTAAGCTGACA 1500
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QY      1501 TCAGAGGAAGATGCAAAAAGCTTGAAGGCACTGAAATATGCGCAGCGAGAG 1551
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2000	100.0	2000	US-09-759-143-374	Sequence 374, App
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4	2000	100.0	2000	US-09-810-936-302	Sequence 302, App
5	2000	100.0	2000	US-09-822-827-374	Sequence 374, App
6	2000	100.0	2000	US-09-429-755-302	Sequence 302, App
7	2000	100.0	2000	US-09-924-400-302	Sequence 302, App
8	2000	100.0	2000	US-09-895-793-374	Sequence 374, App
9	2000	100.0	2000	US-09-895-814-374	Sequence 374, App
10	2000	100.0	2000	US-10-012-896-374	Sequence 374, App
11	2000	100.0	2000	US-10-010-940-374	Sequence 374, App
12	2000	100.0	2000	US-10-212-679-302	Sequence 302, App
13	2000	100.0	2000	US-10-144-678A-374	Sequence 374, App
14	2000	100.0	2000	US-10-033-527-6	Sequence 6, App1
15	2000	100.0	2000	US-10-294-025-374	Sequence 374, App
16	2000	100.0	2000	US-10-079-137B-302	Sequence 302, App
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18	1551	77.5	2040	US-09-759-143-375	Sequence 375, App
19	1551	77.5	2040	US-09-780-669-375	Sequence 375, App
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21	1551	77.5	2040	US-09-822-827-375	Sequence 375, App
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23	1551	77.5	2040	US-09-924-400-303	Sequence 303, App

24	1551	77.5	2040	3	US-09-895-793-375	Sequence 375, App
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ALIGNMENTS

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Sequence 6, Application US/09825301																		
Patent No. US2002009738A1																		
GENERAL INFORMATION:																		
APPLICANT: Houghton, Raymond L.																		
APPLICANT: Dillon, David C.																		
APPLICANT: Molesh, David A.																		
APPLICANT: Xu, Jiangchun																		
APPLICANT: Zehentner, Barbara																		
APPLICANT: Persing, David H.																		
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION																		
FILE REFERENCE: 210121.513																		
CURRENT APPLICATION NUMBER: US/09/825,301																		
CURRENT FILING DATE: 2001-04-02																		
NUMBER OF SEQ ID NOS: 77																		
SOFTWARE: FastSeq for Windows Version 3.0																		
SEQ ID NO 6																		
LENGTH: 2000																		
TYPE: DNA																		
ORGANISM: Homo sapien																		
US-09-825-301-6																		
Query Match																		
Best Local Similarity 100.0%; Score 2000; DB 3; Length 2000;																		
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;																		
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DB	1	ATG	GTG	TTG	AGT	TGAT	TCA	TGC	CGG	CTT	CTT	GTG	AAG	CA	TTG	GTG	CTC	60
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DB	61	AGG	AGC	AAG	TGG	CGA	AGT	GTC	GCC	TTC	TCC	TCT	GTC	GAG	GAG	CGG	CAAG	120
QY	121	ACG	CA	CGT	GCG	CACT	TTC	TGG	AGC	AGC	AGC	ACT	GTG	TAT	GAG	CACT	GAG	180
DB	121	ACG	CA	CGT	GCG	CACT	TTC	TGG	AGC	AGC	AGC	ACT	GTG	TAT	GAG	CACT	GAG	180
QY	181	ATG	GCG	AAG	TGG	TGC	CGC	CACT	GTG	CTT	CCC	CTG	TCA	GAG	GAG	AGT	GCA	240
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DB	241	GCG	CTT	CTG	GAG	CACT	GTG	TAT	GAG	CACT	GTG	TAT	GAG	CACT	GTG	GCA	300	

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RESULT 2
US-09-759-143-374
Sequence 374, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759.143
CURRENT FILING DATE: 2001-01-12


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; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-780-669-374

/ Sequence 374, Application US/09780669

/ Patent No. US2002005197A1

/ GENERAL INFORMATION:

/ APPLICANT: Xu, Jiangchun

/ APPLICANT: Dillon, David C.

/ APPLICANT: Mitcham, Jennifer L.

/ APPLICANT: Harlocker, Susan L.

/ APPLICANT: Jiang, Yuqun

/ APPLICANT: Henderson, Robert A.

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Reiter, Marc W.

/ APPLICANT: Stolk, John A.

/ APPLICANT: Day, Craig H.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Carter, Derrick

/ APPLICANT: Li, Samuel

/ APPLICANT: Wang, Aijun

/ APPLICANT: Skelley, Yaelir A.W.

/ APPLICANT: Hepler, William

/ APPLICANT: Hurai, John

/ APPLICANT: McNeill, Patricia D.

/ APPLICANT: Houghton, Raymond L.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

/ FILE REFERENCE: 210121.427C24

/ CURRENT APPLICATION NUMBER: US/09/780,669

/ CURRENT FILING DATE: 2001-02-09

/ NUMBER OF SEQ ID NOS: 943

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 374

/ LENGTH: 2000

/ TYPE: DNA

/ ORGANISM: Homo sapien

US-09-780-669-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGACAGAACACTGAAATATGCAAAATT 1380

Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGACAGAACACTGAAATATGCAAAATT 1380

QY 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGATCAAAAGAA 1440

Db 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGATCAAAAGAA 1440

QY 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGATCAAAAGAA 1440

Db 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGATCAAAAGAA 1440

QY 1441 AAAAGAGTCCAAATATCTCTTCTGAAAAACACCAACCCAGAACTTAATAGCTGAA 1500

Db 1441 AAAAGAGTCCAAATATCTCTTCTGAAAAACACCAACCCAGAACTTAATAGCTGAA 1500

QY 1441 AAAAGAGTCCAAATATCTCTTCTGAAAAACACCAACCCAGAACTTAATAGCTGAA 1500

Db 1441 AAAAGAGTCCAAATATCTCTTCTGAAAAACACCAACCCAGAACTTAATAGCTGAA 1500

QY 1501 TCAGAGAAAGATCAAAAAGCTTGAAGGCAAGTGAATAATGTGCACAGCAAGCTTAGAAAT 1560

Db 1501 TCAGAGAAAGATCAAAAAGCTTGAAGGCAAGTGAATAATGTGCACAGCAAGCTTAGAAAT 1560

Db 1501 TCAGAGGAGAGTCAAGAGCTTGAAGGAGTGAATGCGCAGCCAGGCTGAGAAAT 1560
Qy 1561 TTTATGGCTATCGAAGAAATGAAGACGAGAGTACTATGCTGGATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGAGTACTATGCTGGATTTCCAGAAAC 1620
Qy 1621 CTGACTAATGGTCCCTGCTGGCAATGATGATGATTAATTTCTCCAGAGAGAGC 1680
Db 1621 CTGACTAATGGTCCCTGCTGGCAATGATGATGATTAATTTCTCCAGAGAGAGC 1680
Qy 1681 AGAACACTGGAAGCAGCAATTTCTGACACTGAGATGAAGATACAGTACGAA 1740
Db 1681 AGAACACTGGAAGCAGCAATTTCTGACACTGAGATGAAGATACAGTACGAA 1740
Qy 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTACAGATGAG 1800
Db 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAGCAGATGAGTGTGAAAAATGAAATTTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATGAGTGTGAAAAATGAAATTTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAAAGAAAGAAAGCATCTTGCATGAAATAGTGGCGGAGAAAT 1920
Db 1861 CTTAGTTGTAAAGAAAGAAAGCATCTTGCATGAAATAGTGGCGGAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4

US-09-810-936-302
Sequence 302, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, Devin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
THERAPY AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810.936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTGGAGTGGATTCATGCGGGCTGCTCTTCTGTGAAGAGCCATTTGTCTC 60
Db 1 ATGGTGGTGGAGTGGATTCATGCGGGCTGCTCTTCTGTGAAGAGCCATTTGTCTC 60
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Db 61 AGAGCAAGATGGGCAAGTGTGCTGCCCTTCTCCCTGCTGACGAGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGGCGCACTGCTTCCCTGCTGACGAGGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGTGCGGCGCACTGCTTCCCTGCTGACGAGGAGTGGCAAGCAAGT 240
Qy 241 GGGCTTCTGAGAGACGAGACGACTGCTATGAGACACTCAGAAACAAGTGGCAAG 300
Db 241 GGGCTTCTGAGAGACGAGACGACTGCTATGAGACACTCAGAAACAAGTGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGACGAGGAGGCGGCAAGAGAGTGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGACGAGGAGGCGGCAAGAGAGTGGCGCTTGG 360
Qy 361 GGAAGCTTACGATGACAGTGTGCTTATGAGAGCCAGGTACAGTCCGTGGAGAAATCTG 420
Db 361 GGAAGCTTACGATGACAGTGTGCTTATGAGAGCCAGGTACAGTCCGTGGAGAAATCTG 420
Qy 421 GACAACTCCACAGAGCTGCTGAGGAGGAAAGTCCCAAGAAAGATCATGCTATG 480
Db 421 GACAACTCCACAGAGCTGCTGAGGAGGAAAGTCCCAAGAAAGATCATGCTATG 480
Qy 481 CTCAGGAGACATGACCTGAGACAGAAAGCAAGCAAGAGAGAGTCTCTACATCTG 540
Db 481 CTCAGGAGACATGACCTGAGACAGAAAGCAAGCAAGAGAGAGTCTCTACATCTG 540
Qy 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGAGACAGAGTCAATTTAT 600
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Qy 601 GTCCCTGACACAAAGAGAGCAGCTGTGATTAAGCCGTAAAGCCAGAGAAATGAG 660
Db 601 GTCCCTGACACAAAGAGAGCAGCTGTGATTAAGCCGTAAAGCCAGAGAAATGAG 660
Qy 661 TGTGCTTATGTTGTGTGAGACATGACAGTCCAAATATTCAGATGATGAGAAAT 720
Db 661 TGTGCTTATGTTGTGTGAGACATGACAGTCCAAATATTCAGATGATGAGAAAT 720
Qy 721 ACCACTCTGACACTGCTATCTATTAATGAAGATTAATGAGCCAAAGACTGCTCTTA 780
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Qy 781 TATGCTGCTGATTCGAATCAAAACCAAGCATGGCTCACACACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATTCGAATCAAAACCAAGCATGGCTCACACACTGTTACTTGGTGA 840
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Db 841 CATGACCAAAAACAGCAAGTGTGGAATTTTATCAAGAAAAACGAATTTAAATGCA 900
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Db 901 CTGAGATAGATGAGAGAGAGCTGCTCAATCTTGTGATGATGAGATGATGATGAT 960
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Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATATATCTGACAGAG 1020
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Db 1021 GCCAGAGATAGCTTTCTAGTCAATCAATGATTAATTTGACAGTTACTTCTGACTAC 1080
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Db 1081 AAGAGAAAACAGATGTAATAATCTTCTGAAAACAGCAATCAGAAACAGCTTTAAG 1140
Qy 1141 CTGACATCAGAGAAAGTCAAAAGTTCAAGAGATGAATAATGCCAGCCAGAGAAA 1200

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Db      1141 CTGACATCAGAGAGAGATCACAAAGTTCAAAGGAGTGAATAATAGCCAGCCAGAGAAA 1200
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Db      1201 ATGTCTCAAGAACCCAGAAATTAATAAGATGTGTATAGAGAGGTGAAGAATAATGAAG 1260
Qy      1261 AAGCATGAAAGTAATAATGTGGATTACTAGAAAACCTGACTAATGTGTCTGTGGC 1320
Db      1261 AAGCATGAAAGTAATAATGTGGATTACTAGAAAACCTGACTAATGTGTCTGTGGC 1320
Qy      1321 AATGTGTATATAGATTAACTTCTCAAGAGAGAGCAACACTGTAATGCAATTT 1380
Db      1321 AATGTGTATATAGATTAACTTCTCAAGAGAGAGCAACACTGTAATGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTAAGAA 1440
Qy      1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
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Db      1561 TTTATGCTATCGAAGAAATGAAGAAAGCACGAAAGTACTGATGTGGATTTCCAGAAAC 1620
Qy      1621 CTGACTAATGTGTCACATGCTGCAATGTGATGATGATTAATCTCCAGAGAAAGC 1680
Db      1621 CTGACTAATGTGTCACATGCTGCAATGTGATGATGATTAATCTCCAGAGAAAGC 1680
Qy      1681 AGAACCCTGAAAAGCCAGCAATTTCTGACACTGAGATGAGAGATCACACTGACGAA 1740
Db      1681 AGAACCCTGAAAAGCCAGCAATTTCTGACACTGAGATGAGAGATCACACTGACGAA 1740
Qy      1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
Db      1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAATAATGAAATCTGAGCTTTC 1860
Db      1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAATAATGAAATCTGAGCTTTC 1860
Qy      1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGAAATATGTAAGTTCGGGGAAGAAAT 1920
Db      1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGAAATATGTAAGTTCGGGGAAGAAAT 1920
Qy      1921 GCCATGCTAGACTGAGAGCTGAGACAAATGAAACATCAGAGCAGCTTAAAAAATAA 1980
Db      1921 GCCATGCTAGACTGAGAGCTGAGACAAATGAAACATCAGAGCAGCTTAAAAAATAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 5
US-09-822-827-374
; Sequence 374, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374

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; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374
Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGTGTGTGAGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGTCTC 60
Db      1 ATGTGTGTGAGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGTCTC 60
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Db      61 AGAGAGAGATGAGGCAAGTGTGCTGCCGTTTCCCTGCTGCAGGAGAGCGGCAAG 120
Qy      121 AGCAACGTGGGCACTTCTGAGACCAAGACGACTGTCTATGAAAGCACTCAGAGACAG 180
Db      121 AGCAACGTGGGCACTTCTGAGACCAAGACGACTGTCTATGAAAGCACTCAGAGACAG 180
Qy      181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAG 240
Db      181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAG 240
Qy      241 GCGGCTTCTGAGAGCAAGACGACTGTCTATGAAAGCACTCAGAGAAAGATGGCAAG 300
Db      241 GCGGCTTCTGAGAGCAAGACGACTGTCTATGAAAGCACTCAGAGAAAGATGGCAAG 300
Qy      301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
Db      301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
Qy      361 GGAAGTACAGATGACAGTGTCTTCAATGAGGCCAGTACCACTGCTGTGAGAAATCTG 420
Db      361 GGAAGTACAGATGACAGTGTCTTCAATGAGGCCAGTACCACTGCTGTGAGAAATCTG 420
Qy      421 GACAAAGCTCAAGAGCTGCTGCTGTGAGAGAGCGGCAAGAGTGTGAGTCACTG 480
Db      421 GACAAAGCTCAAGAGCTGCTGCTGTGAGAGAGCGGCAAGAGTGTGAGTCACTG 480
Qy      481 CTCAAGGACACTGAGCTGTAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTG 540
Db      481 CTCAAGGACACTGAGCTGTAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTG 540
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Db      541 TCTGCCAATGGGAATTCAGAAATGTAATCTCTGCTGCAAGACATGTCACTTAAT 600
Qy      601 GTCTTGAACAACAAAAGAGGACAGCTGATGAAGGCGCTCAATGCGAGGAAGTGA 660
Db      601 GTCTTGAACAACAAAAGAGGACAGCTGATGAAGGCGCTCAATGCGAGGAAGTGA 660
Qy      661 TGTGCTTAATGTGTGCTGAGACATGCACTGATCAATATTCAGATGAGTATGAAAT 720
Db      661 TGTGCTTAATGTGTGCTGAGACATGCACTGATCAATATTCAGATGAGTATGAAAT 720
Qy      721 ACCACTCTGCACTAGGCTATCTTAATGAAGTAAATTAATGCGCAAGACCTGCTT 780
Db      721 ACCACTCTGCACTAGGCTATCTTAATGAAGTAAATTAATGCGCAAGACCTGCTT 780
Qy      781 TATGGGTGATGATGAAATCAAAAAACAGATGAGCTGCAACCACTGTTACTGGTGA 840
Db      781 TATGGGTGATGATGAAATCAAAAAACAGATGAGCTGCAACCACTGTTACTGGTGA 840
Qy      841 CATGAGCAAAAAACAGAACTGTGAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
Db      841 CATGAGCAAAAAACAGAACTGTGAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
Qy      901 CTGATAGATATGAAAGCACTGCTCATATCTTGTCTGTATGTTGTGATCAGCAAGTATA 960
Db      901 CTGATAGATATGAAAGCACTGCTCATATCTTGTCTGTATGTTGTGATCAGCAAGTATA 960

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Db      661 TGGGCTTATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
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Db      721 ACCACTCTGCACTAGGCTATCTATATGAAATTAATGAGCCCAAGACCTGCTT 780
QY      781 TATGCTGATATCTGCAATCAAAAAAAGCATGAGCTGCAACACTGTTACTTGAT 840
Db      781 TATGCTGATATCTGCAATCAAAAAAAGCATGAGCTGCAACACTGTTACTTGAT 840
QY      841 CATGAGCAAAAACAGCAAGCTGGAATTTTATCAAGAAAAAGCGAATTTAAATGA 900
Db      841 CATGAGCAAAAACAGCAAGCTGGAATTTTATCAAGAAAAAGCGAATTTAAATGA 900
QY      901 CTGGATGATATGGAAGGAGCTGCTCATATCTGCTGATGTTGTTGATGAGACAGAT 960
Db      901 CTGGATGATATGGAAGGAGCTGCTCATATCTGCTGATGTTGTTGATGAGACAGAT 960
QY      961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020
Db      961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020
QY      1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db      1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY      1081 AAAAGAAAAACAGATGCTTAAAAATCTCTTCTGAAAAACGCAATCTCAACAACATTAAG 1140
Db      1081 AAAAGAAAAACAGATGCTTAAAAATCTCTTCTGAAAAACGCAATCTCAACAACATTAAG 1140
QY      1141 CTGACATCAGAGGAGATGCACAAAGTTTCAAGGAGTGAATAGCCAGCCAGAGAA 1200
Db      1141 CTGACATCAGAGGAGATGCACAAAGTTTCAAGGAGTGAATAGCCAGCCAGAGAA 1200
QY      1201 ATGCTTCAAGAACCAAAATTAATTAAGATGATGATGAGAGTTGAAGAAATGAAG 1260
Db      1201 ATGCTTCAAGAACCAAAATTAATTAAGATGATGATGAGAGTTGAAGAAATGAAG 1260
QY      1261 AAGCATGAAGATTAATGATGGAATTAATGAAACCTGACTAATGCTGCTGAC 1320
Db      1261 AAGCATGAAGATTAATGATGGAATTAATGAAACCTGACTAATGCTGCTGAC 1320
QY      1321 AATGCTGATTAATGATTAATCTCTCAAGGAGAGAGCAACCTGAAAAATCGCAATTT 1380
Db      1321 AATGCTGATTAATGATTAATCTCTCAAGGAGAGAGCAACCTGAAAAATCGCAATTT 1380
QY      1381 CCTGACAGAGAGATGAAGATYCAAGAAATTTGGAATTAATTTCTGACTACAAAGAA 1440
Db      1381 CCTGACAGAGAGATGAAGATYCAAGAAATTTGGAATTAATTTCTGACTACAAAGAA 1440
QY      1441 AAAACAATGCCAAATATCTCTTCTGAAAAACGCAACCCCAAGAACAACTTTAAAGCTGACA 1500
Db      1441 AAAACAATGCCAAATATCTCTTCTGAAAAACGCAACCCCAAGAACAACTTTAAAGCTGACA 1500
QY      1501 TCAGAGGAGAGATGCACAAAGCTTGAAGGAGTGAATGAGCCAGGCAAGATGAGAAAT 1560
Db      1501 TCAGAGGAGAGATGCACAAAGCTTGAAGGAGTGAATGAGCCAGGCAAGATGAGAAAT 1560
QY      1561 TTTATGCTATGCAAGAAATGAAGAGACGAAAGTACTATGTCGGAATTTCCAGAAAG 1620
Db      1561 TTTATGCTATGCAAGAAATGAAGAGACGAAAGTACTATGTCGGAATTTCCAGAAAG 1620
QY      1621 CTGACATTAATGATGCTGCTGCAATGATGATGATTAATTTCTCTCAAGAGAGAG 1680
Db      1621 CTGACATTAATGATGCTGCTGCAATGATGATGATTAATTTCTCTCAAGAGAGAG 1680
QY      1681 AGAACAAGTGAAGAGAGCAATTTCTGACATGAGAAATGAAGATGATCAAGTGAAG 1740
Db      1681 AGAACAAGTGAAGAGAGCAATTTCTGACATGAGAAATGAAGATGATCAAGTGAAG 1740
QY      1741 CAAATATGATCTGAGAGCAATTTTGTGAAGAACAGAACATGAAATATTACAGATGAG 1800

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Db      1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACAGAACATGATATTAACAGATGAG 1800
QY      1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGGTTGAAAAATGAAATTCGAGCTTCT 1860
Db      1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGGTTGAAAAATGAAATTCGAGCTTCT 1860
QY      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAAAAATGATCGTTGCGGAGAAATTT 1920
Db      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAAAAATGATCGTTGCGGAGAAATTT 1920
QY      1921 GCCATGCTPAGACTGAGAGCTAGACATGAAATCACTGAGGCACTTAAAAATTTAA 1980
Db      1921 GCCATGCTPAGACTGAGAGCTAGACATGAAATCACTGAGGCACTTAAAAATTTAA 1980
QY      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 7
US-09-924-400-302
; Sequence 302, Application US/09924400
; Patent No. US20020165371A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Lynda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C12
; CURRENT APPLICATION NUMBER: US/09/924,400
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-924-400-302

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Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGCTGTTGAGGATGATTCATGCGCGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
Db      1 ATGCTGTTGAGGATGATTCATGCGCGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
QY      61 AAGAGCAAGATGAGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
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QY      121 ACGAAGTGGGAGCTTCTGGAAGACAGAGCACTGCTATGAAGACATCTCAGAGAGCAAG 180
Db      121 ACGAAGTGGGAGCTTCTGGAAGACAGAGCACTGCTATGAAGACATCTCAGAGAGCAAG 180
QY      181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAACGTG 240
Db      181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAACGTG 240
QY      241 GCGGCTTCTGAGAGCAAGCACTCTGCTATGAAGACATGAGAGCAAGATGGGCAAG 300
Db      241 GCGGCTTCTGAGAGCAAGCACTCTGCTATGAAGACATGAGAGCAAGATGGGCAAG 300

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QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGGAGGCGAAGAGCAAGGTGGCGCTTGG 360
 DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGGAGGCGAAGAGCAAGGTGGCGCTTGG 360
 QY 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCCAAGTACACGTCCTGGAGAGATCTG 420
 DB 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCCAAGTACACGTCCTGGAGAGATCTG 420
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 DB 841 CATGAGCAAAAAACAGAGTCTGGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
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DB 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGCGAATTAAGTTTCTGATCAAAAGAA 1440
 QY 1441 AAACAGATGCCAAAATACTTCTGTAAGAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 DB 1441 AAACAGATGCCAAAATACTTCTGTAAGAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCGAGTGAATGGCCAGCAGAGCTAGAAAT 1560
 DB 1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCGAGTGAATGGCCAGCAGAGCTAGAAAT 1560
 QY 1561 TTTATGGCTATGGAAGAAATGAAGAGACGGAAGTCACTGATGGATTTCCAGAAAGAC 1620
 DB 1561 TTTATGGCTATGGAAGAAATGAAGAGACGGAAGTCACTGATGGATTTCCAGAAAGAC 1620
 QY 1621 CTGACTAATGCTGCACTGCTGGCAATGGTGAATGAATTAATTTCTTCAAGAGAGAGC 1680
 DB 1621 CTGACTAATGCTGCACTGCTGGCAATGGTGAATGAATTAATTTCTTCAAGAGAGAGC 1680
 QY 1681 AGAACACTGAAG 1740
 DB 1681 AGAACACTGAAG 1740
 QY 1741 CAAATGATATCTCAG 1800
 DB 1741 CAAATGATATCTCAG 1800
 QY 1801 ATTCTGATTCATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
 DB 1801 ATTCTGATTCATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
 QY 1861 CTTAGTTGTAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
 DB 1861 CTTAGTTGTAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
 QY 1921 GCCATGCTTAAGCTGAGAGTGAACAATGAAGAACTCAGAGGCACTTAAAGAGAGAG 1980
 DB 1921 GCCATGCTTAAGCTGAGAGTGAACAATGAAGAACTCAGAGGCACTTAAAGAGAGAG 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
 US-09-895-793-374
 ; Sequence 374, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yaelir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carloca
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Ranger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER


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FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGATTGATTCATGCGCGCTGCTCTTCTGTGAAGGCAATTTGGTCTC 60
DB 1 ATGGTGGTTGAGATTGATTCATGCGCGCTGCTCTTCTGTGAAGGCAATTTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTCCCTGGCTGCAGGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAAGACTCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAAGCAAGACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTCCGCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGTGG 240
DB 181 ATGGGCAAGTGGTGGTGGTCCGCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGTGG 240
QY 241 GGGGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGGAGGCAAGGATGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGGAGGCAAGGATGGGCGCTTGG 360
QY 361 GGAAGACTAGATGACAGTGGCTTCTGATGAGGCCAGAGTCAAGTCCGCTGAGAGAGTCTG 420
DB 361 GGAAGACTAGATGACAGTGGCTTCTGATGAGGCCAGAGTCAAGTCCGCTGAGAGAGTCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGGATCTACATCGCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGGATCTACATCGCATG 480
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DB 481 CTCAGGAGCACTGACCTGGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
QY 541 TCTGCCAAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGAGATGTCAATTAAT 600
DB 541 TCTGCCAAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGAGATGTCAATTAAT 600
QY 601 GTGCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGGCGGTAAATTCAGAGAGATGAA 660
DB 601 GTGCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGGCGGTAAATTCAGAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACCTCTATCTAATAAGAAATTAATGAGCAAGCACTGCTCTTA 780
DB 721 ACCACTCTGCACTACCTCTATCTAATAAGAAATTAATGAGCAAGCACTGCTCTTA 780
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DB 781 TATGGTGTGATATGCAATCAAAAACAGCATGGCTCAACACATGTTACTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGAAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGAAATTTAAATGCA 900
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DB 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGAAATTTAAATGCA 900
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DB 901 CTGGATATGATGGAAGAGCTGCTCATACTTGGCTGATATGTTGGATACAGCAATATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGGAACAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGGAACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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DB 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGAAATCCAGAACAACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCAAGTGAATTAAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCAAGTGAATTAAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAAACAGAAATAAATAGATGGTATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAAACAGAAATAAATAGATGGTATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGATTTACTAGAAAACTGACATTAATGTTCTACTGTGGC 1320
DB 1261 AAGCATGAAAGTAAATATGTTGGATTTACTAGAAAACTGACATTAATGTTCTACTGTGGC 1320
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DB 1321 AATGGTGAATATGATTAATTCCTCAAGGAAGAGCAGAACACCTGAAAAATCAGCAATTT 1380
QY 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
DB 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
DB 1441 AAAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCACTGAAAAATGGCCAGCAGAGCTAGAAAAAT 1560
DB 1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCACTGAAAAATGGCCAGCAGAGCTAGAAAAAT 1560
QY 1561 TTTATGGCTATCGAAAGAAATGAAGAGCAAGAGTACTCATGTGGATTTCCAGAAAAAC 1620
DB 1561 TTTATGGCTATCGAAAGAAATGAAGAGCAAGAGTACTCATGTGGATTTCCAGAAAAAC 1620
QY 1621 CTGACTAATGTTGGCCACTGCTGGCAATGGTATGATGATTAATTCCTCCAGAGAAAGAC 1680
DB 1621 CTGACTAATGTTGGCCACTGCTGGCAATGGTATGATGATTAATTCCTCCAGAGAAAGAC 1680
QY 1681 AGAACACCTGAAAGCAGAGCAATTTCTGCACTGAGAAATGAAGAGATCAAGTGCAGAA 1740
DB 1681 AGAACACCTGAAAGCAGAGCAATTTCTGCACTGAGAAATGAAGAGATCAAGTGCAGAA 1740
QY 1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
DB 1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
QY 1801 AATTCGATTCATGAAAGAAAGCAGATGAGAGTGTGTAAGAAAAATGAATTCAGACTTTCT 1860
DB 1801 AATTCGATTCATGAAAGAAAGCAGATGAGAGTGTGTAAGAAAAATGAATTCAGACTTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGAAAGCAATCTTGCAATGAATTAAGTACGTGGGGAAGAAAT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGAAAGCAATCTTGCAATGAATTAAGTACGTGGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAGCAATCAGAGCCAGCTTAATTAATTAATTA 1980
DB 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAGCAATCAGAGCCAGCTTAATTAATTAATTA 1980
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QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 9

US-09-895-814-374
Sequence 374, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepner, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTGTGTGAAGCAATTTGCTTC 60
Db 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTGTGTGAAGCAATTTGCTTC 60
QY 61 AGAGCAAGTGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGAGCAAGTGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGTGTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGTGTG 240
QY 241 GGGGCTTTGAGACAAGCAAGCACTGCTATGAAGCACTCAGAACTGAGGAGCAAG 300
Db 241 GGGGCTTTGAGACAAGCAAGCACTGCTATGAAGCACTCAGAACTGAGGAGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGCAAGTGTGAGGAGCTTGG 360
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGCAAGTGTGAGGAGCTTGG 360

QY 361 GGAGACTAGATGACATGCTTCATGAGCCCAAGTACCAGTCCGTGAGAAATCTG 420
Db 361 GGAGACTAGATGACATGCTTCATGAGCCCAAGTACCAGTCCGTGAGAAATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCGCAAGAAAGATCTCATGCTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCGCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGAGACATGACCTGGAACAAGAGCAAGCAAAAGAGAGTCTCTACATCTGGCC 540
Db 481 CTCAGGAGACATGACCTGGAACAAGAGCAAGCAAAAGAGAGTCTCTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTCTGGAACAGAGATCTCACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTCTGGAACAGAGATCTCACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGGACAGCTGATTAAGGCGGTACAAATGCGAGAAATGAA 660
Db 601 GTCTTGAACAACAAAAGAGGACAGCTGATTAAGGCGGTACAAATGCGAGAAATGAA 660
QY 661 TGTGCTTATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCTTATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTCTGACTACCTATCTATTAATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
Db 721 ACCACTCTGACTACCTATCTATTAATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
QY 781 TATGTGCTGATATGCAATCAAAAACAGCATGCGCTCACACACTGTTACTTGCTGA 840
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QY 901 CTGATATGATATGGAAGAGCTGCTCATATCTGCTGATATGTTGTGATCAGCAATATA 960
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QY 961 GTACGCTTCTACTGAGCAAAATATGATATCTTCAAGATATATCTGAGCAGAGC 1020
Db 961 GTACGCTTCTACTGAGCAAAATATGATATCTTCAAGATATATCTGAGCAGAGC 1020
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Db 1021 GCCAGAGATATGCTGTTCTATGTCATCATATGATTTGCAATTAATTTCTGACTAC 1080
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Db 1081 AAGAAAAACAGATGCTAAAAATCTCTGTAACAGCAATCTCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGTCAAAAGGTTCAAAAGGATGAAATATGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGGAAGTCAAAAGGTTCAAAAGGATGAAATATGCCAGCCAGAGAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGAATTAAGAAACCTGACTAATGATGTCTGCTGCGC 1320
Db 1261 AAGCATGAAGATTAATATGTTGGAATTAAGAAACCTGACTAATGATGTCTGCTGCGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGGAAGAGCAACCTGAAAAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGGAAGAGCAACCTGAAAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGTATCAGAAATTTTGAATTTGATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAAGTATCAGAAATTTTGAATTTGATTTCTGACTACAAAGAA 1440

QY 1441 AAACAGATGCCAAATATCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGTGACA 1500
Db 1441 AAACAGATGCCAAATATCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGTGACA 1500
QY 1501 TCAGAGAAAGAGTCACAAAGGCTTGAAGGCACTGAAATGCGCCAGCCAGCTAGAAAT 1560
Db 1501 TCAGAGAAAGAGTCACAAAGGCTTGAAGGCACTGAAATGCGCCAGCCAGCTAGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGCAAGTACTATGCGAATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGCAAGTACTATGCGAATTTCCAGAAAC 1620
QY 1621 CTGACTAATGCTGCCAATGCTGCAATGATGATGATTAATCTCCAGAAAGAGC 1680
Db 1621 CTGACTAATGCTGCCAATGCTGCAATGATGATGATTAATCTCCAGAAAGAGC 1680
QY 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGAGATGAGATGATCAAGTGACGA 1740
Db 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGAGATGAGATGATCAAGTGACGA 1740
QY 1741 CAAAAATGATCTAGAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATTTTACAGATGAG 1800
Db 1741 CAAAAATGATCTAGAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATTTTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAGAAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1860
Db 1801 ATTCTGATTCATGAGAAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGCAATCTTGCATGAAATGTAAGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAAGAAAGAAAGCAATCTTGCATGAAATGTAAGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAGAGCTGAGAGTACAGCAATGAAACATCAGAGCCAGCTTAAAGAAAGAA 1980
Db 1921 GCCATGCTAGAGCTGAGAGTACAGCAATGAAACATCAGAGCCAGCTTAAAGAAAGAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-10-012-896-374
; Sequence 374, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvik, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yaelir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27

; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-374

Query Match 100.0%; Score 2000; DB 5; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGGGTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGTCGCGTGTCTTCCCTGCTGAGGAGAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGTCGCGTGTCTTCCCTGCTGAGGAGAGCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGCTATGAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGCTATGAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGTCGCGTGTCTTCCCTGCTGAGGAGAGTGGCAAGCACTG 240
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QY 421 GACAAGCTCCAGAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCAGCATG 480
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Db 541 TCTGCCAATGGGAATTCAGAAATTAAGTCTGCTGAGACAGAGATGTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTGTAAGAGCCGTAATCCAGAGAAAGTGA 660
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Db 781 TATGGTGTGATATGCAATCAAAAAGAGATGCTCAGACCACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAAAGCAAGTGTGGAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAAAGCAAGTGTGGAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900


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QY 541 TCTGCAATGGGAATTGAGAGTGTAAATCTCTGTGGACAGAGATGTCAATTAAT 600
DB 541 TCTGCAATGGGAATTGAGAGTGTAAATCTCTGTGGACAGAGATGTCAATTAAT 600
QY 601 GTCTTGAACAACAAAAAGAGAGACAGCTGTGATTAAGCCGTACATGCGAGAAATGAA 660
DB 601 GTCTTGAACAACAAAAAGAGAGACAGCTGTGATTAAGCCGTACATGCGAGAAATGAA 660
QY 661 TGTGCGTTAATGTGTGGACATGGACATGCCAATATTCGAGATGAGTGTGAAT 720
DB 661 TGTGCGTTAATGTGTGGACATGGACATGCCAATATTCGAGATGAGTGTGAAT 720
QY 721 ACCACTGTGACCTACCTATCTATTAATGAAGATTAATTAAGCCAAAGACCTGCTTTA 780
DB 721 ACCACTGTGACCTACCTATCTATTAATGAAGATTAATTAAGCCAAAGACCTGCTTTA 780
QY 781 TATGTGTGTGATATCGAATCAAAAAAACAAGCATGGCCTCACACACTGTTACTTGTGTA 840
DB 781 TATGTGTGTGATATCGAATCAAAAAAACAAGCATGGCCTCACACACTGTTACTTGTGTA 840
QY 841 CATGACCAAAAAAGAGAGAGCTGTGAAATTTTATCAAGAAAAAAGCGAATTTAATGCA 900
DB 841 CATGACCAAAAAAGAGAGAGCTGTGAAATTTTATCAAGAAAAAAGCGAATTTAATGCA 900
QY 901 CTGATAGATATGAGAGAGACCTGCTCATATCTGTATGTGTGATCAGCAAGTATA 960
DB 901 CTGATAGATATGAGAGAGACCTGCTCATATCTGTATGTGTGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAACAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCCTTCTACTTGAACAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGAGATAGCTGTCTTACTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGAGATAGCTGTCTTACTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCAGAAACAGACTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGAGTGAATAATAGCCAGAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGAGTGAATAATAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATAGATGTGATGAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATAGATGTGATGAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATATATGTGGATTACTAGAAAACTGACTAATGCTGTCATGCTGGC 1320
DB 1261 AAGCATGAAGATATATGTGGATTACTAGAAAACTGACTAATGCTGTCATGCTGGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAATAATGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAATAATGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCACAAGATTTTGGAAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCACAAGATTTTGGAAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCGCAAAATCTCTTCTGAAAAACAGCAACCGAACAAGCTTAAGCTGACA 1500
DB 1441 AAACAGATGCGCAAAATCTCTTCTGAAAAACAGCAACCGAACAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGATCACAAGAGCTTGAAGGAGTGAATAATGCGCAGAGCTTAAGAAAT 1560
DB 1501 TCAGAGAGAGAGATCACAAGAGCTTGAAGGAGTGAATAATGCGCAGAGCTTAAGAAAT 1560
QY 1561 TTTATGGCTATTCGAAGAAATGAAGAGACAGAAATGTAATCTATGTGGATTTCCAGAAAC 1620
DB 1561 TTTATGGCTATTCGAAGAAATGAAGAGACAGAAATGTAATCTATGTGGATTTCCAGAAAC 1620

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QY 1621 CTGACTAATGTGTGCACTGTGGCAATGGTGAATGATTAATTTCTTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTGTGCACTGTGGCAATGGTGAATGATTAATTTCTTCAAGAAAGAC 1680
QY 1681 AGAAGACCTGAAAGCCAGCAATTTCTGTGACACTGAGATGAAGATATCAGTGAAGAA 1740
DB 1681 AGAAGACCTGAAAGCCAGCAATTTCTGTGACACTGAGATGAAGATATCAGTGAAGAA 1740
QY 1741 CAAATGATATCTCAGAAAGCAATTTTGTGAAGAACGAACACTGGAATATTAACAATGAG 1800
DB 1741 CAAATGATATCTCAGAAAGCAATTTTGTGAAGAACGAACACTGGAATATTAACAATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGAAAAATGAATTTCTGAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGAAAAATGAATTTCTGAGCTTTCT 1860
QY 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGATGAATAATGATACGTTGCGGAGAAATTT 1920
DB 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGATGAATAATGATACGTTGCGGAGAAATTT 1920
QY 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAATCATCAGAGCCAGTAAAAAATTTT 1980
DB 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAATCATCAGAGCCAGTAAAAAATTTT 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 12
US-10-212-679-302
; Sequence 302, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hixel, Shannon Kathleen
; APPLICANT: Dillon, David
; APPLICANT: Roy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Petersing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSB for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-302

Query Match      100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGTCTC 60
DB 1 ATGTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCTTCCCTGTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCTTCCCTGTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACGACGACTCTGATATGAAGACATCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACGACGACTCTGATATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAAGCTG 240

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QY 241 GGGCTTTGGAGACGACGACTCTGATGAGACACTCAGAACAGATGGGCAAG 300
 Db 241 GGGCTTTGGAGACGACGACTCTGATGAGACACTCAGAACAGATGGGCAAG 300
 QY 301 TGGTGCTGCACTGCTTCCCTCTGCGAGGGGAGCGGCAAGAGAGATGGGCGCTTGG 360
 Db 301 TGGTGCTGCACTGCTTCCCTCTGCGAGGGGAGCGGCAAGAGAGATGGGCGCTTGG 360
 QY 361 GGAGACTACGATGACAGTCTTCTATGAGCCGAGTACCACTCCGTGAGAGAGATCTG 420
 Db 361 GGAGACTACGATGACAGTCTTCTATGAGCCGAGTACCACTCCGTGAGAGAGATCTG 420
 QY 421 GACAGCTCAGAGAGTCTGCTGGTGGGAGTAAAGTCCCGCAAGAGATCTGATGATG 480
 Db 421 GACAGCTCAGAGAGTCTGCTGGTGGGAGTAAAGTCCCGCAAGAGATCTGATGATG 480
 QY 481 CTCAGGACACTGACGTCGAAACAAGAGACAGCAAGAGAGAGAGAGAGAGAGAGAG 540
 Db 481 CTCAGGACACTGACGTCGAAACAAGAGACAGCAAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 TCTGCCAATGGGAATTCAGAAATGATGAAATCTCTGTGAGACAGAGATCTCACTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAATGATGAAATCTCTGTGAGACAGAGATCTCACTTAAT 600
 QY 601 GTCTCTGACAAACAAAAAGAGACAGCTCTGATGAAAGGCGTACATGCGAGAAAGATGA 660
 Db 601 GTCTCTGACAAACAAAAAGAGACAGCTCTGATGAAAGGCGTACATGCGAGAAAGATGA 660
 QY 661 TGTGCGTTAATGTTGTGTCGAAACATGCGACATGATCCAAATTTTCAGATGATGGAAT 720
 Db 661 TGTGCGTTAATGTTGTGTCGAAACATGCGACATGATCCAAATTTTCAGATGATGGAAT 720
 QY 721 ACCACTCTGACACTACGCTATCTATTAATGATGATTAATGAGCAAGAGAGAGAGAG 780
 Db 721 ACCACTCTGACACTACGCTATCTATTAATGATGATTAATGAGCAAGAGAGAGAGAG 780
 QY 781 TATGCTGCTGATATTCGATTAACAAAAACAGCATGCGCTCACACATCTGTTACTGGTGA 840
 Db 781 TATGCTGCTGATATTCGATTAACAAAAACAGCATGCGCTCACACATCTGTTACTGGTGA 840
 QY 841 CATGACAAAAACAGCAAGTCTGATGATTTTATATCAAGAAAAAGGAAATTTAAATGCA 900
 Db 841 CATGACAAAAACAGCAAGTCTGATGATTTTATATCAAGAAAAAGGAAATTTAAATGCA 900
 QY 901 CTGATGATGATGAGAGAGCTGCTCTCATCTTCTGATGATGTTGTGATGAGCAAGATGA 960
 Db 901 CTGATGATGATGAGAGAGCTGCTCTCATCTTCTGATGATGTTGTGATGAGCAAGATGA 960
 QY 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 Db 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 QY 1021 GCCAGAGAGATGCTGTTCTAGTCATCATGATGATTTTGCAGTTACTTCTGACTAC 1080
 Db 1021 GCCAGAGAGATGCTGTTCTAGTCATCATGATGATTTTGCAGTTACTTCTGACTAC 1080
 QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCAGAACAGACTTTAAAG 1140
 Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCAGAACAGACTTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGCGTGAAGAAATGACCGACAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGCGTGAAGAAATGACCGACAGAGAAA 1200
 QY 1201 ATGCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATGAAG 1260
 Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAAATTAATGATGATTAATTAAGAAACCTGACTAATGCTGCTGCGC 1320
 Db 1261 AAGCATGAAAGTAAATTAATGATGATTAATTAAGAAACCTGACTAATGCTGCTGCGC 1320

QY 1321 AATGATGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 Db 1321 AATGATGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 QY 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTTGGATTTGTTCTGACTCAAGAAAG 1440
 Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTTGGATTTGTTCTGACTCAAGAAAG 1440
 QY 1441 AAAAGATGCAAAAAATTAATCTTCTGAAAAACAGCAACCAAGAACAGACTTTAAAGCTGACA 1500
 Db 1441 AAAAGATGCAAAAAATTAATCTTCTGAAAAACAGCAACCAAGAACAGACTTTAAAGCTGACA 1500
 QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 QY 1561 TTTATGCTATCGAAGAAATGAAAGAGACAGGAGTACTCATGTCGATTTCCAGAGAAAG 1620
 Db 1561 TTTATGCTATCGAAGAAATGAAAGAGACAGGAGTACTCATGTCGATTTCCAGAGAAAG 1620
 QY 1621 CTGACTAATGCTGCACTGTCGCAATGATGATGATTAATTCCTCAAGAGAGAGAG 1680
 Db 1621 CTGACTAATGCTGCACTGTCGCAATGATGATGATTAATTCCTCAAGAGAGAGAG 1680
 QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAAAGAGAGATGACAGTGAAGAA 1740
 Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAAAGAGAGATGACAGTGAAGAA 1740
 QY 1741 CAAAAATGATCTAGAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
 Db 1741 CAAAAATGATCTAGAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
 QY 1801 ATTCTGATTCATGAGAGAGAGAGAGAGATGATGATGATTAATTCCTGAGCTTTCT 1860
 Db 1801 ATTCTGATTCATGAGAGAGAGAGAGAGATGATGATGATTAATTCCTGAGCTTTCT 1860
 QY 1861 CTTAGTTTGAAG 1920
 Db 1861 CTTAGTTTGAAG 1920
 QY 1921 GCCATGCTAAG 1980
 Db 1921 GCCATGCTAAG 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 RESULT 13
 US-10-144-678A-374
 / Sequence 374, Application US/10144678A
 / Publication No. US20030157089A1
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yugu
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick L.
 / APPLICANT: Wang, Aijun
 / APPLICANT: Skeiky, Yasir A. W.
 / APPLICANT: Hepler, William T.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.

```
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals Y de Bassols, Carlota
/ APPLICANT: Roy, Teresa M.
/ APPLICANT: Matanabe, Yoshihiro
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C28
/ CURRENT APPLICATION NUMBER: US/10/144,678A
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-144-678A-374

Query Match      100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGTGCTTGAAGTTGATTCATGCGCGCTCTCTTCTGTGAAGACCATTTGGTCTC 60
DB      1  ATGTGCTTGAAGTTGATTCATGCGCGCTCTCTTCTGTGAAGACCATTTGGTCTC 60

QY      61  AGGAGCAAGATGGGCAAGTGTGCTGCGCTTGTCTCCCTGCTGCAAGGAGCGGCAAG 120
DB      61  AGGAGCAAGATGGGCAAGTGTGCTGCGCTTGTCTCCCTGCTGCAAGGAGCGGCAAG 120

QY      121  AGCAACGTGGGCACTTCTGAGACAAGACGACTGTCTATGAAGACACTCAGAGCAAG 180
DB      121  AGCAACGTGGGCACTTCTGAGACAAGACGACTGTCTATGAAGACACTCAGAGCAAG 180

QY      181  ATGGGCAAGTGTGCGCGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGCG 240
DB      181  ATGGGCAAGTGTGCGCGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGCG 240

QY      241  GGGGCTTCTGGAGACCAAGCAAGCACTGTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
DB      241  GGGGCTTCTGGAGACCAAGCAAGCACTGTGCTATGAAGACACTCAGAAAGATGGGCAAG 300

QY      301  TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
DB      301  TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGCAAGTGGCGCTTGG 360

QY      361  GGAAGACTACATGACAGTGTCTTCAATGAGCCCAAGGTACCAAGTGTGAGAGATCTTG 420
DB      361  GGAAGACTACATGACAGTGTCTTCAATGAGCCCAAGGTACCAAGTGTGAGAGATCTTG 420

QY      421  GACAACTCCACAGAGCTGCTGTGTGGGGTTAAAGTCCCGCAAGAAAGATCTCATGCTATG 480
DB      421  GACAACTCCACAGAGCTGCTGTGTGGGGTTAAAGTCCCGCAAGAAAGATCTCATGCTATG 480

QY      481  CTCAGAGGACACTGACGTGAACAAAGAAAGCAAGCAAAAGAGAGACTGCTTCAATCTGGCC 540
DB      481  CTCAGAGGACACTGACGTGAACAAAGAAAGCAAGCAAAAGAGAGACTGCTTCAATCTGGCC 540

QY      541  TCTGCCAATGGGAATTCAGAAAGTAACTCTCTGTCGACAGAGATGTCAACTTAAT 600
DB      541  TCTGCCAATGGGAATTCAGAAAGTAACTCTCTGTCGACAGAGATGTCAACTTAAT 600

QY      601  GTCCTTGAACAACAAAAGAGAGACAGCTCTGATAAAGCGGTAAATGCCAGAGAAATGGA 660
DB      601  GTCCTTGAACAACAAAAGAGAGACAGCTCTGATAAAGCGGTAAATGCCAGAGAAATGGA 660

QY      661  TGTGCGTTATGTTGTGCAACATGCACTGATCCAAATTTCCAGATGATGGAAT 720
DB      661  TGTGCGTTATGTTGTGCAACATGCACTGATCCAAATTTCCAGATGATGGAAT 720

QY      721  ACCACTCTGACCTACCGTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCTTGA 780
DB      721  ACCACTCTGACCTACCGTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCTTGA 780
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QY      781  TATGGTCTGATATGGAATCAAAAAACAAGATGGCTCAGACCACTGTTACTGGGTGA 840
DB      781  TATGGTCTGATATGGAATCAAAAAACAAGATGGCTCAGACCACTGTTACTGGGTGA 840

QY      841  CATGAGCAAAAAACAGAGTGTGAAATTTTATCAAGAAAAAAGCAATTTAATGCA 900
DB      841  CATGAGCAAAAAACAGAGTGTGAAATTTTATCAAGAAAAAAGCAATTTAATGCA 900

QY      901  CTGATATGATATGGAAGACTGCTCATACTTGGTGTATGTTGGATACACCAAGTAA 960
DB      901  CTGATATGATATGGAAGACTGCTCATACTTGGTGTATGTTGGATACACCAAGTAA 960

QY      961  GTCAAGCTTCTACTGAGCAAAATATATGATCTTCTCAAGATCTATCTGGAACAGAG 1020
DB      961  GTCAAGCTTCTACTGAGCAAAATATATGATCTTCTCAAGATCTATCTGGAACAGAG 1020

QY      1021  GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB      1021  GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

QY      1081  AAAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACGCAATCCAGAACAAACTTAAAG 1140
DB      1081  AAAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACGCAATCCAGAACAAACTTAAAG 1140

QY      1141  CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAAGTAAATAGCCAGCCAGAGAA 1200
DB      1141  CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAAGTAAATAGCCAGCCAGAGAA 1200

QY      1201  ATGTCTCAAGAAACAGAAATTAATAAGATGAGTATGAGAGGTTGAAGAAATGAAG 1260
DB      1201  ATGTCTCAAGAAACAGAAATTAATAAGATGAGTATGAGAGGTTGAAGAAATGAAG 1260

QY      1261  AAGCATGAAAGTAAATATGTTGGATTTCTAGAAAACTGACTAATGTGTCTCTGTGGC 1320
DB      1261  AAGCATGAAAGTAAATATGTTGGATTTCTAGAAAACTGACTAATGTGTCTCTGTGGC 1320

QY      1321  AATGGTAAATATGATTAATTTCTCAAGAGAAAGAGAGAACACTGAAATCAGCAATTT 1380
DB      1321  AATGGTAAATATGATTAATTTCTCAAGAGAAAGAGAGAACACTGAAATCAGCAATTT 1380

QY      1381  CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
DB      1381  CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440

QY      1441  AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
DB      1441  AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500

QY      1501  TCAGAGAAAGATGCAAAAAGCTTGAAGGCAAGTGAATGGCCAGCAGAGCTAGAAAT 1560
DB      1501  TCAGAGAAAGATGCAAAAAGCTTGAAGGCAAGTGAATGGCCAGCAGAGCTAGAAAT 1560

QY      1561  TTTATGCTATGAAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAAAC 1620
DB      1561  TTTATGCTATGAAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAAAC 1620

QY      1621  TTTATGCTATGAAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAAAC 1680
DB      1621  TTTATGCTATGAAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAAAC 1680

QY      1681  AGAACACCTGAAAGCAGAGCAATTTCTGTCACATGAAATGAAGAGATCAGAGTGCAGAA 1740
DB      1681  AGAACACCTGAAAGCAGAGCAATTTCTGTCACATGAAATGAAGAGATCAGAGTGCAGAA 1740

QY      1741  CAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
DB      1741  CAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800

QY      1801  ATTCTGATTCATGAAGAAAGAGATGAGAGTGTGTAAGAAAAATGAATTTCTGAGCTTTCT 1860
DB      1801  ATTCTGATTCATGAAGAAAGAGATGAGAGTGTGTAAGAAAAATGAATTTCTGAGCTTTCT 1860
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Accession	Sequence	Year
Oy	TTTGTTGTAGAAGAAAAGACACTCTTGATGAAATAGTACGTCGGGGAAGAAATT	1920
Db	CTTGTTGTAGAAGAAAAGACACTCTTGATGAAATAGTACGTCGGGGAAGAAATT	1920
Oy	GCCATGCTAAGACTGAGAGCTAGACACAAATGAAACATCAGAGCCAGCTTAAAAA	1980
Db	GCCATGCTAAGACTGAGAGCTAGACACAAATGAAACATCAGAGCCAGCTTAAAAA	1980
Oy	AAAAA	2000
Db	AAAAA	2000

RESULT 14

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US-10-033-527-6
Sequence 6, Application US/10033527
Publication No. US20030170631A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, Davin C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jianshun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
OF INFECTION: AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.513C1
CURRENT APPLICATION NUMBER: US/10/033,527
CURRENT FILING DATE: 2001-10-27
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-10-033-527-6

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Query Match	100.0%;	Score 2000;	DB 6;	Length 2000;
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Best local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGGAGTGTGAGTTGATTCATGCGCGGCTGCTCTTGTGGAGAAACCATTTGGTCTC	60
Db	1	ATGGTGGTTGAGGTTGATTCCATGCCGGCTGCTCTTCTGTGAGAAACCATTTGGTCTC	60
QY	61	AGAGCAAGATGGGCAAGTGGTGTGCTGCCGTTGCTCCCTGCTGACGAGAGCGGCAAG	120
Db	61	AGAGCAAGATGGGCAAGTGGTGGTGGCGCTTGCTTCCCTGCTGACGAGAGCGGCAAG	120
QY	121	AGCAACGTGGGCACTTTCTGGAGACCAACAACAATCTGCTATGAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTTCTGGAGACCAACAACAATCTGCTATGAGACACTCAGAGGCAAG	180
QY	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGTGG	240
Db	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGTGG	240
QY	241	GGCGCTTCTGAGAACCAAGACGACTCTGCTATGAAACACTCAGGAACAAATGGGCAAG	300
Db	241	GGCGCTTCTGAGAACCAAGACGACTCTGCTATGAAACACTCAGGAACAAATGGGCAAG	300
QY	301	TGGTGTGGCCACTGTTTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
Db	301	TGGTGTGGCCACTGTTTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGCCTTCACTGAGGCCAGGTACCAAGTCCCTGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCACTGAGGCCAGGTACCAAGTCCCTGAGAAAGATCTG	420
QY	421	GACCAAGCTCCACAAGAGCTGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATGCTCATG	480
Db	421	GACCAAGCTCCACAAGAGCTGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATGCTCATG	480

OY	4481	TTGAGGGACACTTGAACGTGAAACAAGAAGACACAGCAAAAAGAGACTGCTCTTCAATCTGGCC	540
Dd	4481	CTCAGAGGACACTGACGTGAACAAGAAGACACAAGAAAGAGACTGCTCTTCAATCTGGCC	540
OY	5441	TCTGGCAATGGGAATTTCAGAGTGTAATAAATCTCGCTGGACAGACGATGCACCTTAAT	600
Dd	5441	TCTGCCAATGGGAATTTCAGAGTGTAATAAATCTCGCTGGACAGACGATGCACCTTAAT	600
OY	601	GTCCTTGACAACAAAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCAGGAAGATGAA	660
Dd	601	GTCCTTGACAACAAAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCAGGAAGATGAA	660
OY	661	TGTGGCTTAATGTTGCTGGAACATGCGACTCATCCAAATATTTCCAGATGAGTATGAAAT	720
Dd	661	TGTGGCTTAATGTTGCTGGAACATGCGACTCATCCAAATATTTCCAGATGAGTATGAAAT	720
OY	721	ACCACTCTGCACCTACGCTATCTATATGAAGAATAAATTAATGGCCAAGCACCTGCTCTTA	780
Dd	721	ACCACTCTGCACCTACGCTATCTATATGAAGAATAAATTAATGGCCAAGCACCTGCTCTTA	780
OY	781	TATGGTGCTGATATCGAATCAAAAAACAAGCATGGCCCTCACACCACCTGTTACTTGGTGTA	840
Dd	781	TATGGTGCTGATATCGAATCAAAAAACAAGCATGGCCCTCACACCACCTGTTACTTGGTGTA	840
OY	841	CATGAGCAAAAACAGCAAATGCTGTAATTTTTTAATCAAGAAAAAGCAATTTAATATGCA	900
Dd	841	CATGAGCAAAAACAGCAAATGCTGTAATTTTTTAATCAAGAAAAAGCAATTTAATATGCA	900
OY	901	CTGATATGATATGGAAGAACCTGCTCTCATCTTGGCTGATGTTGTTGGATCAGCAAGTATA	960
Dd	901	CTGATATGATATGGAAGAACCTGCTCTCATCTTGGCTGATGTTGTTGGATCAGCAAGTATA	960
OY	961	GTCAGCCCTTCTACTTGGACAAAATATTGATGTAATCTTCTCAAGATCTATCTGCACAGC	1020
Dd	961	GTCAGCCCTTCTACTTGGACAAAATATTGATGTAATCTTCTCAAGATCTATCTGCACAGC	1020
OY	1021	GCCAGAGAGTAGTGTGTTCTTAGTCATCATCATGTAATTTGCGAGTTACTTCTGACTAC	1080
Dd	1021	GCCAGAGAGTAGTGTGTTCTTAGTCATCATCATGTAATTTGCGAGTTACTTCTGACTAC	1080
OY	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAAAGACTTAAAG	1140
Dd	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAAAGACTTAAAG	1140
OY	1141	CTGCATCATGAGGAAGAGTCACAAAGGTTCAAAGGAGTGAATAATGACCGCAGAGAAA	1200
Dd	1141	CTGCATCATGAGGAAGAGTCACAAAGGTTCAAAGGAGTGAATAATGACCGCAGAGAAA	1200
OY	1201	ATGCTCTAGAACCCAGAAATTAATATGAAGTGTGATAGAGGAGTTGAAGAAATGAAG	1260
Dd	1201	ATGCTCTAGAACCCAGAAATTAATATGAAGTGTGATAGAGGAGTTGAAGAAATGAAG	1260
OY	1261	AAGCATGAAGTAATTAATGTTGGATTTTCTAGAAAACCTGACTAATGTTGTCACCTGCTGGC	1320
Dd	1261	AAGCATGAAGTAATTAATGTTGGATTTTCTAGAAAACCTGACTAATGTTGTCACCTGCTGGC	1320
OY	1321	AATGTTGATATGATTTAAATTCCTCAAGGAAGGACGAACACCTGAAATATACGCAATTT	1380
Dd	1321	AATGTTGATATGATTTAAATTCCTCAAGGAAGGACGAACACCTGAAATATACGCAATTT	1380
OY	1381	CCTGACAAACGAATGGAAGAGTATCAGAGATTTTGGCAATTAAGTTTCTGACTACAAAGAA	1440
Dd	1381	CCTGACAAACGAATGGAAGAGTATCAGAGATTTTGGCAATTAAGTTTCTGACTACAAAGAA	1440
OY	1441	AAACAGATGCCAAATATCTCTTCTGAAAACGCAACCCAGAACAAAGCTTAAAGCTGACA	1500
Dd	1441	AAACAGATGCCAAATATCTCTTCTGAAAACGCAACCCAGAACAAAGCTTAAAGCTGACA	1500
OY	1501	TCACAGGAAGGTACAAAGGCTTGAAGGGACGTGAATATGCCCAGCCAGAGCTTGAAGAAAT	1560
Dd	1501	TCACAGGAAGGTACAAAGGCTTGAAGGGACGTGAATATGCCCAGCCAGAGCTTGAAGAAAT	1560
OY	1561	TTTATGTCATTCGAAGAAATGAAGAACACGGAAGTACTGATGTCGATTTCCAGAAAC	1620

DB 1561 TTATGGCTATCGAATAAAGAAAGACGGAAGTACTATGCGAATTCACAGAAAC 1620
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DB 1621 CTGACTAAATGGTCCCTGCTGGCAATGGATGATGATTAATTTCTCCAGAGAAAGC 1680
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DB 1681 AGAACAACCTGAAAGCAGCAATTTCTGACACTGAGAATGAAGATATCAAGTGCAGAA 1740
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QY 1921 GCCATGCTAAGACTGAGAGCTAGACACATGATAACATCAGAGCCAGCTAAAAA 1980
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QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

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; Sequence 374, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Skolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-374

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCGGCTGCTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGGCGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGACAGT 240
DB 181 ATGGGCAAGTGGGCGGCGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGACAGT 240

QY 241 GCGGCTTCTGAGACCAAGCAAGTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300
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DB 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
QY 361 GGAAGCTACAGTACAGAGGCTTCATGAGAGCCAGGTACCAAGTCCGAGGAATGCG 420
DB 361 GGAAGCTACAGTACAGAGGCTTCATGAGAGCCAGGTACCAAGTCCGAGGAATGCG 420
QY 421 GACAAGCTCCAGAGAGTGCCTGTGGGTAAGTCCCAAGAAAGATCTCATCTCATG 480
DB 421 GACAAGCTCCAGAGAGTGCCTGTGGGTAAGTCCCAAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGGAACCTGACGTGAACAAGAGCAAGCAAAAGAGGACTGCTCATCTGCGC 540
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QY 901 CTGATATGATGAGAGAGCTGCTCATCTGCTGATATGTTGAGATCAGCAAGTATA 960
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QY 1261 AAGCATGAAGATTAATGTTGGATTAATCAAGAAACCTGACTTAATGTTGCTGCGC 1320
DB 1261 AAGCATGAAGATTAATGTTGGATTAATCAAGAAACCTGACTTAATGTTGCTGCGC 1320
QY 1321 AATGATATATGATTAATTTCTCAAGGAAGAGAGCAACTGAAATCAGCAATTT 1380

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Db 1321 ||||| 1380
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Db 1381 CCTGACACGAAAGTAGAGATCAAGAAATTTGCGAATTAGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTGTGAAAACAGCAACCAGAACAGAATTAAAGCTGACA 1500
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QY 1501 TCAGAGGAAAGTCACAAAGGCTTTGAGGCGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
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QY 1861 CTTAGTTGTAGAAAGAAAGAACATCTTGCATGAAATATGTAAGTTGCGGGAAGAAAT 1920
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Job time : 1633.72 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(Without alignments)
4025.047 Million cell updates/sec

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Perfect score: 2000

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Gapop 60.0 , Gapext 60.0

Searched: 4161431 seqs, 245089505 residues

Word size : 0

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Minimum DB seq length: 10

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Post-Processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	37	1.8	201	6	US-10-995-561-30293
C 3	37	1.8	201	6	US-10-995-561-30411
C 4	37	1.8	201	6	US-10-995-561-30414
C 5	37	1.8	148220	7	US-11-121-086-90
C 6	37	1.8	187986	6	US-10-995-561-13252
C 7	35	1.8	201	6	US-10-995-561-26191
C 8	35	1.8	201	6	US-10-995-561-46434
C 9	35	1.8	201	6	US-10-995-561-73430
C 10	35	1.8	600	7	US-11-123-896-256
C 11	35	1.8	722	6	US-10-689-742-79
C 12	35	1.8	1279	7	US-11-179-411-31
C 13	35	1.8	1279	7	US-11-175-766-31
C 14	35	1.8	1478	6	US-10-909-125-1744
C 15	35	1.8	1968	6	US-10-131-826A-163
C 16	35	1.8	2036	6	US-10-996-217A-8
C 17	35	1.8	2120	7	US-11-167-856-29
C 18	35	1.8	3001	7	US-11-145-703-153
C 19	35	1.8	3001	7	US-11-145-703-187
C 20	35	1.8	14082	6	US-10-995-561-13445
C 21	35	1.8	153376	7	US-11-121-086-5
C 22	35	1.8	171732	7	US-11-121-086-98
C 23	35	1.8	172543	7	US-11-121-086-6
C 24	35	1.8	181172	7	US-11-121-086-41

24	35	1.8	186442	7	US-11-121-086-104	Sequence 104, App
25	35	1.8	191684	7	US-11-121-086-2	Sequence 2, Appl1
C 26	35	1.8	200628	7	US-11-121-086-62	Sequence 62, Appl1
C 27	35	1.8	305312	6	US-10-995-561-13236	Sequence 13236, A
C 28	35	1.8	645179	6	US-10-995-561-13293	Sequence 13293, A
C 29	34	1.7	201	6	US-10-995-561-24366	Sequence 24366, A
C 30	34	1.7	201	6	US-10-995-561-24433	Sequence 24433, A
C 31	34	1.7	201	6	US-10-995-561-24470	Sequence 24470, A
C 32	34	1.7	201	6	US-10-995-561-50304	Sequence 50304, A
C 33	34	1.7	201	6	US-10-995-561-50700	Sequence 50700, A
C 34	34	1.7	201	6	US-10-995-561-50702	Sequence 50702, A
C 35	34	1.7	201	6	US-10-995-561-50871	Sequence 50871, A
C 36	34	1.7	201	6	US-10-995-561-55817	Sequence 55817, A
C 37	34	1.7	398	7	US-11-123-896-262	Sequence 262, App
C 38	34	1.7	470	7	US-11-123-896-88	Sequence 88, Appl1
C 39	34	1.7	517	7	US-11-123-896-467	Sequence 467, App
C 40	34	1.7	551	7	US-11-123-896-358	Sequence 358, App
C 41	34	1.7	602	7	US-11-077-386-7	Sequence 7, Appl1
C 42	34	1.7	778	6	US-10-986-501-38	Sequence 38, Appl1
C 43	34	1.7	958	7	US-11-179-411-5	Sequence 5, Appl1
C 44	34	1.7	958	7	US-11-175-766-5	Sequence 5, Appl1
C 45	34	1.7	1088	6	US-10-131-826A-549	Sequence 549, App

ALIGNMENTS

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; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30293
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-30293

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; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30411
; LENGTH: 201
; TYPE: DNA
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/ ORGANISM: Homo sapiens
US-10-995-561-30411

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Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 148 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 112

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; Sequence 30414, Application US/10995561
; Publication No. US20050272054A1

/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559

/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 30414

/ LENGTH: 201

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-995-561-30414

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; Sequence 90, Application US/11121086
; Publication No. US20050266459A1

/ GENERAL INFORMATION:
/ APPLICANT: POUlsen, TIM S.

/ APPLICANT: NIELSEN, KIRSTEN V.

/ TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

/ FILE REFERENCE: 09138.6000-0.00000

/ CURRENT APPLICATION NUMBER: US/11/121,086

/ CURRENT FILING DATE: 2005-05-04

/ PRIOR APPLICATION NUMBER: 60/567,570

/ NUMBER OF SEQ ID NOS: 107

/ SOFTWARE: PatentIn version 3.3

/ SEQ ID NO 90

/ LENGTH: 148220

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-11-121-086-90

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Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ Sequence 13252, Application US/10995561
; Publication No. US20050272054A1

/ GENERAL INFORMATION:

/ APPLICANT: CARGILL, Michele et al.

/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

/ TITLE OF INVENTION: DETECTION AND USES THEREOF

/ FILE REFERENCE: CL001559

/ CURRENT APPLICATION NUMBER: US/10/995,561

/ CURRENT FILING DATE: 2004-11-24

/ NUMBER OF SEQ ID NOS: 85702

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 13252

/ LENGTH: 187986

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY: misc.feature

/ LOCATION: (1)...(187986)

/ OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13252

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Best Local Similarity 100.0%; Pred. No. 1.1e-05;
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; Sequence 26191, Application US/10995561
; Publication No. US20050272054A1

/ GENERAL INFORMATION:

/ APPLICANT: CARGILL, Michele et al.

/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

/ TITLE OF INVENTION: DETECTION AND USES THEREOF

/ FILE REFERENCE: CL001559

/ CURRENT APPLICATION NUMBER: US/10/995,561

/ CURRENT FILING DATE: 2004-11-24

/ NUMBER OF SEQ ID NOS: 85702

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 26191

/ LENGTH: 201

/ TYPE: DNA

/ ORGANISM: Homo sapiens

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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 152 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 118

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; Sequence 46434, Application US/10995561
; Publication No. US20050272054A1

/ GENERAL INFORMATION:

/ APPLICANT: CARGILL, Michele et al.

/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

/ TITLE OF INVENTION: DETECTION AND USES THEREOF

/ FILE REFERENCE: CL001559

/ CURRENT APPLICATION NUMBER: US/10/995,561

/ CURRENT FILING DATE: 2004-11-24

/ NUMBER OF SEQ ID NOS: 85702

APPLICANT: Tumas, Daniel

APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K

Db 603 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 569

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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
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PRIOR FILING DATE: 1997-06-18
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PRIOR FILING DATE: 1997-08-26
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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
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TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-163
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Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
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```
RESULT 15
US-10-996-217A-8/C
Sequence 8, Application US/10996217A
Publication No. US2005026561A1
GENERAL INFORMATION:
APPLICANT: Revivicor, Inc.
APPLICANT: Wells, Kevin
TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
FILE REFERENCE: 10785.105070 REV 1015 US
CURRENT APPLICATION NUMBER: US/10/996,217A
CURRENT FILING DATE: 2004-11-22
PRIOR APPLICATION NUMBER: 60/523,938
PRIOR FILING DATE: 2003-11-21
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 2036
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-996-217A-8
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Query Match 1.8%; Score 35; DB 6; Length 2036;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
|||||
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:08:19 ; Search time 8061.39 Seconds
(without alignment)
11607.702 Million cell updates/sec

Title: US-09-924-400-302

Sequence: 1 atggtggttgaggtgagtcgattc.....aaaaaaaaaaaaaaaaaaaaa 2000

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82154912

Minimum DB seq length: 10
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492	24.6	729	5	BU930826 AGENCOURT
2	184	-9.2	521	9	AO204617 HS 3229 B
3	141	7.0	865	2	BF676987 602084215
4	140	7.0	451	1	AI804773
5	137	6.9	289	1	AA53501
6	129	6.5	531	9	AO615477 HS 5144.8
7	117	5.9	621	3	BM763942 K-EST0045
8	117	5.9	633	3	BM763453 K-EST0044
9	117	5.9	817	5	BQ441373 AGENCOURT
10	90	4.5	263	10	AG192933
11	89	4.5	400	9	AO124119 HS 3122 A
12	87	4.3	399	9	AO030111 RPII1-39
13	87	4.3	544	1	AL703938 DRFP686E
14	79	4.0	279	3	BI461255 603206584
15	76	3.8	6098	4	BSM809370
16	74	3.7	505	5	BX492731
17	73	3.6	385	5	AO063365 CIT-HSP-2
18	73	3.2	232	5	BU584009 2275475H1
19	64	3.2	381	7	CR747857 CR747857
20	59	2.9	707	10	AG045796 Pan trogl
21	57	2.9	607	9	B48260 RPII1-6K4
22	52	2.6	380	2	BF329652 RC6-BN027

23	50	2.5	592	9	AQ372700 RPII1-14
24	49	2.5	493	10	AG193231
25	49	2.5	495	9	AO469831 CITBI-E1-
26	49	2.5	557	9	AO469663 CITBI-E1-
27	49	2.5	667	10	AG156382
28	49	2.5	697	9	AO030113 RPII1-39
29	47	2.4	187	2	BE069869 CM1-RN039
30	46	2.3	351	7	CV383025 QVO-FN018
31	46	2.3	400	9	AO057106
32	45	2.2	218	5	BU584404 3967290H1
33	45	2.2	259	5	BU584020 4133307H1
34	45	2.2	338	5	BU584405 3967290T6
35	45	2.2	423	5	BU584403 3967290F6
36	45	2.2	874	6	CD358418 AGENCOURT
37	45	2.2	894	2	BF675049 602136643
38	45	2.2	5483	4	BC063888 Homo sapi
39	44	2.2	460	9	AO360298 HS 5035 A
40	41	2.1	476	9	AO392059 CITBI-E1-
41	41	2.1	710	10	AG165908 Pan trogl
42	41	2.1	770	5	BU611819 UI-M-F10-
43	40	2.0	184	1	AW302924 XR86907.x
44	40	2.0	199	1	AW302925 XR86908.x
45	40	2.0	224	1	AI344928 TB01804.x

ALIGNMENTS

RESULT 1
BU930826
LOCUS
DEFINITION
AGENCOURT_10425351 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:668956
5', mRNA sequence.
ACCESSION
BU930826
VERSION
BU930826.1 GI:24119645
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 729)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LBLM2943 row: 0 column: 04
High quality sequence stop: 555.
Location/Qualifiers
1. 729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:668956"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccgcctggcc); Site 2: SfiI
(ggccatcggcc); 5' and 3' adaptor were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGACC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGACGCGCCACATG-AT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones

FEATURES

source

ORIGIN and was constructed by Clontech Laboratories (Palo Alto, CA)."

Query Match 24.6%; Score 492; DB 5; Length 729;
Best Local Similarity 100.0%; Pred. No. 4,2e-229;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 AGGCGTACAAATCCGAGAGATGAATGGCGTAAATGGTGGAGAACTGGACGATC 694
DB 89 AGGCGTACAAATCCGAGAGATGAATGGCGTAAATGGTGGAGAACTGGACGATC 148
QY 695 CAAATATCCAGATGAGTATGAAATACCACTGCTGCACTACCTATCTATTAAGAGATA 754
DB 149 CAAATATCCAGATGAGTATGAAATACCACTGCTGCACTACCTATCTATTAAGAGATA 208
QY 755 AATTATGGCCAAAGACATGCTCTTATATGCTGCTGATATCGAATCAAAAAACAGCATG 814
DB 209 AATTATGGCCAAAGACATGCTCTTATATGCTGCTGATATCGAATCAAAAAACAGCATG 268
QY 815 GCCTCACACACTGTTACTTGTGTATCATAGAGCAAAAAACAGAGTCTGAAATTTTAA 874
DB 269 GCCTCACACACTGTTACTTGTGTATCATAGAGCAAAAAACAGAGTCTGAAATTTTAA 328
QY 875 TCAAGAAAAAGCAATTTAATGCACTGATAGATAGAGAGAGCTGCTCATCTTG 934
DB 329 TCAAGAAAAAGCAATTTAATGCACTGATAGATAGAGAGAGCTGCTCATCTTG 388
QY 935 CTGTATGTTGTGATCAGCAAGTATAGTCAAGCTTCTACTTGAAGCAAAATTTGATGAT 994
DB 389 CTGTATGTTGTGATCAGCAAGTATAGTCAAGCTTCTACTTGAAGCAAAATTTGATGAT 448
QY 995 CTCTCAAGATCTATCTGAGCAGAGCGCCAGAGAGTATGCTGTTCTAGCATCATCATG 1054
DB 449 CTCTCAAGATCTATCTGAGCAGAGCGCCAGAGAGTATGCTGTTCTAGCATCATCATG 508
QY 1055 TAATTGGCAGTACTTCTGACTACAAAGAAAAAGATGCTAAATCTCTTGAAA 1114
DB 509 TAATTGGCAGTACTTCTGACTACAAAGAAAAAGATGCTAAATCTCTTGAAA 568
QY 1115 ACAGCAATCCAG 1126
DB 569 ACAGCAATCCAG 580

RESULT 2

AQ204617

LOCUS

DEFINITION

HS 3229 B1 G12 T7 CIT Approved Human Genomic Sperm Library D Homo

sapient genomic clone Plate3229 Col=23 Row=N, genomic survey

sequence.

AQ204617

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

521 bp DNA linear GSS 17-SBP-1998
HS 3229 B1 G12 T7 CIT Approved Human Genomic Sperm Library D Homo
sapient genomic clone Plate3229 Col=23 Row=N, genomic survey
sequence.
AQ204617
AQ204617.1 GI:3615187
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 521)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 Row: N Column: 23
Class: BAC ends
High quality sequence stop: 521.
Location/Qualifiers
1..521
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate3229 Col=23 Row=N"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match 9.2%; Score 184; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 3e-78;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 AGCTGAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTCATGTCGAT 1609
DB 231 AGCTGAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTCATGTCGAT 290
QY 1610 TCCGAAAACTGCTAATGTTGCGACATGTCGCAATGATGATTAATTCCTC 1669
DB 291 TCCGAAAACTGCTAATGTTGCGACATGTCGCAATGATGATTAATTCCTC 350
QY 1670 CAAGAAAGCAGAAACACCTGAAAGCCAGCAATTTCTGCACTGAAATGAAGATATC 1729
DB 351 CAAGAAAGCAGAAACACCTGAAAGCCAGCAATTTCTGCACTGAAATGAAGATATC 410
QY 1730 ACAG 1733
DB 411 ACAG 414

RESULT 3

BF676987

LOCUS

DEFINITION

602084215P1 NIH-MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',

mRNA sequence.

BF676987

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

865 bp mRNA linear EST 21-DEC-2000
602084215P1 NIH-MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',
mRNA sequence.
BF676987
BF676987.1 GI:11950882
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 865)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers
1..865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/lab_host="DH10B (T1 phage-resistant)"

FEATURES

source

Query Match 6.9%; Score 137; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 3.1e-55;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1743 AATGATCTCAGAGCAATTTTGTGAAGACAGAACTGTGAATTTACAGATGAGAT 1802
 |||||
 DB 9 AATGATCTCAGAGCAATTTTGTGAAGACAGAACTGTGAATTTACAGATGAGAT 68
 |||||

QY 1803 TCTGATTCATGAAGAAAGACAGATAGAGTGTGTAAGAAATGATTCGAGCTTCTCT 1862
 |||||
 DB 69 TCTGATTCATGAAGAAAGACAGATAGAGTGTGTAAGAAATGATTCGAGCTTCTCT 128
 |||||

QY 1863 TAGTGTGAAGAAAGAAA 1879
 |||||
 DB 129 TAGTGTGAAGAAAGAAA 145
 |||||

RESULT 6
 A0615477 531 bp DNA linear GSS 15-JUN-1999
 LOCUS HS_5144.B1.G01.T7A.RPCT-11.Human Male BAC library Homo sapiens
 DEFINITION genomic clone Plate=720 Col=1 Row=N, genomic survey sequence.
 ACCESSION A0615477 GI:5076753
 VERSION A0615477.1
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 531)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCT-11. For BAC
 library availability, please contact Pletcher de Jong
 (pleterdejong.med.buflalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buflalo.edu/ordering/bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
 http://www.htec.washington.edu
 Plate: 720 row: N column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 531.

FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="plate=720 Col=1 Row=N"
 /sex="male"
 /clone_1lb="RPCT-11 Human Male BAC library"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"

ORIGIN
 Query Match 6.5%; Score 129; DB 9; Length 531;
 Best Local Similarity 100.0%; Pred. No. 2.6e-51;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CATGGCACTGATCCAAATTTCCAGATGAGTATGGAATATACCACTTCGACTACGCTATC 741
 |||||
 DB 117 CATGGCACTGATCCAAATTTCCAGATGAGTATGGAATATACCACTTCGACTACGCTATC 176
 |||||

QY 742 TATATGAAGATTAATTAATGCGCAAGACACTGCTTTATATGATGCTGATATCGAATCA 801
 |||||
 DB 177 TATATGAAGATTAATTAATGCGCAAGACACTGCTTTATATGATGCTGATATCGAATCA 236
 |||||

QY 802 AAAAACCAAG 810
 |||||
 DB 237 AAAAACCAAG 245
 |||||

RESULT 7
 BM763942 621 bp mRNA linear EST 04-MAR-2002
 LOCUS K-EST0045367.S13KMS5.Homo sapiens cDNA clone S13KMS5-25-A11.5',
 DEFINITION mRNA sequence.
 ACCESSION BM763942 GI:19093557
 VERSION BM763942.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 621)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsun@mail.kribb.re.kr
 Plate: 25 row: A column: 11
 High quality sequence stop: 621.

FEATURES
 source
 Location/Qualifiers
 1..621
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-25-A11"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10P"
 /clone_1lb="S13KMS5"
 /note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI. The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tobacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dt-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10P by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

ORIGIN
 Query Match 5.9%; Score 117; DB 3; Length 621;
 Best Local Similarity 99.1%; Pred. No. 2e-45;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 510 CAGCAAAAGAGAGCTCTTACATCTGGCTCTGCCAATGGAAATTCAGAACTAGTAA 569
 |||||
 Db 1 CAGCAAAAGAGAGCTCTTACATCTGGCTCTGCCAATGGAAATTCAGAACTAGTAA 60
 QY 570 ACTCTGTGTGACAGACGATGTCACTTAATGTCTTGCACAAACAAAGAGACACTCT 629
 |||||
 Db 61 ACTCGTGTGACAGACGATGTCACTTAATGTCTTGCACAAACAAAGAGACACTCT 120
 QY 630 GATTAAGCCCGTACAAATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGACAC 689
 |||||
 Db 121 GACAAAGCCGTACATGACAGAAATGAATGTGCTTAATGTCTGGAACATGACAC 180
 QY 690 TGATCCAAATATTCAGATGATGAATGAAATACACTCT 728
 |||||
 Db 181 TGATCCAAATATTCAGATGATGAATGAAATACACTCT 219
 RESULT 8
 BM763453 633 bp mRNA linear EST 04-MAR-2002
 LOCUS K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5',
 DEFINITION mRNA sequence.
 ACCESSION BM763453
 VERSION BM763453.1 GI:19093068
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 633)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Kim,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 16 row: A column: 11
 High quality sequence stop: 633.
 Location/Qualifiers
 1..633
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-16-A11"
 /issue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10F"
 /clone_1ib="S13KMS5"
 /note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then deapped with tobacco acid
 pyrophosphatase (TAP). The deapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dT-selected mRNA by priming with
 dT-tailed vector. The dT-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10F by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

ORIGIN

Query Match 5.9%; Score 117; DB 3; Length 633;
 Best Local Similarity 99.1%; Pred. No. 2e-45;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 510 CAGCAAAAGAGAGCTCTTACATCTGGCTCTGCCAATGGAAATTCAGAACTAGTAA 569
 |||||
 Db 1 CAGCAAAAGAGAGCTCTTACATCTGGCTCTGCCAATGGAAATTCAGAACTAGTAA 60
 QY 570 ACTCTGTGTGACAGACGATGTCACTTAATGTCTTGCACAAACAAAGAGACACTCT 629
 |||||
 Db 61 ACTCGTGTGACAGACGATGTCACTTAATGTCTTGCACAAACAAAGAGACACTCT 120
 QY 630 GATTAAGCCCGTACAAATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGACAC 689
 |||||
 Db 121 GACAAAGCCGTACATGACAGAAATGAATGTGCTTAATGTCTGGAACATGACAC 180
 QY 690 TGATCCAAATATTCAGATGATGAATGAAATACACTCT 728
 |||||
 Db 181 TGATCCAAATATTCAGATGATGAATGAAATACACTCT 219

RESULT 9
 BQ441373 817 bp mRNA linear EST 24-MAY-2002
 LOCUS AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ441373
 VERSION BQ441373.1 GI:21180449
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA library Preparation: CLONTECH Laboratories, Inc.
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: L1CM2340 row: m column: 08
 High quality sequence stop: 516.
 Location/Qualifiers
 1..817
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6103855"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1ib="NIH MGC 82"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggcgccctggcgc); Site 2: SfiI (ggccatcatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATATATGACC-3' and 3' adaptor sequence:
 5'-ATTCAGAGCCGACGCGCCACATG-dT (30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Query Match 5.9%; Score 117; DB 5; Length 817;
 Best Local Similarity 100.0%; Pred. No. 2e-45;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1408 AGAATTGGCAATTAGTTCTGACTACAAAGAAAAACAGATGCGAAATTAATCTTCTGAA 1467
    |||||
Db 319 AGAATTGGCAATTAGTTCTGACTACAAAGAAAAACAGATGCGAAATTAATCTTCTGAA 378
    |||||
Oy 1468 AACAGCAACCCGAAACAGACTTAAAGCTGACATCAGAGAAAGTCCAGAAAGGCTT 1524
    |||||
Db 379 AACAGCAACCCGAAACAGACTTAAAGCTGACATCAGAGAAAGTCCAGAAAGGCTT 435
    |||||

RESULT 10
AG192933 263 bp DNA linear GSS 06-MAR-2004
LOCUS AG192933/c
DEFINITION Pan troglodytes DNA, clone: RP43-069L23.TU, genomic survey
ACCESSION AG192933
VERSION AG192933.1 GI:45225109
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.U.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
JOURNAL BAC end sequences of Library RP-43
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 263)
TITLE Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.U.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
JOURNAL Direct Submission
COMMENT Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
BioScience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.krribb.re.kr, URL:http://phs.grc.krribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the Rad process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TU
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 263
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-069L23.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
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Best Local Similarity 100.0%; Pred.No.3.2e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1739 AACCAATGATGATCTGAGAGCAATTTTGGAGAGACAGAACTGGAATATTACAGATG 1798
    |||||
Db 90 AACCAATGATGATCTGAGAGCAATTTTGGAGAGACAGAACTGGAATATTACAGATG 31
    |||||
Oy 1799 AGATTCTGATTCATGAAGAAAAGACAGATG 1828
    |||||
Db 30 AGATTCTGATTCATGAAGAAAAGACAGATG 1
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RESULT 11
AQ124119 400 bp DNA linear GSS 22-SEP-1998
LOCUS AQ124119

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DEFINITION HS 3122 A1 C07 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3122 Col=13 Row=E, genomic survey
sequence.
ACCESSION AQ124119
VERSION AQ124119.1 GI:3501285
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
JOURNAL Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
PROC. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3122 Row: E Column: 13
Class: BAC ends
High quality sequence stop: 400.
Location/Qualifiers
1. 400
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone="Plate=3122 Col=13 Row=E"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/cnote="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Col1 DH10B"

ORIGIN
Query Match 4.5%; Score 89; DB 9; Length 400;
Best Local Similarity 100.0%; Pred.No.1e-31;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 635 AGCCGTCACATGCCAGAGAGATGATGCGTTAATGTTGCTGGAACATGCACTGATC 694
    |||||
Db 237 AGCCGTCACATGCCAGAGAGATGATGCGTTAATGTTGCTGGAACATGCACTGATC 296
    |||||
Oy 695 CAATATTCACAGATGATGGAATATAC 723
    |||||
Db 297 CAATATTCACAGATGATGGAATATAC 325
    |||||

RESULT 12
AQ030111/c 399 bp DNA linear GSS 14-APR-1999
LOCUS AQ030111
DEFINITION RPc111-39K18.TP RPc111 Homo sapiens genomic clone RPc111-39K18,
genomic survey sequence.
ACCESSION AQ030111
VERSION AQ030111.1 GI:3274075
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
AUTHORS Adams,M.D., Rounsailey,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
JOURNAL Use of BAC End Sequences for Sequence-Ready Map Building (1998)

```

JOURNAL COMMENT

Unpublished (1998)
 Other GSSs: RPc11-39K18.TV
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: madam@tigr.org
 Clones are derived from the human BAC library RPc1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: Sp6
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..399

/organism="Homo sapiens"
 /mol_type="genomic DNA"
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 /clone="RPc1-11-39K18"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_11b="RPc1-11"
 /note="Vector: pBACE3.6; Site 1: EcoRI; site_2: EcoRI; RPc11 Human Male BAC Library"

ORIGIN

Query Match 4.3%; Score 87; DB 9; Length 399;
 Best Local Similarity 100.0%; Pred. No. 9.6e-31;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1732 AGTACGACAAATATGATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTA 1791

DB 102 AGTACGACAAATATGATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTA 43

QY 1792 CACGATGAGATTCTGATTGATGAGAA 1818

DB 42 CACGATGAGATTCTGATTGATGAGAA 16

RESULT 13 544 bp mRNA linear EST 04-SEP-2003
 LOCUS AL703938
 DEFINITION DKF26686E1728_r1.686 (synonym: h1cc3) Homo sapiens cDNA clone

ACCESSION AL703938
 VERSION AL703938.1 GI:19687293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 544)
 Othenwaeider, B., Obermaier, B., Mewes, W., Mewes, H.W., Well, B. and Wiemann, S.
 EST (Othenwaeider, B., Obermaier, B., Mewes, H.W., Well, B. and Wiemann, S.)
 Unpublished (2001)
 Contact: MIPS

JOURNAL COMMENT
 MIPS
 Ingstedter Landstr. 1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert.
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by MedGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No 3' sequence available.
 This clone (DKF26686E1728) is available at the RZPD in Berlin.

FEATURES

source

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

ORIGIN

Query Match 4.3%; Score 87; DB 1; Length 544;
 Best Local Similarity 100.0%; Pred. No. 9.8e-31;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 AAGGAAAAACAGATGCTAAATCTTCTGAAAACAGCAATCCAGACAGCTTAAG 1140

DB 432 AAGGAAAAACAGATGCTAAATCTTCTGAAAACAGCAATCCAGACAGCTTAAG 491

QY 1141 CTGACATCAGAGGAGTCACAAAGC 1167

DB 492 CTGACATCAGAGGAGTCACAAAGC 518

RESULT 14
 BI461255/c

LOCUS BI461255 279 bp mRNA linear EST 21-APR-2001
 DEFINITION 603206584P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5', mRNA sequence.
 ACCESSION BI461255
 VERSION BI461255.1 GI:15251911
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 279)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshitaki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11687 row: 9 column: 21
 High quality sequence stop: 236.
 Location/Qualifiers
 1..279

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5272364"
 /lab_host="DH10B"
 /clone_11b="NIH MGC 97"
 /note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to RGT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein

(NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

ORIGIN

Query Match 4.0%; Score 79; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 7.8e-27;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTCATGATTCATGCGGCGCTCTTCGTGAAGAGCCATTGGCTTC 60
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DB 84 ATGGTGGTTCATGATTCATGCGGCGCTCTTCGTGAAGAGCCATTGGCTTC 25
|||||
QY 61 AGGAGCAAGATGGGCAAGT 79
|||||
DB 24 AGGAGCAAGATGGGCAAGT 6
|||||

RESULT 15
HSM809270 6098 bp mRNA linear HTC 20-JAN-2005
LOCUS Homo sapiens mRNA; cDNA DKFZp686J0529 (from clone DKFZp686J0529).
DEFINITION BX649118
ACCESSION BX649118.1 GI:34368290
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 6098)
Bahr,A., Lauber,J., Mewes,H.W., Well,B., Amid,C., Oesinger,A.,
Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
Direct Submission
Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764
Neuerberg, GERMANY

REFERENCE
AUTHORS
CONSRMT
TITLE
JOURNAL
Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764
Neuerberg, GERMANY

COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Ojagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686J0529) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686J0529
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..6098
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFZp686J0529Q"
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/clone="DKFZp686J0529"
/issue_type="testis"
/clone_lib="686 (synonym: hlc03). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="putative transcript"

ORIGIN

Query Match 3.8%; Score 76; DB 4; Length 6098;
Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 986 TTGATGTATCTTCTCAAGATCTATCTGACAGACGGCCAGAGATGCTGTTCTAGTC 1045
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DB 1426 TTGATGTATCTTCTCAAGATCTATCTGACAGACGGCCAGAGATGCTGTTCTAGTC 1485
|||||
QY 1046 ATCATCATGTAATTG 1061
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DB 1486 ATCATCATGTAATTG 1501
|||||

Search completed: December 19, 2005, 20:05:01
Job time : 8066.39 secs

PF	14-JUL-1999 JP	200560247	
PR	14-JUL-1998 US	09/115453_14-JUL-1998 US	09/115134 PR
23-SRP-	1998 US	09/159822_23-SEP-1998 US	09/159812 PR
15-JAN-	1999 US	09/232800_15-JAN-1999 US	09/232149 PR
09-ARR-	1999 US	09/288946	
P1	DAVIN CLIFFORD DILON,SUSAN LOUISE HARLOCKER,JIANG YUQIU,P1 JIANGCIN XU,		
P1	JENNIFER LYNN MITCHAM		
PC	C12N15/09,A6IK38/00,A6IK39/00,A6IK39/395,C07K14/47,C07K16/30		
PC	C12N5/10,		
PC	C12P21/08,C12Q1/68,G01N33/574,G01N33/68/A6IP35/00,C12NI5/00		
PC	A6IK37/02,		
PC	C12N5/00		
CC	Compounds for immunotherapy and diagnosis of prostate cancer		
CC	and methods		
CC	for their use		
FH	Key	Location/Qualifiers	
FT	Source	1..2000	
PT	/organism='Homo sapiens (human)'. 		

FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGTGCTC 60
DB 1 ATGTGTTGAAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGTGCTC 60
QY 61 AGGAGCAATATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
DB 61 AGGAGCAATATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAGACGACGACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAGACGACGACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCACTG 240
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DB 241 GCGGCTTCTGAGACACAGACGACTGTGCTATGAACAACCTCAGAGCAAGATGGGCAAG 300
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DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGAGTGGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGTCTTCAATGAGGCCAGGTACCAAGTCCGTGAGAAAGTCTG 420
DB 361 GGAAGCTACGATGACAGTGTCTTCAATGAGGCCAGGTACCAAGTCCGTGAGAAAGTCTG 420
QY 421 GACAAGCTCCACAGACGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCTGCTGAG 480
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QY 481 CTCAGGAGACATGACGCTGAAACAAGAGACAAAGCAAAAGAGACTCTCTACATCTGGCC 540
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QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGAGATGTCAACTTAAAT 600
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QY 601 GTTCCTTGACAAACAAAAGAGAGACAGCTGTGAATAAGCCGTACAAATGCCAGAGAAATGAA 660
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QY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAATGAGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAATGAGATGGAAT 720
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DB 721 ACCACTCTGACCTAGGCTATCTAATAATGAAGATAAATTAATGAGCAAGCACTGCTTAA 780
QY 781 TATGTGCTGATATGCAATCAAAAACAAAGCATGGGCTCACACACTGTTATCTTGGTGA 840
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DB 841 CATGACCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGCTGCTCATATCTTGCTGTATGTTGTGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGAGCTGCTCATATCTTGCTGTATGTTGTGATCAGCAAGTATA 960
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DB 901 CTGGATAGATATGGAAGAGCTGCTCATATCTTGCTGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTTCAGCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
DB 961 GTTCAGCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCGAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCGAGTTACTTTCTGACTAC 1080
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DB 1261 AAGCATGAAAGTAAATATGTGGGATTAATAGAAAACTGTGCTAATGTGTCACTGTGCGC 1320
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DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGACAGAAACCTGTAATATGCAATTT 1380
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DB 1381 CCTGACAAAGAAAGAGAGATATCAAGAAATTTGCAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
QY 1501 TCGAGAGAAAGATTCAAAAGGCTTGAAGGCAATGAAAATGGCCAGCCAGAGCTAAGAAAT 1560
DB 1501 TCGAGAGAAAGATTCAAAAGGCTTGAAGGCAATGAAAATGGCCAGCCAGAGCTAAGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAGACGAGAAAGTACTCATGTGGAATTTCCAGAAAGAC 1620
DB 1561 TTTATGCTATCGAAGAAATGAAGAGACGAGAAAGTACTCATGTGGAATTTCCAGAAAGAC 1620
QY 1621 CTGACTAATGTGTGCACTGTGCGCAATGTGTGATGATTAATTTCTTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTGTGCACTGTGCGCAATGTGTGATGATTAATTTCTTCAAGAAAGAC 1680
QY 1681 AGAACAACCTGAAAGCCAGCAATTTCTCTGACACTGAGAAAGAAAGATACAGTGCAGAA 1740
DB 1681 AGAACAACCTGAAAGCCAGCAATTTCTCTGACACTGAGAAAGAAAGATACAGTGCAGAA 1740
QY 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTCTGAAATATTAACAGATGAG 1800
DB 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTCTGAAATATTAACAGATGAG 1800
QY 1801 ATTCTGATTCATGAGAAAGAAAGAGATAGAAAGTGTGAATAATGAAATTTCTGAGCTTCT 1860
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LOCUS	AR350943		
DEFINITION	Sequence 302 from patent US 6586570.		
ACCESSION	AR350943		
VERSION	AR350943.1	GI:33752583	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2000)		
TITLE	Frudakis,T.N., Reed,S.G., Smith,J.M. and Mishner,L.		
JOURNAL	Compositions and methods for the treatment and diagnosis of breast		
FEATURES	Patent: US 6586570-A 302 01-JUL-2003;		
source	Corixa Corporation; Seattle, WA		
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Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2000;	Conservative 0;	Mismatches 0;	Indels 0;
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QY	121	AGCAACGTGGGCACTTCTGAGAACGACGACGACTCTGCTATGAAGACACTCAGAGCAAG	180
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QY	181	ATGGGCAAGTGTGTGCGCCGACCTGTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG	240
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QY	301	TGTTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360
Db	301	TGTTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGTCTTATGAGGCCCAAGTACACGTCCTGTGAGAGAAAGATCTG	420

Db		361	GGAGACCTACGATGCACTGCTTCATGAGCCGAGATCCACAGTCCGTGAGAAAGATCTG	420
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Qy		481	CTCAGGGACACTGACCTGGAACAGAGAGACAGCAAGCAAAAGAGACTGCTTCACATCTG	540
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Db		961	GTCAGCCTTCTACTTGGAGCAAAATATGATGATCTTCTCAAGATCTTATCTGACAGCG	1020
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Qy		1321	AATGATGATATGATTAATCTCTCAAGAGAGAGCAACAACCTGAAATATCAGCAATTT	1380
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Qy		1381	CCTGACAAAGAAAGTGAAGATATCACGAATTTGGCAATTAATGTTTCTGACTACAAAGAA	1440
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Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 4
AR367175 2000 bp DNA linear PAT 12-SEP-2003
LOCUS AR367175
DEFINITION Sequence 374 from patent US 6329505.
ACCESSION AR367175
VERSION AR367175.1 GI:34600150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yugi,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6329505-A 374 11-DEC-2001;
FEATURES
source Corixa Corporation; Seattle, WA
location/Qualifiers
1..2000
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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Dp	1381	CCTGCACACGAAAGTAGAGAGTATCACAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA	1440
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RESULT 5			
LOCUS	AR371071	2000 bp	DNA
DEFINITION	Sequence 374 from patent US 6395278.	linear	PAT 12-SEP-2003
ACCESSION	AR371071		
VERSION	AR371071.1	GI:34607964	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2000)		
TITLE	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L. and Yugu,J.		
JOURNAL	Prostate specific fusion protein compositions		
	Patent: US 6395278-A 374 28-MAY-2002;		
	Corixa Corporation; Seattle, WA		

FEATURES		Location/Qualifiers
SOURCE		1. 2000
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Query Match	100.0%; Score 2000; DB 6; Length 2000;	
Best Local Similarity	100.0%; Pred. No. 0;	
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QY	121 AGCAACGGGGGCACTTCTGAGAACCAAGACGACTGTGCTATGAAAGCACTCAGAGCAAG	180
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LOCUS Sequence 374 from patent US 6620922.
DEFINITION AR400211
ACCESSION AR400211
VERSION AR400211.1 GI:40143375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
Kalos M.D., Fanger G.R., Retter M.W., Stolk J.A., Day C.H.,
Vedrick T.S., Carter D., Li S.X., Wang A., Skelley Y.A.W.,
Hepler W.T. and Henderson R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 374 16-SEP-2003;
Corixa Corporation; Seattle, WA
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AR405478 2000 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 374 from patent US 6630305.
ACCESSION AR405478
VERSION AR405478.1 GI:40154315
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kadosh,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
COMPOSITIONS AND METHODS for the therapy and diagnosis of prostate
cancer
PATENT: US 6630305-A 374 07-OCT-2003;
CORIXA Corporation; Seattle, WA;
WOX;

FEATURES
source location/Qualifiers
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR433319
DEFINITION Sequence 302 from patent US 6656480.
ACCESSION AR433319
VERSION AR433319.1 GI:40196101
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Rether, M.W. and Dillon, D.C.
TITLES Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6656480-A 302 02-DEC-2003;
Corixa Corporation; Seattle, WA
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 9
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LOCUS AR563858 2000 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 374 from patent US 6759515.
ACCESSION AR563858
VERSION AR563858.1 GI:53978909
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolck,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,

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RESULT 10
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LOCUS Sequence 374 from patent US 6800746.
DEFINITION ARS88844
ACCESSION ARS88844
VERSION ARS88844.1 GI:56635741
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 Unpublished.
AUTHORS Xu, D., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kales, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Veddyck, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6800746-A 374 05-OCT-2004;
Corixa Corporation; Seattle, WA
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
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RESULT 11
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LOCUS Sequence 374 from patent US 6818751.
DEFINITION AR605664
ACCESSION AR605664
VERSION AR605664.1 GI:56657328
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,
Vedvyck,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6818751-A 374 16-NOV-2004;
Corixa Corporation, Seattle, WA
FEATURES
source 1..2000
/organism="unknown"
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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 ARE15063
 LOCUS ARE15063 2000 bp DNA linear PAT 15-DEC-2004
 DEFINITION Sequence 302 from patent US 6828431.
 ACCESSION ARE15063
 VERSION ARE15063.1 GI:56671467
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2000)
 AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
 TITLE Reiter,M.W., Wang,A., Skeiky,Y.A.W. and Harlocke,S.L.
 JOURNAL Compositions and methods for the therapy and diagnosis of breast
 PATENT Patent: US 6828431-A 302 07-DEC-2004;
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 Best Local Similarity 100.0%; Pred. No. 0;
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ACCESSION AR642105
VERSION    AR642105.1 GI:62778253
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SOURCE     Unknown.
ORGANISM   Unknown.

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REFERENCE 1 (bases 1 to 2000)
AUTHORS   Fridakis,T.N., Smith,J.M., Reed,S.G., Misher,L.B., Retter,M.W. and
           Dillon,D.C.
TITLE      Compositions and methods for the treatment and diagnosis of breast
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JOURNAL    Patent: US 6861506-A 302 01-MAR-2005;
           Corixa Corporation; Seattle, WA
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ACCESSION	AR657003		
VERSION	AR657003.1	GI:67590123	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2000)		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: US 6894146-A 374 17-MAY-2005;		
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 VERSION AX106593.1 GI:13922264
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 Homidae; Homo.
 REFERENCE 1 Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
 AUTHORS Compositions and methods for therapy and diagnosis of prostate
 TITLE Cancer
 JOURNAL Patent: WO 0125272-A 374 12-APR-2001;
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QY 1921 GCCATGCTAAGACTGAGCTAGACAAATGAAAACATCAGAGCCAGCTAATAAAAAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACAAATGAAAACATCAGAGCCAGCTAATAAAAAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

Search completed: December 18, 2005, 21:07:08
Uod time : 10119.4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:12:25 ; Search time 1195.05 Seconds
(without alignments) 11153.835 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000
Sequence: 1 atgctgcttgctgctgctgcttc.....aaaaaaaaaaaaaaaaaaaaa 2000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2000	100.0	2000	3 AAC81012	AAC81012 Human B11
2	2000	100.0	2000	4 AAH93715	Aah93715 Human pro
3	2000	100.0	2000	4 AA167212	AA167212 B305D iso
4	2000	100.0	2000	4 AA63808	AA63808 Human pro
5	2000	100.0	2000	4 AAH02780	Aah02780 Prostate
6	2000	100.0	2000	4 AAH85029	Aah85029 Human pro
7	2000	100.0	2000	4 ACAS59616	Acas59616 Prostate
8	2000	100.0	2000	6 AB195179	Ab195179 Human B30
9	2000	100.0	2000	6 AA899858	Aa899858 Breast tu
10	2000	100.0	2000	8 ACC95343	Acc95343 Prostate
11	2000	100.0	2000	8 ADA11381	Ada11381 Human bre
12	2000	100.0	2000	10 ADC15354	Adc15354 Human bre
13	2000	100.0	2000	10 ADB13824	Adb13824 Human pro
14	2000	100.0	2000	10 ADG26240	Adg26240 Human pro
15	1998.4	99.9	2000	3 AAA06599	Aaa06599 Human imm
16	1940	97.0	2040	4 AAC81013	Aac81013 Human B11
17	1940	97.0	2040	4 AAH93716	Aah93716 Human pro
18	1940	97.0	2040	4 AA167213	AA167213 B305D iso
19	1940	97.0	2040	4 AA63809	Aa63809 Human pro

20	1940	97.0	2040	4 AAH02781	Aah02781 Prostate
21	1940	97.0	2040	4 AAH85030	Aah85030 Human pro
22	1940	97.0	2040	5 ACAS9617	Acas9617 Prostate
23	1940	97.0	2040	6 AB195180	Ab195180 Human B30
24	1940	97.0	2040	6 AA899859	Aa899859 Breast tu
25	1940	97.0	2040	8 ACC95344	Acc95344 Prostate
26	1940	97.0	2040	8 ADA11382	Ada11382 Human bre
27	1940	97.0	2040	10 ADC15355	Adc15355 Human bre
28	1940	97.0	2040	10 ADB13825	Adb13825 Human pro
29	1940	97.0	2040	10 ADG26241	Adg26241 Human pro
30	1938.4	96.9	2040	3 AAA06600	Aaa06600 Human imm
31	1170.8	58.5	1449	11 ACN90068	Acn90068 Breast ca
32	1147.6	57.4	1853	2 AA689996	Aa689996 DNA molec
33	1147.6	57.4	1853	3 AAA06594	Aaa06594 Human imm
34	1147.6	57.4	1853	3 AAC81007	Aac81007 Human B11
35	1147.6	57.4	1853	4 AAH93710	Aah93710 Human pro
36	1147.6	57.4	1853	4 AA63803	Aa63803 Human pro
37	1147.6	57.4	1853	4 AAH02775	Aah02775 Prostate
38	1147.6	57.4	1853	4 AAH85024	Aah85024 Human pro
39	1147.6	57.4	1853	5 ACAS59611	Acas59611 Prostate
40	1147.6	57.4	1853	6 AB195174	Ab195174 Human B30
41	1147.6	57.4	1853	6 AA899853	Aa899853 Breast tu
42	1147.6	57.4	1853	6 ABR46897	Ab46897 Human bre
43	1147.6	57.4	1853	8 ACC95338	Acc95338 Prostate
44	1147.6	57.4	1853	8 ADA11374	Ada11374 Human bre
45	1147.6	57.4	1853	10 ADC15347	Adc15347 Human bre

ALIGNMENTS

RESULT 1
AAC81012
ID AAC81012 strand; cDNA; 2000 BP.
XX
XX AAC81012;
AC
XX
DT 13-FEB-2001 (first entry)
XX
DE Human B11Ag1 antigen splice isoform B11C-8 cDNA.
XX
XX Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B11Ag1; B11Ag1; B15Ag1; ss.
XX
XX Homo sapiens.
OS
PN WO200061753-A2.
XX
PD 19-OCT-2000.
XX
XX 07-APR-2000; 2000WO-US009312.
XX
XX 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TM, Smith JM, Reed SG, Misher LB, Retter MW, Dillon DC;
DR WPI; 2000-628403/60.
XX P-PSDB; AAB28629.
XX
XX An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient.
XX
XX Claim 4; Page 177-178; 187pp; English.
XX
XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumor tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in

CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTTGAGGTTTATTCATGCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGTGGTTGAGGTTTATTCATGCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAGAACTCTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAGAACTCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGAGGAGGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGAGGAGGAGTGGCAAGCACTG 240
QY 241 GGGGCTTCTGAGAGCACACGACTCTGCTATGAGAACTCTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGAGCACACGACTCTGCTATGAGAACTCTCAGAGCAAGTGGCAAG 300
QY 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
DB 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
QY 361 GGAAGATGAGTACAGTGTCTTCAAGAGCCCAAGTACCACTGCTGAGAGAGTCTG 420
DB 361 GGAAGATGAGTACAGTGTCTTCAAGAGCCCAAGTACCACTGCTGAGAGAGTCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTCCCAAGAAAGGATCTCATCGCATG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTCCCAAGAAAGGATCTCATCGCATG 480
QY 481 CTCAGGAGCACTGACGCTGAAACAAGAGACAAGCAAAAGAGACTGCTTACATCGGC 540
DB 481 CTCAGGAGCACTGACGCTGAAACAAGAGACAAGCAAAAGAGACTGCTTACATCGGC 540
QY 541 TCTGCCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGACAGAGATGCTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGACAGAGATGCTCACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCGGTACATGCGAAGATGAA 660
DB 601 GTCCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCGGTACATGCGAAGATGAA 660
QY 661 TGTGCTTAATGTTGTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGACCTAACCTATCTAATGAAGATTAATTAAGGCCAAAGCATGCTCTTA 780
DB 721 ACCACTCTGACCTAACCTATCTAATGAAGATTAATTAAGGCCAAAGCATGCTCTTA 780
QY 781 TATGTGCTGATATTCGAATCAAAAACAAGATGGCTCACACCATGTTTACTGGATGA 840
DB 781 TATGTGCTGATATTCGAATCAAAAACAAGATGGCTCACACCATGTTTACTGGATGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900

DB 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGACGTGCTCATCTACTGCTGATATGTTGGATACAGAGTATA 960
DB 901 CTGATATGATATGGAAGACGTGCTCATCTACTGCTGATATGTTGGATACAGAGTATA 960
QY 961 GTCAACCTTCTTACCTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
DB 961 GTCAACCTTCTTACCTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCGAGTACTTCTGATAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCGAGTACTTCTGATAC 1080
QY 1081 AAAAGAAAAACGATCTAAAAATCTCTGTAACAGCAATCCAGAACTTAAG 1140
DB 1081 AAAAGAAAAACGATCTAAAAATCTCTGTAACAGCAATCCAGAACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGTCACAAGGTTCAAAAGCAGTGAATATAGCCAGAGAGAA 1200
DB 1141 CTGACATCAGAGGAAGTCACAAGGTTCAAAAGCAGTGAATATAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAAGATGTGATAGAGCTTGAAGAAATGAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAAGATGTGATAGAGCTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAGATTAATATGTGGATTACTAGAAACCTGACTAATGTGTCTGCTGGC 1320
DB 1261 AAGCATGAAGATTAATATGTGGATTACTAGAAACCTGACTAATGTGTCTGCTGGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAAAGGAAGACAGAACACTGAAATAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAAAGGAAGACAGAACACTGAAATAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440
QY 1441 AAAAGATGCCAAATCTCTTCTGAAAAACGAAACCAAGAACAACTTAAGCTGAGA 1500
DB 1441 AAAAGATGCCAAATCTCTTCTGAAAAACGAAACCAAGAACAACTTAAGCTGAGA 1500
QY 1501 TCAGAGGAAGATCACAAAAGCTTGAAGGCAAGTGAATATGCGCAGAGCTAGAAAT 1560
DB 1501 TCAGAGGAAGATCACAAAAGCTTGAAGGCAAGTGAATATGCGCAGAGCTAGAAAT 1560
QY 1561 TTTATGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGAATTTCCAGAAAC 1620
DB 1561 TTTATGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGAATTTCCAGAAAC 1620
QY 1621 CTGACTAATGTGCGCACTGCTGGCAATGATATGATTTAATTTCTTCCAGAGAAAGC 1680
DB 1621 CTGACTAATGTGCGCACTGCTGGCAATGATATGATTTAATTTCTTCCAGAGAAAGC 1680
QY 1681 AGAAGACCTGAAAGCAGCAATTTTCTGCACTGAGAAATGAAGATATCAAGTACGAA 1740
DB 1681 AGAAGACCTGAAAGCAGCAATTTTCTGCACTGAGAAATGAAGATATCAAGTACGAA 1740
QY 1741 CAAAATGATCTCAGAAAGATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
DB 1741 CAAAATGATCTCAGAAAGATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
QY 1801 ATTTGATTTCAAGAAAGAAAGAGATAGAGGTGTGAAGAAATATTAATTTGAGCTTCT 1860
DB 1801 ATTTGATTTCAAGAAAGAAAGAGATAGAGGTGTGAAGAAATATTAATTTGAGCTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGTCAATGAATATGATGCTTGGGGAAGAAATTT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGTCAATGAATATGATGCTTGGGGAAGAAATTT 1920
QY 1921 GGCATGCTAAGACTGAGCTAGACCAATGAAGACATCAGAGCCAGCTAATTAATTAATTA 1980
DB 1921 GGCATGCTAAGACTGAGCTAGACCAATGAAGACATCAGAGCCAGCTAATTAATTAATTA 1980

QY 1981 AAAAAAAAAAAAAAAAAA 2000
 DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 2
 ID AAH93715 standard; cDNA; 2000 BP.

AAH93715;
 04-OCT-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #9.
 Human; prostate cancer; prostate-specific; diagnosis; vaccine;
 KM cytotoxic; gene therapy; metastasis; ss.

OS Homo sapiens.
 PN WO200151633-A2.
 PD 19-JUL-2001.
 PF 16-JAN-2001; 2001MO-US001574.
 PR 14-JAN-2000; 2000US-00483672.
 PA (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
 PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM;
 PI Wang A, Meagher MJ;
 XX MPI; 2001-425873/45.

PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
 PT monitoring and treating prostate cancer in a patient and for use in
 PT vaccines.

PS Claim 1; Page 347-348; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
 CC prostate-specific proteins (II). (I) and (II) have cytotoxic activity,
 CC and can be used in vaccine production and gene therapy. (I), (II),
 CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
 CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
 CC the antibodies are also used in the detection of cancer in a patient. The
 CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
 CC and (II) can be used in vaccines. The antibodies or (I) can be used for
 CC monitoring the progression of cancer in a patient. (I) and (II) can also
 CC be used to improve diagnostic and therapeutic methods for prostate
 CC cancer. They can indicate the level of metastasis as well as the prostate
 CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
 CC polynucleotide and amino acid sequences used in the exemplification of
 CC the present invention

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 2000; DB 4; Length 2000;
 DB Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTTGTAAGAAGCATTTGGTCTC 60
 DB 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTTGTAAGAAGCATTTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
 DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACATCAGAGCAAG 180

DB 121 AGCAAGTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACATCAGAGCAAG 180
 QY 181 ATGGGCAAGTGGTGGCGCCATGCTTCCCTGCTGCAAGGAGATGGCAAGCAAGTGG 240
 DB 181 ATGGGCAAGTGGTGGCGCCATGCTTCCCTGCTGCAAGGAGATGGCAAGCAAGTGG 240
 QY 241 GGGGCTTCTGAGACCAAGCAAGCTCTGCTATGAAGACATCAGCAAGCAAGTGGCAAG 300
 DB 241 GGGGCTTCTGAGACCAAGCAAGCTCTGCTATGAAGACATCAGCAAGCAAGTGGCAAG 300
 QY 301 TGGTGTGCTGACGTCTTCCCTGCTGCAAGGAGATGGCAAGTGGGCGCTTGG 360
 DB 301 TGGTGTGCTGACGTCTTCCCTGCTGCAAGGAGATGGCAAGTGGGCGCTTGG 360
 QY 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCAGGTACAGGTCCGTGAGAGATCTG 420
 DB 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCAGGTACAGGTCCGTGAGAGATCTG 420
 QY 421 GACAGCTTCAAGAGCTGCTGCTGGGCTTAAAGTCCCAAGAAAGATCTCATGCTAG 480
 DB 421 GACAGCTTCAAGAGCTGCTGCTGGGCTTAAAGTCCCAAGAAAGATCTCATGCTAG 480
 QY 481 CTCAGGGACACTGACGTGTGAACAAAGACAAAGCAAGAGAGATCTCATGCTAG 540
 DB 481 CTCAGGGACACTGACGTGTGAACAAAGACAAAGCAAGAGAGATCTCATGCTAG 540
 QY 541 TCTGCAATGGGAATTCAGAGATGATTAATCTCTGCTGAGACAGATGCAATTAAT 600
 DB 541 TCTGCAATGGGAATTCAGAGATGATTAATCTCTGCTGAGACAGATGCAATTAAT 600
 QY 601 GTCTCTTGAACAATAAAGAGAGACAGCTGATTAAGGCGGTACATGCAAGAAATGAA 660
 DB 601 GTCTCTTGAACAATAAAGAGAGACAGCTGATTAAGGCGGTACATGCAAGAAATGAA 660
 QY 661 TGTGGTTAATGTTGTGTAAGATGAGCACTGATCCAAATATTCAGATGATGAAAT 720
 DB 661 TGTGGTTAATGTTGTGTAAGATGAGCACTGATCCAAATATTCAGATGATGAAAT 720
 QY 721 ACCACTGTGACATGCTATCTATATGAAAGATTAATTAAGGCCAAGCACTGCTT 780
 DB 721 ACCACTGTGACATGCTATCTATATGAAAGATTAATTAAGGCCAAGCACTGCTT 780
 QY 781 TATGCTGATGATGATCAATAAAGCAAGCTGCTCAACCACTGTTACTTGGTGA 840
 DB 781 TATGCTGATGATGATCAATAAAGCAAGCTGCTCAACCACTGTTACTTGGTGA 840
 QY 841 CATGAGCAAAACAGCAAGTGTGAATTTTAATCAAGAAAGCGAATTAATGCA 900
 DB 841 CATGAGCAAAACAGCAAGTGTGAATTTTAATCAAGAAAGCGAATTAATGCA 900
 QY 901 CTGAGATGATGAAAGAGCTGCTCATACTTGTGTAATGTTGATGATCAAGCAATTA 960
 DB 901 CTGAGATGATGAAAGAGCTGCTCATACTTGTGTAATGTTGATGATCAAGCAATTA 960
 QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATCTTCTCAAGATCTATCTGACAGAG 1020
 DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATCTTCTCAAGATCTATCTGACAGAG 1020
 QY 1021 GCCAGAGATGATGCTTTCTGATCATCATCAATGTAATTTGCAAGTACTTCTGACTAG 1080
 DB 1021 GCCAGAGATGATGCTTTCTGATCATCATCAATGTAATTTGCAAGTACTTCTGACTAG 1080
 QY 1081 AAAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAGCTTAAAG 1140
 DB 1081 AAAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAGCTTAAAG 1140
 QY 1141 CTGACATCAGAGAAAGATCAAAAGTTCAAAAGGATGAAATATGCGCAGCAAGGAAA 1200
 DB 1141 CTGACATCAGAGAAAGATCAAAAGTTCAAAAGGATGAAATATGCGCAGCAAGGAAA 1200
 QY 1201 ATGCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260

Db 361 GGAGACTACGATGACAGTGGCTTTCATGAGCCCAAGGTACCACTGCTGGAGGAAGATCTG 420
Qy 421 GACAACTCCACAGAGCTGCTGCTGGGGGTAAAGTCCCGAAGAAAGATCTCATCTGTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGCTGGGGGTAAAGTCCCGAAGAAAGATCTCATCTGTCATG 480
Qy 481 CTCAGGAGACCTGACCTGAAACAAGAAAGAACCAAAAGAGAGCTGCTCAACATCTGAGCC 540
Db 481 CTCAGGAGACCTGACCTGAAACAAGAAAGAACCAAAAGAGAGCTGCTCAACATCTGAGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGGACAGACGATCTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGGACAGACGATCTCACTTAAT 600
Qy 601 GTCTTGGACAACAAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGAAAGATGAA 660
Db 601 GTCTTGGACAACAAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGAAAGATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAAACATGGCACTGATCCAAATTTCCAGATGATGTAATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAAACATGGCACTGATCCAAATTTCCAGATGATGTAATGAAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAAGCCAAAGCAGCTGCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAAGCCAAAGCAGCTGCTTA 780
Qy 781 TATGATGCTGATATCGAATCAAAAACAGCATGGCTCAACACACTGTTACTTGGTGA 840
Db 781 TATGATGCTGATATCGAATCAAAAACAGCATGGCTCAACACACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATAGATATGGAAGGAGCTGCTCATACCTTGATGTTGGATGAGCAAGATTA 960
Db 901 CTGGATAGATATGGAAGGAGCTGCTCATACCTTGATGTTGGATGAGCAAGATTA 960
Qy 961 GTGAGCGTTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTGAGCGTTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAATACTCTCTGAAAAACAGCAATGCAGAAACAAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATACTCTCTGAAAAACAGCAATGCAGAAACAAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAAAGCAGTGAATAATGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAAAGCAGTGAATAATGCCAGCAGAGAAA 1200
Qy 1201 ATGTCTCAAGAACCAAAATTAAGATGTTGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAAGATGTTGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATGTTGGAATTACTAGAAAACTGACTAATGCTGCTGCG 1320
Db 1261 AAGCATGAAGATTAATGTTGGAATTACTAGAAAACTGACTAATGCTGCTGCG 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGACACTGTAATAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGACACTGTAATAATCAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGACTCAAGAA 1440
Qy 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500

Db 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
Qy 1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCACTGAAATGGCCAGCAGATTAAGAAAT 1560
Db 1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCACTGAAATGGCCAGCAGATTAAGAAAT 1560
Qy 1561 TTTATGGCTATGCAAAAGATTAAGAAAGACAGAAAGTCACTCAATGCGATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATGCAAAAGATTAAGAAAGACAGAAAGTCACTCAATGCGATTTCCAGAAAC 1620
Qy 1621 CTGACTAATGATGTCACCTGCTGCAATGGTGAATGATGATTAATTTCTCCAGAAAGAGC 1680
Db 1621 CTGACTAATGATGTCACCTGCTGCAATGGTGAATGATGATTAATTTCTCCAGAAAGAGC 1680
Qy 1681 AGAACCTGAAAAGCCAGCAATTTCTTGAACACTGAGAAATGAAGATATCACTGACGAA 1740
Db 1681 AGAACCTGAAAAGCCAGCAATTTCTTGAACACTGAGAAATGAAGATATCACTGACGAA 1740
Qy 1741 CAAAATGATATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
Db 1741 CAAAATGATATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
Qy 1801 ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGTGAAGAAATGAATTTCTGACTTTCT 1860
Db 1801 ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGTGAAGAAATGAATTTCTGACTTTCT 1860
Qy 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGAAATATGATCGTTGGGGAGAAATTT 1920
Db 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGAAATATGATCGTTGGGGAGAAATTT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACATGAATCATCAAGCCAGCTTAATAAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAATCATCAAGCCAGCTTAATAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
AAS63808
ID AAS63808 standard; cdna; 2000 BP.
XX
XX AAS63808;
AC
XX
XX 29-JAN-2002 (first entry)
DT
XX
XX Human prostate cdna clone B305D splice variant #9.
DE
XX Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.
XX
XX Homo sapiens.
OS
XX
XX MO200173032-A2.
PN
XX
XX 04-OCT-2001.
PD
XX
XX 27-MAR-2001; 2001WC-US009919.
PF
XX
XX 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
XX
XX (CORI-) CORIXA CORP.
PA
XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Rietter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX MPI, 2001-639232/73.
DR P-PSDB; AAU69778.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
PT
PS Claim 1, Page 349-350; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polynucleotide of the invention
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGTTCATGCGCGTCTCTTCTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGTTGAGTTCATGCGCGTCTCTTCTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGTGGCAAGTGTGTGCTGCTTCTCTGTCGAGGAGAGCGCAAG 120
DB 61 AGGAGCAAGTGGCAAGTGTGTGCTGCTTCTCTGTCGAGGAGAGCGCAAG 120
QY 121 ACCAAGCTGGGACCTTCTGAGACCAAGCACTGTCTATGAAGACATCAGAGCAAG 180
DB 121 ACCAAGCTGGGACCTTCTGAGACCAAGCACTGTCTATGAAGACATCAGAGCAAG 180
QY 121 ACCAAGCTGGGACCTTCTGAGACCAAGCACTGTCTATGAAGACATCAGAGCAAG 180
DB 121 ACCAAGCTGGGACCTTCTGAGACCAAGCACTGTCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGT 240
QY 241 GGGGCTTCTGAGACCAAGCACTGTCTATGAAGACATCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGACCAAGCACTGTCTATGAAGACATCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTCACCTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTGGGCGTTGG 360
DB 301 TGGTGTCACCTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTGGGCGTTGG 360
QY 361 GGAAGCTAAGTACAGTGTCTTCAATGAGCCAGGTACAGTCCGTGGAAGATCTG 420
DB 361 GGAAGCTAAGTACAGTGTCTTCAATGAGCCAGGTACAGTCCGTGGAAGATCTG 420
QY 421 GACCAAGCTCAGAGCTGCTGCTGAGGGTAAAGTCCCAAGAAAGATCTATCGTC 480
DB 421 GACCAAGCTCAGAGCTGCTGCTGAGGGTAAAGTCCCAAGAAAGATCTATCGTC 480
QY 481 CTCAGGAGACCTGACCTGGAACAAGAGCAAGCAAAAGAGATCTTCAATCTGCGC 540
DB 481 CTCAGGAGACCTGACCTGGAACAAGAGCAAGCAAAAGAGATCTTCAATCTGCGC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTGTAAGAGAGATGTCAATTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTGTAAGAGAGATGTCAATTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTTGATTAAGGCGTACATGCAAGAGATGA 660
DB 601 GTCTTGAACAACAAAAGAGACAGCTTGATTAAGGCGTACATGCAAGAGATGA 660

DB 601 GTCTTGAACAACAAAAGAGACAGCTTGATTAAGGCGTACATGCAAGAGATGA 660
QY 661 TGTGGTTAAATGTCTGGAACAATGCACTGATTCCAATATTCAGATGAGTGAAT 720
DB 661 TGTGGTTAAATGTCTGGAACAATGCACTGATTCCAATATTCAGATGAGTGAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGAGTAAATTAATGAGCCAAAGCATGCTCTTA 780
DB 721 ACCACTGCACTACGCTATCTATATGAGTAAATTAATGAGCCAAAGCATGCTCTTA 780
QY 781 TATGTGCTGATATGATCAAAAAACAAGATGCTTCACCACTGTACTTGGTGTGA 840
DB 781 TATGTGCTGATATGATCAAAAAACAAGATGCTTCACCACTGTACTTGGTGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATATGAGAGAGCTGCTCATCTTGTGTATGTTGTGATCAGACAGTATA 960
DB 901 CTGATATGATATGAGAGAGCTGCTCATCTTGTGTATGTTGTGATCAGACAGTATA 960
QY 961 GTGAGCTTTCTATCTGAGCAAAAAATGATATGATCTTCAAGATCTATCTGAGACAG 1020
DB 961 GTGAGCTTTCTATCTGAGCAAAAAATGATATGATCTTCAAGATCTATCTGAGACAG 1020
QY 1021 GGCAGAGATATGCTGTTCTGATCATCATGATATTTGGCAGTTACTTCTGATC 1080
DB 1021 GGCAGAGATATGCTGTTCTGATCATCATGATATTTGGCAGTTACTTCTGATC 1080
QY 1081 AAAGAAAAACAGATCTAAAAATCTCTGAAAAACAGAAATCCAGAACAAAGCTTAAAG 1140
DB 1081 AAAGAAAAACAGATCTAAAAATCTCTGAAAAACAGAAATCCAGAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAAGAGAAAGTCACAAAAGTTCAAAAGCATGAAATATGCCAGCAAGAAA 1200
DB 1141 CTGACATCAAGAGAAAGTCACAAAAGTTCAAAAGCATGAAATATGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGTTGTATGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGTTGTATGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGTGGATTTACTAGAAAACCTGATTAATGTGTCTGCTGTGC 1320
DB 1261 AAGCATGAAGATTAATGTGGATTTACTAGAAAACCTGATTAATGTGTCTGCTGTGC 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAAAGAGCAAGCACTGAAATATGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATCTCTCAAGAAAGAGCAAGCACTGAAATATGCAATTT 1380
QY 1381 CCTGACCAAGAAAGTGAAGATATCAAGAAATTTGCAATTTGATTTCTGACATCAAGAAA 1440
DB 1381 CCTGACCAAGAAAGTGAAGATATCAAGAAATTTGCAATTTGATTTCTGACATCAAGAAA 1440
QY 1441 AAAAGATGCGCAAAATATCTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCGCAAAATATCTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTCAAAAAGGCTTGAAGGCAAGTAAATGTCACAGAGCTAGAAAT 1560
DB 1501 TCAGAGAAAGAGTCAAAAAGGCTTGAAGGCAAGTAAATGTCACAGAGCTAGAAAT 1560
QY 1561 TTTATGCTATGAGAAATTAAGAAAGCAAGAAATTAATCTCATGTGGATTTCCCAAGAAA 1620
DB 1561 TTTATGCTATGAGAAATTAAGAAAGCAAGAAATTAATCTCATGTGGATTTCCCAAGAAA 1620
QY 1621 CTGACTAATGTGCACTGCTGCAATGTGATGATTAATTTCTTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTGCACTGCTGCAATGTGATGATTAATTTCTTCAAGAAAGAC 1680
QY 1681 AGAAGACCTGAAGACCAAGATTTCTGACACTGAGAAATGAAGATATCAAGTACGA 1740
DB 1681 AGAAGACCTGAAGACCAAGATTTCTGACACTGAGAAATGAAGATATCAAGTACGA 1740


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Db 1021 GCAGAGATATGCTTTCTAGTCATCATGTAATTTGCGATTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACGAAATTCAGAAACAAGCTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACGAAATTCAGAAACAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAACAAAGGTTCAAAAGCAGTGAATAATGCGACGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAACAAAGGTTCAAAAGCAGTGAATAATGCGACGAGAGAA 1200
QY 1201 ATGCTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGATGAGTCTAGTAAACCTGATTAATGATGATGATGATG 1320
Db 1261 AAGCATGAAGATTAATTAATGATGAGTCTAGTAAACCTGATTAATGATGATGATGATG 1320
QY 1321 AATGATGATTAATGATTAATTTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGATGATTAATGATTAATTTCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 CCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 AAAAGAGATGCGAAAAATCTCTTCTGAAAAACGAAATTCAGAAACAAGCTTAAAGCTGAC 1500
Db 1441 AAAAGAGATGCGAAAAATCTCTTCTGAAAAACGAAATTCAGAAACAAGCTTAAAGCTGAC 1500
QY 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 TTTATGCTATCGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 CTGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 CTGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 AGAAGACCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 AGAAGACCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 CAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 ATTCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
Db 1801 ATTCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
QY 1861 CTTAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 CTTAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
RESULT 6
AAH85029
ID AAH85029 standard; cDNA; 2000 BP.
XX AC AAH85029;
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XX 25-SBP-2001 (first entry)
DT Human prostate-specific cDNA sequence B305D splice variant #9.
DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
OS Homo sapiens.
PN WO200134802-A2.
PD 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US030904.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
XX (CORI-) CORIXA CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SJ, Jiang Y, Reed SG;
PI Kalos MD, Rector MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX MPI; 2001-308785/32.
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
PS Claim 31; Page 247-248; 325pp; English.
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention.
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGAGTTGATTCATGCCGCTGCTCTTCTGTAAGAGCATTTGGTCTC 60
Db 1 ATGCTGTTGAGAGTTGATTCATGCCGCTGCTCTTCTGTAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGCTGCGTTCCTCCCTGCTGAGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGCTGCGTTCCTCCCTGCTGAGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 GGCCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GGCCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
```

Db	1381	CCTGACAAACGAAGTGAAGAGTATCAGAGAAATTTGGAAATTAAGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCAGACACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCAGACACAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGAGTCCAAAGAGCTTGAAGGGAGTGAATAATGACCCAGAGCTTAGAAAT	1560
Db	1501	TCAGAGGAAGAGTCCAAAGAGCTTGAAGGGAGTGAATAATGACCCAGAGCTTAGAAAT	1560
Qy	1561	TTTATGGCTATCCGAAGAAATGGAAGACAGGAAGTACTCATGTCCGATTTCCAGAAAC	1620
Db	1561	TTTATGGCTATCCGAAGAAATGGAAGACAGGAAGTACTCATGTCCGATTTCCAGAAAC	1620
Qy	1621	CTGACTATATGATGCTGCTGCGCAATGATGATGATTAATTCCTCCAGGAAGAGC	1680
Db	1621	CTGACTATATGATGCTGCTGCGCAATGATGATGATTAATTCCTCCAGGAAGAGC	1680
Qy	1681	AGAACACCTGAAAAGCCAGCAATTTCTGACACTGAGATTAAGATTCACAGTGAAGAA	1740
Db	1681	AGAACACCTGAAAAGCCAGCAATTTCTGACACTGAGATTAAGATTCACAGTGAAGAA	1740
Qy	1741	CAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG	1800
Db	1741	CAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG	1800
Qy	1801	ATTCTGATCATGAGAGAAAGCAGATAGAAATGGTGTGAATAATGAAATTCGAGCTTCT	1860
Db	1801	ATTCTGATCATGAGAGAAAGCAGATAGAAATGGTGTGAATAATGAAATTCGAGCTTCT	1860
Qy	1861	CTTATGTTGTAAAGAAAGAAAGACATCTTGTGATGAAATATGTACCTTGGGAAAGAAAT	1920
Db	1861	CTTATGTTGTAAAGAAAGAAAGACATCTTGTGATGAAATATGTACCTTGGGAAAGAAAT	1920
Qy	1921	GCCATGCTAAGCTGAGAGCTAGACACAATGAAACATGAGGCCAGCTTAAATAAAAA	1980
Db	1921	GCCATGCTAAGCTGAGAGCTAGACACAATGAAACATGAGGCCAGCTTAAATAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 7			
ACAS9616 standard; cDNA; 2000 BP.			
AC	ACAS9616;		
DT	10-JUN-2003 (first entry)		
DE	Prostate cancer therapy associated cDNA #359.		
KW	Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;		
KW	immunogen; cancer; prostate specific antigen; PSA;		
KW	prostatic acid phosphatase; PAP; prostate specific membrane antigen;		
KW	PSMA; gene; ss.		
OS	Homo sapiens.		
FN	US2002192763-A1.		
PD	19-DEC-2002.		
PF	29-JUN-2001; 2001US-00895793.		
PR	04-OCT-1999; 99US-0157455P.		
PR	04-OCT-2000; 2000US-00679272.		
PR	28-MAR-2001; 2001US-00822827.		
PA	(XUJ/) XU J.		
PA	(DIL/) DILON D C.		
PA	(MIT/) MITCHAM J L.		

PA (HARL/) HARLOCKER S. L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M. D.
 PA (FANG/) FANGER G. R.
 PA (RETT/) RETTER M. W.
 PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEL/) SKELLY Y. A. W.
 PA (HEPL/) HEPLER W. T.
 PA (HEND/) HENDERSON R. A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P. D.
 PA (HOUN/) HOUGHTON R. L.
 PA (DBAS/) Y. DE BASSOLS C. V.
 PA (FOYT/) FOY T. M.

PI Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
 PI Li SK, Wang A, Skelly YAW, Hepler WT, Henderson RA, Hural J;
 PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
 DR MPI; 2001-245062/25.
 XX P-PSDB; AB071669.

PT Prostate specific protein and its encoding polynucleotide, useful for the
 XX treatment and diagnosis of prostate cancer.

PS Example 11; SEQ ID NO 374; 85bp; English.

XX The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 3 sequences defined in the USPO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This sequence represents a prostate cancer
 CC therapy associated CDNA. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 5; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
 DB 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
 QY 61 AGAAGCAAGTGGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
 DB 61 AGAAGCAAGTGGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGGAGACGAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
 DB 121 AGCAAGTGGGCACTTCTGGAGACGAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCGAGGAGGAGTGGCAAGCAAGT 240
 DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCGAGGAGGAGTGGCAAGCAAGT 240
 QY 241 GGGGCTTTTGGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
 DB 241 GGGGCTTTTGGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
 QY 241 GGGGCTTTTGGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300

1

QY 301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGGAGGCAAGGATGGGCGCTTGG 360
 DB 301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGGAGGCAAGGATGGGCGCTTGG 360
 QY 361 GGAAGCTAGATGACAGTGCCTTCAATGAGCCAGGTACACGTCCTGTGAGAAATCTG 420
 DB 361 GGAAGCTAGATGACAGTGCCTTCAATGAGCCAGGTACACGTCCTGTGAGAAATCTG 420
 QY 421 GACAACTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 DB 421 GACAACTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 481 CTCAGGAGCACTGAGCTGAGCAAGAAAGCAAGCAAGAAAGAGAGCTCTTCAATCTG 540
 DB 481 CTCAGGAGCACTGAGCTGAGCAAGAAAGCAAGCAAGAAAGAGAGCTCTTCAATCTG 540
 QY 541 TCTGCAATGGGAATTCAGAAAGTAAAGCTCTGCTGAGCAGAGATGTCACTTAAT 600
 DB 541 TCTGCAATGGGAATTCAGAAAGTAAAGCTCTGCTGAGCAGAGATGTCACTTAAT 600
 QY 601 GTCTTTGACAAACAAAGAGGACAGCTCTGATTAAGCCGTACATGCCAGAAATGAA 660
 DB 601 GTCTTTGACAAACAAAGAGGACAGCTCTGATTAAGCCGTACATGCCAGAAATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
 DB 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
 QY 721 ACCACTGTGCACTGATCTATCTATATGAAATTAATTAATGCAAGAGCTGCTCTTA 780
 DB 721 ACCACTGTGCACTGATCTATCTATATGAAATTAATTAATGCAAGAGCTGCTCTTA 780
 QY 781 TATGTTGCTGATATGAAATCAAAAGCAAGTGGCTTCAACACCTGTTACTTGGTGA 840
 DB 781 TATGTTGCTGATATGAAATCAAAAGCAAGTGGCTTCAACACCTGTTACTTGGTGA 840
 QY 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGCAATTTAAATGCA 900
 DB 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGCAATTTAAATGCA 900
 QY 901 CTGATATGATATGAAAGCATGCTCTCATATCTGCTGATATGTTGGATCAAGATATA 960
 DB 901 CTGATATGATATGAAAGCATGCTCTCATATCTGCTGATATGTTGGATCAAGATATA 960
 QY 961 GTACGCTTCTACTTGAAGCAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
 DB 961 GTACGCTTCTACTTGAAGCAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
 QY 1021 GCCAAGAGTATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
 DB 1021 GCCAAGAGTATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
 QY 1081 AAAAGAAAACAGATCTTAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
 DB 1081 AAAAGAAAACAGATCTTAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAGGCAAGTAAATAGCCAGCAAGAAA 1200
 DB 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAGGCAAGTAAATAGCCAGCAAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
 DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAAATATGATGGAATTAATGAAAACCTGACTAATGTGTCACTG 1320
 DB 1261 AAGCATGAAAGTAAATATGATGGAATTAATGAAAACCTGACTAATGTGTCACTG 1320
 QY 1321 AATGTGATTAATGATTAATTTCTTCAAGAGAGAGCAAGAACCTGAAATCAGCAATT 1380
 DB 1321 AATGTGATTAATGATTAATTTCTTCAAGAGAGAGCAAGAACCTGAAATCAGCAATT 1380
 QY 1381 CCTGACAAAGGAAAGTAAAGATATCAAGAAATTTGGGAATTTGTTCTGACTACAAAGAA 1440

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Db      1381 CCTGACACGAAAGTGAAGGTATCACGAATTTGGCAATTAATTTCTGACTCAAGAA 1440
Qy      1441 AAACAGATGCCAAATATCTCTTGTAAAACAGCAACCAGACAAGAATTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATATCTCTTGTAAAACAGCAACCAGACAAGAATTAAAGCTGACA 1500
Qy      1501 TCAGAGGAAGATCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
Db      1501 TCAGAGGAAGATCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
Qy      1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGGAAGTACTATGTCGGATTCGCCAGAAAAC 1620
Db      1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGGAAGTACTATGTCGGATTCGCCAGAAAAC 1620
Qy      1621 CTGACTAATGTCGCACTGCTGGCAATGTGATGATGATTAATTCCTCCAGGAAGAGC 1680
Db      1621 CTGACTAATGTCGCACTGCTGGCAATGTGATGATGATTAATTCCTCCAGGAAGAGC 1680
Qy      1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATGACAGTGAAGAA 1740
Db      1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATGACAGTGAAGAA 1740
Qy      1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
Db      1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAAAGCAGATGAAAGTGGTGAATAATTCGACTTCTTCT 1860
Db      1801 ATTCTGATTCATGAGAAAGCAGATGAAAGTGGTGAATAATTCGACTTCTTCT 1860
Qy      1861 CTTAAGTTGTGAAGAAAGACATTTCTGACATGAATAATGTACGTTGCGGAAAGAAAT 1920
Db      1861 CTTAAGTTGTGAAGAAAGACATTTCTGACATGAATAATGTACGTTGCGGAAAGAAAT 1920
Qy      1921 GCCATGCTAGAGCTGAGCTGAGACACAATGAAACATCAGAGCCAGCTAAAGAAAAA 1980
Db      1921 GCCATGCTAGAGCTGAGCTGAGACACAATGAAACATCAGAGCCAGCTAAAGAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
ABL95179
ID      ABL95179 standard; cDNA; 2000 BP.
XX
AC      ABL95179;
XX
DT      19-JUL-2002 (first entry)
XX
DE      Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
KW      Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX      gene therapy; gene; ss.
OS      Homo sapiens.
XX
PN      US2002022248-A1.
XX
PD      21-FEB-2002.
XX
PF      12-JAN-2001; 2001US-00759143.
XX
PR      25-FEB-1997; 97US-00806099.
PR      10-AUG-1997; 97US-00904804.
PR      10-FEB-1998; 98US-00020956.
PR      25-FEB-1998; 98US-00030607.
PR      14-JUL-1998; 98US-00115453.
PR      23-SEP-1998; 98US-00159812.
PR      15-JAN-1999; 99US-00232149.
PR      09-APR-1999; 99US-00288946.

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PR      13-JUL-1999; 99US-00352616.
PR      12-NOV-1999; 99US-00439313.
PR      18-NOV-1999; 99US-00443686.
PR      14-JAN-2000; 2000US-00483672.
PR      27-MAR-2000; 2000US-00536857.
PR      09-MAY-2000; 2000US-00568100.
PR      12-MAY-2000; 2000US-00570737.
PR      13-JUN-2000; 2000US-00593793.
PR      27-JUN-2000; 2000US-00605783.
PR      10-AUG-2000; 2000US-00636215.
PR      29-AUG-2000; 2000US-00651236.
PR      06-SEP-2000; 2000US-00657129.
PR      02-OCT-2000; 2000US-00679426.
PR      10-OCT-2000; 2000US-00685166.
XX
XX      (XUJ/) XU J.
PA      (DILL/) DILLON D C.
PA      (MITC/) MITCHAM J L.
PA      (HARL/) HARLOCKER S L.
PA      (JIAN/) JIANG Y.
PA      (KALO/) KALOS M D.
PA      (FANG/) FANGER G R.
PA      (RETT/) RETTER M W.
PA      (STOL/) STOLK J A.
PA      (DAYC/) DAY C H.
PA      (VEDV/) VEDVICK T S.
PA      (CART/) CARTER D.
PA      (LISX/) LI S X.
PA      (WANG/) WANG A.
PA      (SKEI/) SKEIKY Y A W.
PA      (HEPL/) HEPLER W T.
PA      (HEND/) HENDERSON R A.
XX
XX      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI      Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX      WPI; 2002-255649/30.
XX
XX      New prostate-specific polynucleotides for diagnosing and treating
PT      diseases, in particular prostate cancer, and as markers for the
PT      progression of cancer.
XX
XX      Claim 1; SEQ ID NO 374; 87bp; English.
XX
XX      The present invention provides prostate-specific coding sequences and
CC      their encoded proteins. These can be used in the diagnosis and treatment
CC      of cancers, particularly prostate cancer. The present sequence is a cDNA
CC      described in the invention
XX
SQ      Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match      100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
Db      1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
Qy      61 AGAGGCAAGATGGGCAAGTGTGCTGCTGTTCCCTGCTGCGAGGAGCGGCAAG 120
Db      61 AGAGGCAAGATGGGCAAGTGTGCTGCTGTTCCCTGCTGCGAGGAGCGGCAAG 120
Qy      121 AGCAAGTGGGCACTTCTGAGACGACGACTGTCTATGAAGACACTCAGAGCAAG 180
Db      121 AGCAAGTGGGCACTTCTGAGACGACGACTGTCTATGAAGACACTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Db      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Qy      241 GGGCTTCTGAGAGCAAGCAAGCACTGTGTAAGACACTCAGAGCAAGAGTGGCAAG 300

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Db      241 GGGGCTTCGAGAGACGACGACTGCTATGAAACACTCAGAAACAAGTGGCAG 300
Qy      301 TGGTGTGGCAGCTGTTCCCTGCTGACGGGGAGGGAGGAGCAAGGGCGGCTTGG 360
Db      301 TGGTGTGGCAGCTGTTCCCTGCTGACGGGGAGGGAGGAGCAAGGGCGGCTTGG 360
Qy      361 GGAAGTACGATGACAGTGGCTTCATGAGGCCAGGTACACGTCCTGGAGAGATCTG 420
Db      361 GGAAGTACGATGACAGTGGCTTCATGAGGCCAGGTACACGTCCTGGAGAGATCTG 420
Qy      421 GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTAG 480
Db      421 GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTAG 480
Qy      481 CTCAGGGACACTGACGTTGAAACAAGAGCAAGCAAAAGAGAGCTGCTACACTGGCC 540
Db      481 CTCAGGGACACTGACGTTGAAACAAGAGCAAGCAAAAGAGAGCTGCTACACTGGCC 540
Qy      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGAGATGCACTTAAT 600
Db      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGAGATGCACTTAAT 600
Qy      601 GTCTTGAACAACAAGAGAGACGCTCTGATTAAGCCGTACATGCCAGAAAGTAA 660
Db      601 GTCTTGAACAACAAGAGAGACGCTCTGATTAAGCCGTACATGCCAGAAAGTAA 660
Qy      661 TGTGCGTTATGTTGCTGGAACATGGACCTGATCCAAATATTCAGATAGATGGAAT 720
Db      661 TGTGCGTTATGTTGCTGGAACATGGACCTGATCCAAATATTCAGATAGATGGAAT 720
Qy      721 ACCACTCTGACACTACCTATCTATAATGAAGATAAATTAATGCGCAAGCACTGCTTA 780
Db      721 ACCACTCTGACACTACCTATCTATAATGAAGATAAATTAATGCGCAAGCACTGCTTA 780
Qy      781 TATGTGCTGATATCGAATCAAAAAACAAGCATGGCTCACACCATGTTACTGGTGTAA 840
Db      781 TATGTGCTGATATCGAATCAAAAAACAAGCATGGCTCACACCATGTTACTGGTGTAA 840
Qy      841 CATGACAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
Db      841 CATGACAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
Qy      901 CTGGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
Db      901 CTGGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
Qy      961 GTTCAGCTTCTACTTGAAGCAAAATTTGATGTATCTTCAAGATCTATCTGGACAGAG 1020
Db      961 GTTCAGCTTCTACTTGAAGCAAAATTTGATGTATCTTCAAGATCTATCTGGACAGAG 1020
Qy      1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCAAGTACTCTTCTGACTAC 1080
Db      1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCAAGTACTCTTCTGACTAC 1080
Qy      1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACGCAATCCAGAACAGCTTAAAG 1140
Db      1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACGCAATCCAGAACAGCTTAAAG 1140
Qy      1141 CTGACATCAGAGAGAGATCAAAAGTTCAAAAGGCAAGTAAATAGCCAGCCAGAGAAA 1200
Db      1141 CTGACATCAGAGAGAGATCAAAAGTTCAAAAGGCAAGTAAATAGCCAGCCAGAGAAA 1200
Qy      1201 ATGCTCAAGAAACAGAAATTAATTAAGATGTGATAGAGAGGTGAAGAAAGAAAGAG 1260
Db      1201 ATGCTCAAGAAACAGAAATTAATTAAGATGTGATAGAGAGGTGAAGAAAGAAAGAG 1260
Qy      1261 AAGCATGAAAGTAAATATGAGATTAGAAAACTGACTAATGCTGCTGAC 1320
Db      1261 AAGCATGAAAGTAAATATGAGATTAGAAAACTGACTAATGCTGCTGAC 1320
Qy      1321 AATGTGATATATGATTTAATTTCTCAAGAGAGAGAGAACCTGAAATACAGCAATTT 1380
Db      1321 AATGTGATATATGATTTAATTTCTCAAGAGAGAGAGAACCTGAAATACAGCAATTT 1380

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Db      1321 AATGTGATATATGATTTAATTTCTCAAGAGAGAGAGAACCTGAAATACAGCAATTT 1380
Qy      1381 CCTGACAAGAAAGTAAAGATATCAAGAAATTTGCGAAATTTGTTCTGATCAAGAAAG 1440
Db      1381 CCTGACAAGAAAGTAAAGATATCAAGAAATTTGCGAAATTTGTTCTGATCAAGAAAG 1440
Qy      1441 AAACAGATGCCAAATACTCTCTGAAAAACAGCAACCAGAAACAAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATACTCTCTGAAAAACAGCAACCAGAAACAAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCGAGTAAATGGCCAGCAGAGCTAGAAAAAT 1560
Db      1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCGAGTAAATGGCCAGCAGAGCTAGAAAAAT 1560
Qy      1561 TTTATGGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAAC 1620
Db      1561 TTTATGGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAAC 1620
Qy      1621 CTGACTAATGGTGCCACTGCTGGCAATGATGATGATTAATTTCTTCAAGAAAGAC 1680
Db      1621 CTGACTAATGGTGCCACTGCTGGCAATGATGATGATTAATTTCTTCAAGAAAGAC 1680
Qy      1681 AGAACACTGAAAGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
Db      1681 AGAACACTGAAAGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
Qy      1741 CAAAATGATACACAGAAAGTTTGTGAAGACAGAACACTGGAATTAACAGATGAG 1800
Db      1741 CAAAATGATACACAGAAAGTTTGTGAAGACAGAACACTGGAATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAAAGAGAGATAGAGTGTGAAAAATGAAATTTCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAGAAAGAGAGATAGAGTGTGAAAAATGAAATTTCTGAGCTTTCT 1860
Qy      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCACTGAAAAATGTAAGTTGCGGGAGAGAAAT 1920
Db      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCACTGAAAAATGTAAGTTGCGGGAGAGAAAT 1920
Qy      1921 GCCATGCTTAAGCTGAGAGTACACAAATGAACATCAGAGCAGCTAAAAAAGAAAAA 1980
Db      1921 GCCATGCTTAAGCTGAGAGTACACAAATGAACATCAGAGCAGCTAAAAAAGAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 9
AAS99858
ID AAS99858 standard; cDNA; 2000 BP.
XX
AC AAS99858;
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11g1 splice variant B11C-8.
XX
KW Human; breast cancer; PCR primer; ss; cytosolic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN MO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX

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(CORI-) CORIXA CORP.

PA Frudekis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
PI Wang A, Skeiky YAM, Harlocker SL, Day CH;
XX WPI; 2002-089919/12.
DR P-PSDB; AAU74378.

XX New breast tumor proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response.

Claim 1: Page 224; 245pp; English.

XX The invention relates to novel breast tumour polynucleotides and
XX polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response.
CC Particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
CC represent novel human breast cancer protein coding sequences and PCR
CC primers of the invention

Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 6; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTGATTCATGCGGCTGCTCTTGTGGAAGCCATTGTGCTC 60
DB 1 ATGGTGTGAGGTGATTCATGCGGCTGCTCTTGTGGAAGCCATTGTGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCTGT 240
DB 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCTGT 240
QY 241 GGGGCTTCTGGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTCTGGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGAGTGGGCTGTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGAGTGGGCTGTGG 360
QY 361 GGAAGTACGATACAGTGTGCTTCAATGAGCCAGGTACCAAGTGTGGAGAAAGTCTG 420
DB 361 GGAAGTACGATACAGTGTGCTTCAATGAGCCAGGTACCAAGTGTGGAGAAAGTCTG 420
QY 421 GACAACTCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAACTCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTGAGGGAACCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 CTGAGGGAACCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGCAAGAGATGCTCAATTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGCAAGAGATGCTCAATTAAT 600
QY 601 GTCTTGAACAACAAAAGAGGACGCTGTATTAAGGCGGTACAAATGCCAGAAAGTGA 660

DB 601 GTCTTGAACAACAAAAGAGGACGCTGTATTAAGGCGGTACAAATGCCAGAAAGTGA 660
QY 661 TGTGCTTAATGTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGGCTATCTATATGAAGTAAATTAATGCGCAAGACCTGCTTA 780
DB 721 ACCACTCTGCACTAGGCTATCTATATGAAGTAAATTAATGCGCAAGACCTGCTTA 780
QY 781 TATGCTGATATGGAATCAAAAACAGATGCTGCAAGATCTATCTGATGCTGTA 840
DB 781 TATGCTGATATGGAATCAAAAACAGATGCTGCAAGATCTATCTGATGCTGTA 840
QY 841 CATGACAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAACGAAATTTAAATGCA 900
DB 841 CATGACAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAACGAAATTTAAATGCA 900
QY 901 CTGATATGATGGAAGAGCTGCTCATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 CTGATATGATGGAAGAGCTGCTCATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 GTGAGCTTCTATGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTATGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGCTTCTATGATCATCATGTAATTTGCAAGTCTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGCTTCTATGATCATCATGTAATTTGCAAGTCTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAATTTCTTCTGAAAAACGAAATCCAGAACTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAATTTCTTCTGAAAAACGAAATCCAGAACTTAAG 1140
QY 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAGGAGTAAATGCGACAGAGAA 1200
DB 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAGGAGTAAATGCGACAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATAGAGAGTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATAGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATGATGAGATTAATGAGTAACTGAGAAACCTGATATGCTGCTG 1320
DB 1261 AAGCATGAAGTAAATGATGAGATTAATGAGTAACTGAGTAACTGATATGCTGCTG 1320
QY 1321 AATGATGAATATGATTAATTTCTCAAGAGAGAGAGACACCTGAATATGAGCAATT 1380
DB 1321 AATGATGAATATGATTAATTTCTCAAGAGAGAGAGACACCTGAATATGAGCAATT 1380
QY 1381 CCTGACAAAGAGAGAGATATCAAGAAATTTGCAATTAATGATTAATGATTAATG 1440
DB 1381 CCTGACAAAGAGAGAGATATCAAGAAATTTGCAATTAATGATTAATGATTAATG 1440
QY 1441 AAAAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAACTTAAGCTGACA 1500
DB 1441 AAAAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAACTTAAGCTGACA 1500
QY 1501 TCAAGAGAGAGATCAAAAGGCTTGAAGGCACTGAAATAGGCGACAGAGCTAGAAAT 1560
DB 1501 TCAAGAGAGAGATCAAAAGGCTTGAAGGCACTGAAATAGGCGACAGAGCTAGAAAT 1560
QY 1561 TTTATGCTATGAGAAATGAAAGACAGGAAGTACTCATGTGAGATTTCCAGAAAC 1620
DB 1561 TTTATGCTATGAGAAATGAAAGACAGGAAGTACTCATGTGAGATTTCCAGAAAC 1620
QY 1621 CTGACTAATGTGCTCACTGCTGCAATGCTGATATTAATTTCTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTGCTCACTGCTGCAATGCTGATATTAATTTCTCAAGAAAGAC 1680
QY 1681 AAGAACCTGGAAGCAGCAATTTCTGCACTGGAATGAAGAGTATCACTGACGA 1740

Db 1681 AGAACAAGCTGAAAGCAATTTCTGACACTGAGATGAAGATATCATACAGTACGAA 1740
QY 1741 CAATAATGATCTAGAGAGCAATTTTGTGAAGACAGAACTGGAATATTATACAGATGAG 1800
Db 1741 CAATAATGATCTAGAGAGCAATTTTGTGAAGACAGAACTGGAATATTATACAGATGAG 1800
QY 1801 ATTCTGATTCATGAGAGAGAGAGATGAGATGAGTGTGAAATTAATGATTCGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAGAGAGAGAGATGAGATGAGTGTGAAATTAATGATTCGAGCTTTCT 1860
QY 1861 CTTAGTGTGAGAGAGAGAGAGATCTTGTGATGAAATATGATCGTTGCGGAGAAATTT 1920
Db 1861 CTTAGTGTGAGAGAGAGAGAGATCTTGTGATGAAATATGATCGTTGCGGAGAAATTT 1920
QY 1921 GCCATGCTAGAGCTGAGAGCTAGACATGAAATCATGAGCGAGCTTAAAAA 1980
Db 1921 GCCATGCTAGAGCTGAGAGCTAGACATGAAATCATGAGCGAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
RESULT 10
ACC95343
ID ACC95343 standard; cDNA; 2000 BP.
XX
AC ACC95343;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific cDNA sequence SEQ ID 374.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW Immune response; prostate cancer; ss.
OS Homo sapiens.
XX
PN MO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002MO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-0085814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA,
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CR, Vedrick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepner WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Baesisc, Foy TM, Watanabe Y;
PI Deng T;
XX
DR MPI; 2003-167130/16.
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Example 11; Page 415-416; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTGAGGTTGATTCATGCGCGGCTGCTCTTGTGTAAGAGCCATTGGTCTC 60
Db 1 ATGGTGTGAGGTTGATTCATGCGCGGCTGCTCTTGTGTAAGAGCCATTGGTCTC 60
QY 61 AGAGCAGAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCGAGGAGCGGCAAG 120
Db 61 AGAGCAGAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCGAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAAGCACTGCTGATGAAGCACTCAGGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGGAAGCAAGCACTGCTGATGAAGCACTCAGGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCAGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCTTG 240
Db 181 ATGGGCAAGTGTGCGCCAGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCTTG 240
QY 241 GCGGCTTCTGAGAGCAAGCACTCTGCTATGAAGCACTCAGGAACAAGTGGCAAG 300
Db 241 GCGGCTTCTGAGAGCAAGCACTCTGCTATGAAGCACTCAGGAACAAGTGGCAAG 300
QY 301 TGGTGTGCTGACGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAGAGTGGCGCTTGG 360
Db 301 TGGTGTGCTGACGCTTCCCTGCTGCGAGGAGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAAGCTAGATGAGAGAGTGCCTTCAATGAGAGCCAGGTACCACTGCTGAGAGATCTTG 420
Db 361 GGAAGCTAGATGAGAGAGTGCCTTCAATGAGAGCCAGGTACCACTGCTGAGAGATCTTG 420
QY 421 GACAAGCTCCAGAGAGCTGCTGCTGAGGAGTAAAGTCCCGAAGAGATCTCATGCTCAG 480
Db 421 GACAAGCTCCAGAGAGCTGCTGCTGAGGAGTAAAGTCCCGAAGAGATCTCATGCTCAG 480
QY 481 CTCAGGGAACATGAGAGTGAACAAGAGCAAGCAAGAGAGAGTCTTACATCTGGCC 540
Db 481 CTCAGGGAACATGAGAGTGAACAAGAGCAAGCAAGAGAGAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGCTGAGAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGCTGAGAGAGATGCACTTAAT 600
QY 601 GTCTTGTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCTTGTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCGTTAATGTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGCTATCTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTGA 780
Db 721 ACCACTCTGCACTAGCTATCTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTGA 780
QY 781 TATGTGCTGATATGATGATCAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 TATGTGCTGATATGATGATCAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CATGAGCAACAAACAG 900
Db 841 CATGAGCAACAAACAG 900
QY 901 CTGATATGATATGAT 960
Db 901 CTGATATGATATGAT 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020

QY	1021	GGCCAGAGATATGCTGTTTCTTAGTATCATATGTAATTTGGCAGTTACTTTCTGACTAC	1080
Db	1021	GGCAAGAGATATGCTGTTTCTTAGTATCATATGTAATTTGGCAGTTACTTTCTGACTAC	1080
QY	1081	AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACACATCCAGAACCAAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACACATCCAGAACCAAGACTTAAAG	1140
QY	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAAGGCACTGAAAAATAGCCACAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAAGGCACTGAAAAATAGCCACAGAGAA	1200
QY	1201	ATGTCCTCAAGAACCCGAAATTAATTAAGATGGTGTATAGAGGTTGAAAGAAATGAAG	1260
Db	1201	ATGTCCTCAAGAACCCGAAATTAATTAAGATGGTGTATAGAGGTTGAAAGAAATGAAG	1260
QY	1261	AAGCATGAAGTAATTAATGTGGATTTACTAGAAAACCTGAATATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAGTAATTAATGTGGATTTACTAGAAAACCTGAATATGTGTCACTGTGGC	1320
QY	1321	AATGTGTAAATGATTAATTCCTCAAGAAAGCAGAACACCTGAAATCAGCAATTT	1380
Db	1321	AATGTGTAAATGATTAATTCCTCAAGAAAGCAGAACACCTGAAATCAGCAATTT	1380
QY	1381	CCTGACAAAGAAAGTAAAGATATCACAAATTTGCGAATAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAAGAAAGTAAAGATATCACAAATTTGCGAATAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACGATATGCCAAATTACTCTTCTGAAAAACAGCAACCCAGAACAAAGATTAAAGTACA	1500
Db	1441	AAACGATATGCCAAATTACTCTTCTGAAAAACAGCAACCCAGAACAAAGATTAAAGTACA	1500
QY	1501	TCAGAGAAAGAGTCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTGAAAT	1560
Db	1501	TCAGAGAAAGAGTCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTGAAAT	1560
QY	1561	TTTATGTGCTATCGAAGAAATGAAAGACCGGAAGTACTCATGTGCGAATTTCCAGAAAC	1620
Db	1561	TTTATGTGCTATCGAAGAAATGAAAGACCGGAAGTACTCATGTGCGAATTTCCAGAAAC	1620
QY	1621	CTGACTAATTGGTGCACCTGTGGCAATGTGATGATGATTAATTTCTCCAAAGAAAGC	1680
Db	1621	CTGACTAATTGGTGCACCTGTGGCAATGTGATGATGATTAATTTCTCCAAAGAAAGC	1680
QY	1681	AGAACACCTGAAAGCAGCAATTTCTCTGACACTGAGATGAAGAGTATCAAGTGAAGAA	1740
Db	1681	AGAACACCTGAAAGCAGCAATTTCTCTGACACTGAGATGAAGAGTATCAAGTGAAGAA	1740
QY	1741	CAAAATGATTACTCAGAAAGCAATTTTGTGAAAGACAGAACTGGAATATTACAGATGAG	1800
Db	1741	CAAAATGATTACTCAGAAAGCAATTTTGTGAAAGACAGAACTGGAATATTACAGATGAG	1800
QY	1801	ATTCTGATTCATGAAAGAAAGCAGATAGAAAGTGGTTGAAAAATGAATTCGAGCTTTCT	1860
Db	1801	ATTCTGATTCATGAAAGAAAGCAGATAGAAAGTGGTTGAAAAATGAATTCGAGCTTTCT	1860
QY	1861	CTTGTGTTGTAAGAAAGAAAGACATCTTGATGAAAAATAGTAACTTGGCGGAAAGAAAT	1920
Db	1861	CTTGTGTTGTAAGAAAGAAAGACATCTTGATGAAAAATAGTAACTTGGCGGAAAGAAAT	1920
QY	1921	GCCATGTCTAAAGTCTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATGAAAT	1980
Db	1921	GCCATGTCTAAAGTCTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATGAAAT	1980
QY	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	
RESULT 11			
ADAL1381			
ID	ADAL1381	standard; cDNA; 2000 BP.	
XX			

ADAl1381;
06-NOV-2003 (first entry)
Human breast cancer specific cDNA B11C-8.
ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.
Homo sapiens.
US2002165371-A1.
07-NOV-2002.
07-AUG-2001; 2001US-00924400.
11-JAN-1996; 96US-00585392.
10-JAN-1997; 97WO-US000485.
09-APR-1997; 97US-00838762.
11-DEC-1997; 97US-00991789.
17-APR-1998; 98US-00062451.
09-APR-1999; 99US-00289128.
28-OCT-1999; 99US-00429755.
23-MAR-2000; 2000US-00534825.
24-MAY-2000; 2000US-00577505.
08-JUN-2000; 2000US-00590583.
26-OCT-2000; 2000US-00699295.
16-MAR-2001; 2001US-00810936.
FRUD./ FRUDAKIS T N.
REED./ REED S G.
SMIT./ SMITH J M.
MISH./ MISHER L E.
DILL./ DILLON D C.
RETT./ RETTER M W.
WANG./ WANG A.
SKEI./ SKEIKY Y A W.
HARL./ HARLOCKER S L.
DAYC./ DAY C H.
LISX./ LI S X.
DENG./ DENG T.
Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW, Wang A, Skelky YAW, Harlocker SL, Day CH, Li SX, Deng T; P-PSDB; ADAl1384.
WPI: 2003-247262/24.
New breast tumor proteins nucleic acids encoding such proteins, useful in diagnosing, preventing and/or treating diseases such as cancer, particularly breast cancer, and as markers for detecting the presence of a cancer.
Claim 1; Page 140; 190pp; English.
The invention relates to a breast tumour polynucleotide selected from one of the 275 fully defined nucleotide sequences (a) given in the specification, including their complements, sequences consisting of at least 20 contiguous residues of a sequence in (a), sequences that hybridise to a sequence in (a) under moderately stringent conditions, sequences having at least 75% or 90% identity to a sequence in (a), or degenerate variants of a sequence in (a). Also included are an isolated polypeptide (II) (comprising an amino acid sequence selected from sequences encoded by (a), sequences having at least 70% or 90% identity to a sequence encoded by (a), sequences of 30 fully defined amino acid sequences (c), and sequences having at least 70% or 90% identity to a sequence in (c)), expression vectors comprising (a), a host cell transformed or transfected with the expression vector, an isolated antibody or its antigen-binding fragment that specifically binds to (II), a method for detecting the presence of a cancer in a patient, a fusion protein comprising at least one polypeptide (II), an oligonucleotide that hybridises to (a), under moderately stringent conditions, a method for stimulating and/or expanding T cells specific for a tumour protein (bv


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Db      1141 CTGACATCAGAGGAAAGTCACAAAAGTTCAAAAGCAGTGAATAATGACGACAGAGAA 1200
Qy      1201 ATGTCTCAAGAACCGAATAATTAAGATGTGTATGAGAGCTTGAAATAAATATGAG 1260
Db      1201 ATGTCTCAAGAACCGAATAATTAAGATGTGTATGAGAGCTTGAAATAAATATGAG 1260
Qy      1261 AAGCATGAAAGTATATATGTGGATTACTAGAAAACCTACTATATGTGTCACTGCTGAC 1320
Db      1261 AAGCATGAAAGTATATATGTGGATTACTAGAAAACCTACTATATGTGTCACTGCTGAC 1320
Qy      1321 AATGTGTATATATGATTAATTTCTCTCAAGAGAGACAGAACCTTGAAATATGACAAATT 1380
Db      1321 AATGTGTATATATGATTAATTTCTCTCAAGAGAGACAGAACCTTGAAATATGACAAATT 1380
Qy      1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGATTTGTTCTGACTACAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGATTTGTTCTGACTACAAAGAA 1440
Qy      1441 AAACAGATGCCAAAATATCTCTTCTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAAATATCTCTTCTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGGAAAGAGTCACAAAGGCTTGAGGCGAGTGAATGCGCAGCCAGAGCTAGAAAT 1560
Db      1501 TCAGAGGAAAGAGTCACAAAGGCTTGAGGCGAGTGAATGCGCAGCCAGAGCTAGAAAT 1560
Qy      1561 TTTATGGCTATGAGAAATGAAAGACGGAAGTACTCATGTGGATTTCCCAAGAAAC 1620
Db      1561 TTTATGGCTATGAGAAATGAAAGACGGAAGTACTCATGTGGATTTCCCAAGAAAC 1620
Qy      1621 CTGACTAATGTGTCACCTGCTGCGCAATGTGTATGATGATTAATTTCTTCAAGAGAGAC 1680
Db      1621 CTGACTAATGTGTCACCTGCTGCGCAATGTGTATGATGATTAATTTCTTCAAGAGAGAC 1680
Qy      1681 AGAACAACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAAGATATACAGTACGAA 1740
Db      1681 AGAACAACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAAGATATACAGTACGAA 1740
Qy      1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACAGATGAG 1800
Db      1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAAAGAGAGATAGAGTGTGTTGAAATAATGATTTCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAGAAAGAGAGATAGAGTGTGTTGAAATAATGATTTCTGAGCTTTCT 1860
Qy      1861 CTTAGTTGTAGAGAAAGAAAGACATCTTGCAATGAAAATATGATGCTTGGCGAGAAATT 1920
Db      1861 CTTAGTTGTAGAGAAAGAAAGACATCTTGCAATGAAAATATGATGCTTGGCGAGAAATT 1920
Qy      1921 GCCATGCTAAGACTGGAGCTAGACAAATGAAACATCAGAGCAGCTAATAAAAAAAAAA 1980
Db      1921 GCCATGCTAAGACTGGAGCTAGACAAATGAAACATCAGAGCAGCTAATAAAAAAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 13
ADBI3824
ID      ADBI3824 standard; cDNA; 2000 BP.
XX
AC      ADBI3824;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Human prostate specific cDNA B305 splice variant #9.
XX
KW      Human; 88; prostate specific cDNA; cytosolic; immunostimulant;
KW      gene therapy; cell therapy; vaccine; T-cell epitope;
KW      class I major histocompatibility complex allele; MHC; prostate cancer;
KW      tumour; antigen presenting cell.

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XX      XX      Homo sapiens.
OS      XX      US2003185830-A1.
PN      XX      02-OCT-2003.
PD      XX      12-NOV-2002; 2002US-00294025.
PF      XX      25-FEB-1997; 97US-00806099.
PR      XX      01-AUG-1997; 97US-00904804.
PR      XX      09-FEB-1998; 98US-00202956.
PR      XX      25-FEB-1998; 98US-00030607.
PR      XX      14-JUL-1998; 98US-00115453.
PR      XX      23-SEP-1998; 98US-00159812.
PR      XX      15-JAN-1999; 99US-00232149.
PR      XX      09-APR-1999; 99US-00288946.
PR      XX      13-JUL-1999; 99US-00352616.
PR      XX      12-NOV-1999; 99US-00439313.
PR      XX      18-NOV-1999; 99US-00443686.
PR      XX      14-JAN-2000; 2000US-00483672.
PR      XX      27-MAR-2000; 2000US-00536857.
PR      XX      09-MAY-2000; 2000US-00568100.
PR      XX      12-MAY-2000; 2000US-00570737.
PR      XX      13-JUN-2000; 2000US-00593793.
PR      XX      27-JUN-2000; 2000US-00605783.
PR      XX      09-AUG-2000; 2000US-00636215.
PR      XX      29-AUG-2000; 2000US-00651236.
PR      XX      06-SEP-2000; 2000US-00657279.
PR      XX      02-OCT-2000; 2000US-00679426.
PR      XX      10-OCT-2000; 2000US-00685166.
PR      XX      09-NOV-2000; 2000US-00709729.
PR      XX      12-JAN-2001; 2001US-00759143.
PR      XX      09-FEB-2001; 2001US-00780669.
PR      XX      09-MAY-2001; 2001US-00852911.
PR      XX      29-JUN-2001; 2001US-00895814.
PR      XX      10-DEC-2001; 2001US-00012896.
PR      XX      09-MAY-2002; 2002US-00144678.

(CORI-) CORIXA CORP.
PA
XX
PI      Xu J, Stolk JA, Kalos MD;
XX
DR      MPI: 2003-756193/71.
XX
DR      P-PSDB; ADBI3829.
XX
PT      New isolated polypeptide for use in a vaccine for stimulating an immune
PT      response, or for treating or diagnosis cancer, preferably prostate
PT      cancer.
XX
PS      Example 11; Page; 101pp; English.
XX
CC      The invention relates to an isolated polypeptide comprising no more than
CC      11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC      peptides comprise a fragment ADBI3563 of that contain naturally processed
CC      T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC      alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC      cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC      encoding the proteins and peptides, expression vectors, a host cell
CC      transformed with the vector, an isolated antibody (or antigen binding
CC      fragment) that specifically binds to the protein or peptide, detecting
CC      the presence of a cancer in a patient (comprising contacting a patient
CC      sample with a binding agent that binds to the peptide or a polypeptide
CC      appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC      the agent and comparing the amount of polypeptide to a predetermined cut-
CC      off value to determine the presence of cancer), a fusion protein
CC      comprising the peptides or proteins, stimulating or expanding T cells
CC      specific for a tumour protein comprising contacting T cells with the
CC      peptides or the isolated T cell population, treating prostate cancer in a
CC      patient comprising administering a composition comprising the peptides,
CC      nucleic acids, antibodies or compounds, determining the presence of a
CC      cancer in a patient and treating prostate cancer in a patient comprising
CC      incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

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CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridizes to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030185830.

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 10; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGGTTGATTCATGCGCGCTGCTTCTGTGAAAGACCATTTGCTTC 60
DB 1 ATGGTGGTGAAGGTTGATTCATGCGCGCTGCTTCTGTGAAAGACCATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCCGTTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCCGTTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAACCAAGAGACTCTGCTATGAAAGACTCAGAGACAG 180
DB 121 AGCAACGTGGGCACTTCTGGAACCAAGAGACTCTGCTATGAAAGACTCAGAGACAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACAG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACAG 240
QY 241 GGGGCTTCTGGAAGCAAGCAAGCTCTGCTATGAAAGACTCAGAGACAGATGGGCAAG 300
DB 241 GGGGCTTCTGGAAGCAAGCAAGCTCTGCTATGAAAGACTCAGAGACAGATGGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 GGAAGCTAAGATGAGTGAAGTCAAGAGCCAGGATCAAGCTCGTGGAGAAATCTG 420
DB 361 GGAAGCTAAGATGAGTGAAGTCAAGAGCCAGGATCAAGCTCGTGGAGAAATCTG 420
QY 421 GACAACTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAACTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGGAAGCTGAGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CTCAGGGAAGCTGAGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCCAATGGGAAATTCAGAAAGTAAATCTCTGCTGGAAGAGAGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAAATTCAGAAAGTAAATCTCTGCTGGAAGAGAGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAG 660
DB 601 GTCTTGAACAACAAAAG 660
QY 661 TGTGCTTAATGTTGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TGTGCTTAATGTTGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACCACTGTGCACTAGCTATCTAATTAAGAAATTAATGAGCAAGAGAGAGAGAGAG 780
DB 721 ACCACTGTGCACTAGCTATCTAATTAAGAAATTAATGAGCAAGAGAGAGAGAGAG 780

QY 781 TATGCTGCTGATATGCAATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TATGCTGCTGATATCAAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CATGAGCAAAAACAGAACTCGGAAATTTTAAATCAAGAAAAGAGAAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGAACTCGGAAATTTTAAATCAAGAAAAGAGAAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAG 960
DB 901 CTGATATGATATGGAAG 960
QY 961 GTGAGCTTCTAATTGAGCAAAATATGATATCTTCTCAAGATATCTGAGAGAGAG 1020
DB 961 GTGAGCTTCTAATTGAGCAAAATATGATATCTTCTCAAGATATCTGAGAGAGAG 1020
QY 1021 GCGAGAGATATGCTGTTCTGATCAATCATATGATATTTGCGAGTACTTCTGACTAC 1080
DB 1021 GCGAGAGATATGCTGTTCTGATCAATCATATGATATTTGCGAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATGCTAAATAATCTCTGAAAAAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 AAAAGAAAACAGATGCTAAATAATCTCTGAAAAAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 CTGACATCAG 1200
DB 1141 CTGACATCAG 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATGATATGATATGATATGATATGATATGATATG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATGATATGATATGATATGATATGATATGATATG 1260
QY 1261 AAGCATGAAGATATATATGATGAGATTAATGAGAAACCTGATATATGATATGATG 1320
DB 1261 AAGCATGAAGATATATATGATGAGATTAATGAGAAACCTGATATATGATATGATG 1320
QY 1321 AATGTGATATGATATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380
DB 1321 AATGTGATATGATATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380
QY 1381 CCTGCAAG 1440
DB 1381 CCTGCAAG 1440
QY 1441 AAAAGATGCAAAATATCTTCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 AAAAGATGCAAAATATCTTCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TCAGAT 1560
DB 1501 TCAGAT 1560
QY 1561 TTTATGCTATGAG 1620
DB 1561 TTTATGCTATGAG 1620
QY 1621 CTGATATATGAG 1680
DB 1621 CTGATATATGAG 1680
QY 1681 AGAAGACCTGAAG 1740
DB 1681 AGAAGACCTGAAG 1740
QY 1741 CAAGATGATATCAAG 1800
DB 1741 CAAGATGATATCAAG 1800
QY 1801 ATTTGATATCAAG 1860
DB 1801 ATTTGATATCAAG 1860

Db	661	GTGGGTTAAATGTTCTCTGGAAACATGGCACTGATTCCAAATATTCCAGATGAGTATGGAAT	720
Qy	721	ACCACTTGCACCTACGCTATCTTAATAGAAAGATAAATTATGCGCAAGCACTGCTCTTA	780
Db	721	ACCACTTGCACCTACGCTATCTTAATAGAAAGATAAATTATGCGCAAGCACTGCTCTTA	780
Qy	781	TATGTCGTGATNTGGAATTCAAAAACAAGCATGGCTTCACACCACTGTATCTTGCTGT	840
Db	781	TATGTCGTGATNTGGAATTCAAAAACAAGCATGGCTTCACACCACTGTATCTTGCTGT	840
Qy	841	CATGAGCAAAAAACAGCAAGTCGTGAAATTTTTTAATCAAGAAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTCGTGAAATTTTTTAATCAAGAAAAAAGCAATTTAAATGCA	900
Qy	901	CTGATAGATATGGAAGACATGCTCTCATCTTGCTGATGTTGATGATCAGCAAGTATA	960
Db	901	CTGATAGATATGGAAGACATGCTCTCATCTTGCTGATGTTGATGATCAGCAAGTATA	960
Qy	961	GTGACGCTTTCTACTTGAGCAAAATTTGATGATTTTCTCAAGATCTATCTGCAACAGC	1020
Db	961	GTGACGCTTTCTACTTGAGCAAAATTTGATGATTTTCTCAAGATCTATCTGCAACAGC	1020
Qy	1021	GCCAGAGATGATGCTGTTTCTAGTCATGATCATGTAATTTGCCAGTTACTTTTGACATAC	1080
Db	1021	GCCAGAGATGATGCTGTTTCTAGTCATGATCATGTAATTTGCCAGTTACTTTTGACATAC	1080
Qy	1081	AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Qy	1141	CTGACATCAGAGAAAGAGTCACAAAAGTTCAAGGCACTGAAATAATGCGACCCAGAGAA	1200
Db	1141	CTGACATCAGAGAAAGAGTCACAAAAGTTCAAGGCACTGAAATAATGCGACCCAGAGAA	1200
Qy	1201	ATGTCCTCAAGAACCGAAATTAATTAAGATGGTGTATAGAGGTTGAAAGAAATGAAG	1260
Db	1201	ATGTCCTCAAGAACCGAAATTAATTAAGATGGTGTATAGAGGTTGAAAGAAATGAAG	1260
Qy	1261	AAGCATGAAGTAAATTAATGTTGGGATTAATCAAAAACTGTAATGAGTCACTGCTGGC	1320
Db	1261	AAGCATGAAGTAAATTAATGTTGGGATTAATCAAAAACTGTAATGAGTCACTGCTGGC	1320
Qy	1321	AATGGTGAATATGATTAATTTCTTCAAAAGAAAGCAGAACACCTGAAATCAGCAATTT	1380
Db	1321	AATGGTGAATATGATTAATTTCTTCAAAAGAAAGCAGAACACCTGAAATCAGCAATTT	1380
Qy	1381	CCTGACAAACGAAAGTGAAGATATACAGAAATTTGCCAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAAGTGAAGATATACAGAAATTTGCCAATTAAGTTTCTGACTACAAAGAA	1440
Qy	1441	AAACGATGCCAAATACTCTTCTGAAACAAGCAACCCAGAAACAAGACTTAAAGCTGACA	1500
Db	1441	AAACGATGCCAAATACTCTTCTGAAACAAGCAACCCAGAAACAAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGTCACAAAAGGCTTGAGGGCAGTGAATAATGCGCACGACAGACTGAAAT	1560
Db	1501	TCAGAGGAAGTCACAAAAGGCTTGAGGGCAGTGAATAATGCGCACGACAGACTGAAAT	1560
Qy	1561	TTTATGCTATTCGAAGAAATGAAGAAGACGGAAGTCACTCATGTTCGATTTCCCAAAAC	1620
Db	1561	TTTATGCTATTCGAAGAAATGAAGAAGACGGAAGTCACTCATGTTCGATTTCCCAAAAC	1620
Qy	1621	CTGACTAATGCTGCACTGCTGGCAATGGTATGATGATTAATTTCTTCCAGAAAGAC	1680
Db	1621	CTGACTAATGCTGCACTGCTGGCAATGGTATGATGATTAATTTCTTCCAGAAAGAC	1680
Qy	1681	AGAACACTGAAAGCCAGACAAATTTCTTGACACTGGAATGAAGAGTATCAACGTGACGAA	1740
Db	1681	AGAACACTGAAAGCCAGACAAATTTCTTGACACTGGAATGAAGAGTATCAACGTGACGAA	1740
Qy	1741	CAAAATGATATCTCGAAGACAAATTTTGTGAAGAACAGAACACTCGAATATTTACAGATGAG	1800
Db	1741	CAAAATGATATCTCGAAGACAAATTTTGTGAAGAACAGAACACTCGAATATTTACAGATGAG	1800

QY	1801	ATTCTGATTCATGAAGAAAAAGCATGTGAAGTGGTTGAAAAAATGAAATTCGTGAGCTTCT	1860		
Db	1801	ATTCTGATTCATGAAGAAAAAGCATGTGAAGTGGTTGAAAAAATGAAATTCGTGAGCTTCT	1860		
QY	1861	CTTAGTGTGTAAAGAAAGAAAAAGACATCTTCATCATGAAATAGTACGTTGCCGGAAGAAAT	1920		
Db	1861	CTTAGTGTGTAAAGAAAGAAAAAGACATCTTCATCATGAAATAGTACGTTGCCGGAAGAAAT	1920		
QY	1921	GCCATGCTTAAGACTGGAGCTTGACACATATGAAACATCAGAGCCAGCTAAAAA	1980		
Db	1921	GCCATGCTTAAGACTGGAGCTTGACACATATGAAACATCAGAGCCAGCTAAAAA	1980		
QY	1981	AAAAAAAAAAAAAAAAAAAA 2000			
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000			
RESULT 15					
AA06599					
ID	AAA06599	standard; cDNA; 2000 BP.			
AC	AAA06599;				
XX					
DT	13-JUN-2000	(first entry)			
XX					
DE	Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:374.				
XX					
KW	Human; prostate cancer; diagnosis; tumour; gene therapy; detection;				
KW	immunogenic; cytosolic; vaccinia; ss.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200004149-A2.				
PD					
XX	27-JAN-2000.				
PF	14-JUL-1999;	99WO-US015838.			
XX					
PR	14-JUL-1998;	98US-00115453.			
PR	14-JUL-1998;	98US-00116134.			
PR	23-SEP-1998;	98US-00159812.			
PR	23-SEP-1998;	98US-00159822.			
PR	15-JAN-1999;	99US-00232149.			
PR	15-JAN-1999;	99US-00232880.			
PR	09-APR-1999;	99US-00288946.			
PA	(CORI-) CORIXA CORP.				
XX					
PI	Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;				
XX					
DR	WPI; 2000-171268/15.				
XX					
PT	New polypeptide useful for treating and diagnosing prostate cancer				
PT	comprises an immunogenic portion of prostate tumor protein.				
XX					
PS	Claim 50; Page 222-223; 263pp; English.				
XX					
CC	The present invention describes isolated polypeptides, comprising an				
CC	immunogenic portion of a prostate tumour protein (pTP). The polypeptides				
CC	and polynucleotides encoding them have cytosolic activity and can be				
CC	used in vaccines and in gene therapy. The polypeptides and				
CC	polynucleotides encoding them, antigen presenting cells which express the				
CC	polypeptides, antibodies against the polypeptides and vaccines comprising				
CC	them can be used for inhibiting the development of prostate cancer in a				
CC	patient. The polypeptides can be used to generate antibodies or anti-				
CC	idiotypic antibodies for passive immuno therapy. A portion of the				
CC	polynucleotides encoding the polypeptides can be used as a probe or to				
CC	modulate the expression of the polypeptides. AA065241 to AA065691 and				
CC	AA065200 to AA065202 represent sequences used in the exemplification of				
CC	the present invention				
QZ	Sequence 2000 BP; 698 A; 387 C; 489 G; 426 T; 0 U; 0 Other;				

Query Match 99.9%; Score 1998.4; DB 3; Length 2000;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Perfect score: 2000
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Searched: 1303057 seqs, 888780828 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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2	2000	100.0	2000	US-09-352-616A-374	Sequence 374, App
3	2000	100.0	2000	US-09-289-198-302	Sequence 302, App
4	2000	100.0	2000	US-09-636-215-374	Sequence 374, App
5	2000	100.0	2000	US-09-685-166A-374	Sequence 374, App
6	2000	100.0	2000	US-09-429-755-302	Sequence 302, App
7	2000	100.0	2000	US-09-679-426-374	Sequence 374, App
8	2000	100.0	2000	US-09-759-143-374	Sequence 374, App
9	2000	100.0	2000	US-09-651-236-374	Sequence 374, App
10	2000	100.0	2000	US-09-699-295-302	Sequence 302, App
11	2000	100.0	2000	US-09-534-825A-302	Sequence 302, App
12	2000	100.0	2000	US-09-657-279-374	Sequence 374, App
13	2000	100.0	2000	US-10-012-896-374	Sequence 374, App
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16	1940	97.0	2040	US-09-289-198-303	Sequence 303, App
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ALIGNMENTS

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; Sequence 374, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocke, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalo, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-374
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ Sequence 374, Application US/09352616A
/ Patent No. 6395278
/ GENERAL INFORMATION:
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Uiang, Yungui
/ APPLICANT: Xu, Jianshun
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
/ FILE REFERENCE: 210121.427C8
/ CURRENT APPLICATION NUMBER: US/09/352,616A
/ NUMBER OF SEQ ID NOS: 472
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
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Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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DB 1381 CCTGACAAAG 1440
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DB 1561 TTTATGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
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DB 1681 AGAACAAG 1740
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QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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RESULT 3
US-09-289-198-302
; Sequence 302, Appl: cation US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
EARLIER FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 09/062,451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-636-215-374
Sequence 374, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kales, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636, 215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-636-215-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1981 AAAAAAAAAAAAAAAAAA 2000
1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 5
US-09-685-166A-374
Sequence 374, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun
APPLICANT: Skelley, Yasir A.W.
APPLICANT: Hepher, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-685-166A-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1921 GCCATCTAAGACTGAGCTAGACAAATGAAGAAATCAGAGCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 6
US-09-429-755-302
; Sequence 302, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda G.
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1921 GCCATGCTAAGACTGAGAGTGAACAAATGAACATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-679-426-374
Sequence 374, Application US/09679426
Patent No. 6759315
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Liang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGTGTTGAGCTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTC 60

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RESULT 8

US-09-759-143-374
 ; Sequence 374, Application US/09759143
 ; Patent No. 6800746
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yeair A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ATGGTGTGAGGTTGATTCATGCGCGGCTCTTCTGTGAAGAAGCCATTTGGTCTC 60
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RESULT 10
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; Sequence 302, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
; APPLICANT: Frudakie, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Linda B.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelley, Yaelir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-302

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Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      121 AGCAACGTGGGCACTTTCTGAGAGCAAGCAAGCTGCTGATGAAGACATCTGAGGCAAG 180
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Db      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY      241 GCGGCTTCTGAGACCAAGAGCACTCTGCTATGAAGACATCTAGAGAACAAATGGGCAAG 300
Db      241 GCGGCTTCTGAGACCAAGAGCACTCTGCTATGAAGACATCTAGAGAACAAATGGGCAAG 300
QY      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Db      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
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RESULT 12
US-09-657-279-374
Sequence 374, Application US/09657279
Patent No. 6894146
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuyui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepier, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C19
CURRENT APPLICATION NUMBER: US/09/657,279
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-657-279-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 RESULT 13
 US-10-012-896-374
 ; Sequence 374, Application US/10012896
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Micham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retler, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yashir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hurel, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Basbols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Mantanabe, Yoshinhiro

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; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ Patent No. 6329505			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Davin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocker, Susan Louise			
APPLICANT: Jiang Yuqul			
APPLICANT: Reed, Steven G.			
APPLICANT: Kaios, Michael			
APPLICANT: Fanger, Gary			
APPLICANT: Retter, Mark			
APPLICANT: Solk, John			
APPLICANT: Day, Craig			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
FILE REFERENCE: 210121.427C9			
CURRENT APPLICATION NUMBER: US/09/439,313			
CURRENT FILING DATE: 1999-11-12			
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13	2000	100.0	2000	6	US-10-144-678A-374 Sequence 374, App
14	2000	100.0	2000	6	US-10-033-527-6 Sequence 6, App11
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ALIGNMENTS

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; Sequence 6, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Petersen, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
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; ORGANISM: Homo sapien
US-09-825-301-6

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Qy 421 GACAACTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTGAG 480
Db 421 GACAACTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTGAG 480
Qy 481 CTCAGGAGACCTGACCTGAAACAAAGAGCAAGCAAAAGAGAGCTGCTCAATCTGGGC 540
Db 481 CTCAGGAGACCTGACCTGAAACAAAGAGCAAGCAAAAGAGAGCTGCTCAATCTGGGC 540
Qy 541 TCTGCAATGGGAATTCAGAAAGTAAAACTCTGCTGGAACAGAGATGCTCACTTAAT 600
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Qy 601 GTCTTGTACAAACAAAAGAGAGCAGCTGTGATTAAGGCGGTACAATGCGAGAAAGATGA 660
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Qy 661 TGTGCTTATGTTGTGTGGAACATGGCACTGATCCAAATTTTCCAGATGAGATGGAAT 720
Db 661 TGTGCTTATGTTGTGTGGAACATGGCACTGATCCAAATTTTCCAGATGAGATGGAAT 720
Qy 721 ACCACTGTGCACTACGCTATCTATATGAAGATTAATGAGCCAAAGCATGCTCTTA 780
Db 721 ACCACTGTGCACTACGCTATCTATATGAAGATTAATGAGCCAAAGCATGCTCTTA 780
Qy 781 TATGTGTGATATGCAATCAAAAAACAAGCATGCTGCAACACATGTTACTGGTGA 840
Db 781 TATGTGTGATATGCAATCAAAAAACAAGCATGCTGCAACACATGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAACAGAAATGCTGGAATTTTAAATCAAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGAAATGCTGGAATTTTAAATCAAAAAAGCGAATTTAAATGA 900
Qy 901 CTGATATGATATGGAAGAGCTGCTCATATCTGATGTTGTTGATGAGCAAGATATA 960
Db 901 CTGATATGATATGGAAGAGCTGCTCATATCTGATGTTGTTGATGAGCAAGATATA 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCGAGAGATATGCTGTTCTAGTCAATCATATGTAATTTGCGAGTACTTCTGACTAC 1080
Db 1021 GCGAGAGATATGCTGTTCTAGTCAATCATATGTAATTTGCGAGTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCAGAACTTAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCAGAACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAGGAGTGAATAATGACCAAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAGGAGTGAATAATGACCAAGAGAA 1200
Qy 1201 ATGTCTCAAGAAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTATATGAGGATTAAGAAAACTGACTATGCTGCTGCTGAG 1320
Db 1261 AAGCATGAAAGTATATGAGGATTAAGAAAACTGACTATGCTGCTGCTGAG 1320
Qy 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
Db 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380

Qy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGCAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGCAATTAATGTTCTGACTACAAAGAA 1440
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Db 1441 AAAAGATGCGCAAAATTAATCTCTCTGAAAAACAGCAACCCAGAACTTAAGCTGACA 1500
Qy 1501 TCAGAGAAAGTCAACAAAGCTTGAAGGCACTGAAATGAGCAGCAGAGCTTAAGAAAT 1560
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Db 1561 TTTATGCTATATGAAAGAAATGAAGAGACGGAATTAATCTCATGATGAGATTTCCAGAAAAC 1620
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Db 1681 AGAACACTGAAAGCGCAGCAATTTCTGACACTGAGAAATGAAGATATCAGATGAGAA 1740
Qy 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATTAACAGATGAG 1800
Db 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATTAACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGAAAAATGAAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGAAAAATGAAATTTCTGAGCTTTCT 1860
Qy 1861 CTTAGTGTAGAAAGAAAGACATCTTGTGCAATGAATATGATGCTTGGGAGAGAAAT 1920
Db 1861 CTTAGTGTAGAAAGAAAGACATCTTGTGCAATGAATATGATGCTTGGGAGAGAAAT 1920
Qy 1921 GCGATGCTTAAGCTGAGAGTACACAAATGAAACATCGAGGCACTTAATTAATTAATTA 1980
Db 1921 GCGATGCTTAAGCTGAGAGTACACAAATGAAACATCGAGGCACTTAATTAATTAATTA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-759-143-374
Sequence 374, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, DAVID C.
APPLICANT: Mitcham, JENNIFER L.
APPLICANT: Harlocker, SUSAN L.
APPLICANT: Jiang, YUQI
APPLICANT: Henderson, ROBERT A.
APPLICANT: Kalos, MICHAEL D.
APPLICANT: Fanger, GARY R.
APPLICANT: Retter, MARC W.
APPLICANT: Stolk, JOHN A.
APPLICANT: Day, CRAIG H.
APPLICANT: Vedvick, THOMAS S.
APPLICANT: Carter, DARICK
APPLICANT: Li, SAMUEL
APPLICANT: Wang, AIJUN
APPLICANT: Skeiky, YASIR A.W.
APPLICANT: Hepler, WILLIAM
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12

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; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1  ATGGTGGTGAAGGTGATTCATGCGCGGCTGCTTCTGTGAAGAACCATTTGGCTC 60
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DB      61  AGGAGCAAGATGGGCAAGTGGTCTGCGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY      121  AGCAACGTGGGCACTTCTGAGACAAGACGACTGTGTAAGAACACTCAGAGCAAG 180
DB      121  AGCAACGTGGGCACTTCTGAGACAAGACGACTGTGTAAGAACACTCAGAGCAAG 180
QY      181  ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCTG 240
DB      181  ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCTG 240
QY      241  GGGCTTCTGAGAGACCAAGCACTGCTGTAAGAACACTCAGAGCAAGTGGCAAG 300
DB      241  GGGCTTCTGAGAGACCAAGCACTGCTGTAAGAACACTCAGAGCAAGTGGCAAG 300
QY      301  TGGTGTCCCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
DB      301  TGGTGTCCCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
QY      361  GGAAGATTAGAGTACAGTGGCTTCATGAGCCCAAGGTACCACTCCGTGGAAGATCTG 420
DB      361  GGAAGATTAGAGTACAGTGGCTTCATGAGCCCAAGGTACCACTCCGTGGAAGATCTG 420
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DB      421  GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCGCAAGAAAGATCTCATGCTAG 480
QY      481  CTCAGGAGACCTGACCTGAAACAAGAAAGACAAAGAGAGCTCTTCAATCTGGCC 540
DB      481  CTCAGGAGACCTGACCTGAAACAAGAAAGACAAAGAGAGCTCTTCAATCTGGCC 540
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DB      541  TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGGAACAGAGTGTCAACTTAAT 600
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DB      601  GTCTTGAACAACAAGAGAGACGCTGATTAAGCGGTAAAGCCAGAGAAATGTA 660
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DB      661  TGTGCGTATATGTTGCTGGAACAGTGCATGATCCAATATTCAGATGATGTAAT 720
QY      721  ACCACTCTGACATGAGCTATCTATATGAAGATTAATTAAGCCAAAGACCTGCTTA 780
DB      721  ACCACTCTGACATGAGCTATCTATATGAAGATTAATTAAGCCAAAGACCTGCTTA 780
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DB      781  TATGCTGATATATCAATCAAAAACAAGCATGGCTCACACCATGTTACTTGGTGA 840
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DB      961  GTGAGCCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGC 1020
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DB      1021  GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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DB      1141  CTGACATCAGAGGAAGTCACAAAGTTCAAAGCAGTGAATAAGCCAGCAGAGAAA 1200
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DB      1201  ATGTCTCAAGAACCAAGAAATTAATAAGATGTGATAGAGGTTGAAGAAATGAAG 1260
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DB      1261  AAGCATGAAGATTAATATGTTGGATTAATGAAAACCTGACTTAATGCTGCTGGC 1320
QY      1321  AATGTGATATATGATTAATATCTTCAAGAGAGAGAGCAACCTGAATAATGCAATTT 1380
DB      1321  AATGTGATATATGATTAATATCTTCAAGAGAGAGAGCAACCTGAATAATGCAATTT 1380
QY      1381  CTTGACAAAGAAAGTGAAGATATCAAGAAATTTGGCAATTAATTTCTGACTACAAAGAA 1440
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QY      1441  AAAAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAAACAACCTTAAAGCTGACA 1500
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DB      1861  CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAATATGATACGTGCGGGAAGAAATTT 1920
QY      1921  GCCATGCTTAAGACTGAGCTAGACACAATGAACAATCAGAGCCAGCTAATAAAAAATTT 1980
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Db 1981 AAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3

US-09-780-669-374

/ Sequence 374, Application US/09780669

/ Patent No. US2002005197A1

/ GENERAL INFORMATION:

/ APPLICANT: Xu, Jiangchun

/ APPLICANT: Dillon, Davin C.

/ APPLICANT: Mitcham, Jennifer L.

/ APPLICANT: Harlocker, Susan L.

/ APPLICANT: Jiang, Yuqi

/ APPLICANT: Henderson, Robert A.

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Stolk, John A.

/ APPLICANT: Day, Craig H.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Carter, Darrick

/ APPLICANT: Li, Samuel

/ APPLICANT: Wang, Aijun

/ APPLICANT: Skelky, Yaelir A.W.

/ APPLICANT: Hepley, William

/ APPLICANT: Hural, John

/ APPLICANT: McNeill, Patricia D.

/ APPLICANT: Houghton, Raymond L.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

/ FILE REFERENCE: 210121.427C24

/ CURRENT APPLICATION NUMBER: US/09/780,669

/ CURRENT FILING DATE: 2001-02-09

/ NUMBER OF SEQ ID NOS: 943

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 374

/ LENGTH: 2000

/ TYPE: DNA

/ ORGANISM: Homo sapien

US-09-780-669-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTGGATTCAGTCCGCGCTGCTCTTGTGAAGAGCATTTGGTCTC 60

Db 1 ATGGTGGTGGAGTGGATTCAGTCCGCGCTGCTCTTGTGAAGAGCATTTGGTCTC 60

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Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120

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Db 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAGCACTTCAAGAGCAAG 180

QY 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGAGAGGAGAGTGGCAAGCAAGCTG 240

Db 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGAGAGGAGAGTGGCAAGCAAGCTG 240

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Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAACGAATTTAAATGA 900

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DB 1501 TCAGAGAGAGATGCTCAAGAGCTTGGAGGAGTGAAGAAATGGCCAGGCAAGCTTGAAGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAAGACGGAAGTACTCATGTGGATTTCCAGAAAAC 1620
DB 1561 TTTATGGCTATCGAAGAAATGAAGAAGACGGAAGTACTCATGTGGATTTCCAGAAAAC 1620
QY 1621 CTGACTTAATGGTCCCATCTGCTGGCATTGGTGAATGATGATTAATTTCTTCCAGAGAAAGAC 1680
DB 1621 CTGACTTAATGGTCCCATCTGCTGGCATTGGTGAATGATGATTAATTTCTTCCAGAGAAAGAC 1680
QY 1681 AGAAGCACTGGAAGCCAGCAATTTCTGCACTGAGATGAAGATGATCAAGTACGAA 1740
DB 1681 AGAAGCACTGGAAGCCAGCAATTTCTGCACTGAGATGAAGATGATCAAGTACGAA 1740
QY 1741 CAAATGATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
DB 1741 CAAATGATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAGATGAAAGTGGTGAAGAAATGCAATTTCTGACTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGCAGATGAAAGTGGTGAAGAAATGCAATTTCTGACTTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTGCAATGAATATGATACGTTGGGGAGAAAT 1920
DB 1861 CTTAGTGTGAAGAAAGAAAGACATCTGCAATGAATATGATACGTTGGGGAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGCTAGACACATGATAACATCAGAGCCAGCTTAAAAA 1980
DB 1921 GCCATGCTAAGACTGAGCTAGACACATGATAACATCAGAGCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-810-936-302
Sequence 302, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121, 419C11
CURRENT APPLICATION NUMBER: US/09/810, 936
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGATGAGTTGATTCATGCGGCTCTTCTGTGAAGAACATTTGGTCTC 60
DB 1 ATGGTGTGATGAGTTGATTCATGCGGCTCTTCTGTGAAGAACATTTGGTCTC 60
QY 61 AGAGAGCAATGGGCAAGTGGTGGCTGCTTCCCTGCTGAGGAGAGAGCGGCAAG 120

DB 61 AGAGAGCAATGGGCAAGTGGTGGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
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DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCTCTGTATGAAGACATCAGAGCAAG 180
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DB 481 CTCAGGGAACAAGCTGAGCAAGAAAGCAAGCAAGAAAGAGCACTCTCATCTGAGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTCTGCTGAGACAGATGCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTCTGCTGAGACAGATGCACTTAAT 600
QY 601 GTGCTTGAACAAGAAAGGACAGCTCTGATTAAGCCGTAACATGACAGAAAGTGA 660
DB 601 GTGCTTGAACAAGAAAGGACAGCTCTGATTAAGCCGTAACATGACAGAAAGTGA 660
QY 661 TGTGCTTAATGTTCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTATCTATATATGAAGATTAATATGAGCCAAAGCTGCTTTA 780
DB 721 ACCACTCTGCACTATCTATATATGAAGATTAATATGAGCCAAAGCTGCTTTA 780
QY 781 TATGTCCTGATATGAAATCAAAAACAAGATGAGCTTCAACCACTGTTACTTGGTGA 840
DB 781 TATGTCCTGATATGAAATCAAAAACAAGATGAGCTTCAACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAAACAGAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATGAGAGAGCTGCTCTCATCTTCTGATGTTGGATCAGCAAGTATA 960
DB 901 CTGATATGATGAGAGAGCTGCTCTCATCTTCTGATGTTGGATCAGCAAGTATA 960
QY 961 GTGACCTTCTATCTGAGAAATATGATATCTTCAAGATCTATCTGAGAGAG 1020
DB 961 GTGACCTTCTATCTGAGAAATATGATATCTTCAAGATCTATCTGAGAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTTCTGATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTTCTGATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATCTTAAATCTTCTGAAAACAGCAATCCAGAACAGATTTAAG 1140
DB 1081 AAGAAAAACAGATCTTAAATCTTCTGAAAACAGCAATCCAGAACAGATTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAGATTCAGAAAGCAAGTGAATATGACAGAGAGAA 1200

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Db      1141 CTGACATCAGAGAAAGTCCAAAGGTTCAAAGCGAGTAAAAATAGCCAGCAGAGAAA 1200
Qy      1201 ATGTCTCAAGAACCGAATAATAAGATGTGTATAGAGAGTTGAAAGAAATATGAAG 1260
Db      1201 ATGTCTCAAGAACCGAATAATAAGATGTGTATAGAGAGTTGAAAGAAATATGAAG 1260
Qy      1261 AAGCATGAAAGTAAATATGTGGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC 1320
Db      1261 AAGCATGAAAGTAAATATGTGGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC 1320
Qy      1321 AATGTGTATATGTGATTAAATCTCTCAAGAGAAAGCAACCTGAAAAATACGAATTT 1380
Db      1321 AATGTGTATATGTGATTAAATCTCTCAAGAGAAAGCAACCTGAAAAATACGAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAAATTAAGTTCTGATCAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAAATTAAGTTCTGATCAAGAA 1440
Qy      1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGATCACAAGAGCTTGAAGGCGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
Db      1501 TCAGAGAAAGATCACAAGAGCTTGAAGGCGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
Qy      1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGGAAATCTCATGTGGGATTTCCAGAAAC 1620
Db      1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGGAAATCTCATGTGGGATTTCCAGAAAC 1620
Qy      1621 CTGACTAATGTGGCCACTGTGGCAATGTGTATGTATGATTAAATCTCTCAAGAAAGAC 1680
Db      1621 CTGACTAATGTGGCCACTGTGGCAATGTGTATGTATGATTAAATCTCTCAAGAAAGAC 1680
Qy      1681 AAGAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAGTATCACTGTGCGAA 1740
Db      1681 AAGAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAGTATCACTGTGCGAA 1740
Qy      1741 CAAATATGATCTCAGAAAGCAATTTGTGAAGAACAGACACTGGAATATTAACAGATGAG 1800
Db      1741 CAAATATGATCTCAGAAAGCAATTTGTGAAGAACAGACACTGGAATATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAAGAAAGCAGATAGAAGTGTGAAGAAATATGAAATCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAAGAAAGCAGATAGAAGTGTGAAGAAATATGAAATCTGAGCTTTCT 1860
Qy      1861 CTTAGTGTGAAGAAAGAAAGACATCTTGACATGAAATATGTAAGTGTGGGAGAAATTT 1920
Db      1861 CTTAGTGTGAAGAAAGAAAGACATCTTGACATGAAATATGTAAGTGTGGGAGAAATTT 1920
Qy      1921 GGCATGCTAAGACTGGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAA 1980
Db      1921 GGCATGCTAAGACTGGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 5
US-09-822-827-374
; Sequence 374, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374

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; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374
Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGTGTGTTAGAGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
Db      1 ATGTGTGTTAGAGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
Qy      61 AGGAGCAAGATGGGCAAGTGGTGGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db      61 AGGAGCAAGATGGGCAAGTGGTGGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Qy      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGCTATGAGACACTCAGAGCAAG 180
Db      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGCTATGAGACACTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGGCCGCACTGCTTCCCCTGCTGAGGGGAGTGGCAAGCAAGTGG 240
Db      181 ATGGGCAAGTGTGGCCGCACTGCTTCCCCTGCTGAGGGGAGTGGCAAGCAAGTGG 240
Qy      241 GGGCGCTTCTGAGACCAAGCACTCTGCTATGAGACCACTGAGAAACAAGATGGGCAAG 300
Db      241 GGGCGCTTCTGAGACCAAGCACTCTGCTATGAGACCACTGAGAAACAAGATGGGCAAG 300
Qy      301 TGGTCTGCACTGCTTCCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
Db      301 TGGTCTGCACTGCTTCCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
Qy      361 GGAAGCTACGATGACAGTGCCTTCAATGAGAGCCAGATACAGTCCGTGGAAGATCTG 420
Db      361 GGAAGCTACGATGACAGTGCCTTCAATGAGAGCCAGATACAGTCCGTGGAAGATCTG 420
Qy      421 GACCAAGCTCCACAGAGCTGCGGTGGGTTAAAGTCCCAAGAAAGATCTACGTCATG 480
Db      421 GACCAAGCTCCACAGAGCTGCGGTGGGTTAAAGTCCCAAGAAAGATCTACGTCATG 480
Qy      481 CTCAGGGAACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTCAATCTGGCC 540
Db      481 CTCAGGGAACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTCAATCTGGCC 540
Qy      541 TCTGCAATGGGAATTCAGAAAGTATGAAATCTCTGCTGAGACAGATGTCACCTTAAT 600
Db      541 TCTGCAATGGGAATTCAGAAAGTATGAAATCTCTGCTGAGACAGATGTCACCTTAAT 600
Qy      601 GTCTTGAACAACAAAGAGAGCAGCTCTGATTAAGGCGGTCAATGCAAGAGATGAA 660
Db      601 GTCTTGAACAACAAAGAGAGCAGCTCTGATTAAGGCGGTCAATGCAAGAGATGAA 660
Qy      661 TGTGCTTAATGTGCTGGAAATGCAAGCACTGATCAAAATATTCAGAGTATGGAAT 720
Db      661 TGTGCTTAATGTGCTGGAAATGCAAGCACTGATCAAAATATTCAGAGTATGGAAT 720
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Db      721 ACCACTCTGACCTAAGCTATCTATATGAAAGTAAATTAATGAGCCAAAGACCTGCTTA 780
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Db      781 TATGTGTGATGATGAAATCAAAAAAAGAGTGGCTCAGACCACTGTTACTTGGTGA 840
Qy      841 CATGACAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db      841 CATGACAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Qy      901 CTGATATGATGAGAGAGTGTCTCATCTTGTGCTGATGTTGTGAGTACAGCAAGTATA 960
Db      901 CTGATATGATGAGAGAGTGTCTCATCTTGTGCTGATGTTGTGAGTACAGCAAGTATA 960

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QY 961 GTGAGCTTCTACTGAGCAAAATATGATCTTCTCAAGATCTATCGACAGC 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATCTTCTCAAGATCTATCGACAGC 1020
QY 1021 GCCAGAGATGCTGTTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATGCTGTTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAGATGCTAAATCTCTCTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
DB 1081 AAGAGAAAAGATGCTAAATCTCTCTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAGAGTTCAAGAGAGTAAATAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCACAAGAGTTCAAGAGAGTAAATAGCCAGCAGAGAAA 1200
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DB 1201 ATGCTCAAGAACAGCAAAATTAATAGATGATGAGAGGTTGAGAGAAATGAAG 1260
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DB 1381 CCTGACAAAGAAAGTGAAGATTAATCAAGAACTGATTAATGATTAATGATTAATG 1440
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DB 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGAGTGAAGAAATGAGGAGAGAGAGTGAAG 1560
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DB 1681 AAGAACCTGAAAGCCAGCAATTTCTGACACTGAAATGAAGATTAATCAAGTGA 1740
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DB 1741 CAAAATGATCTAGAGAGCAATTTTGTGAAGAACAGAACTGGAATTAATCAAGTGA 1800
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DB 1921 GCCATGCTAAGAGTGAAGTGAAGCAATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 6
US-09-429-755-302
Sequence 302, Application US/09429755A
Patent No. US20020111467A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-302
Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
DB 1 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
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DB 61 AG 120
QY 121 AGCAAG 180
DB 121 AGCAAG 180
QY 181 ATGAG 240
DB 181 ATGAG 240
QY 241 GAG 300
DB 241 GAG 300
QY 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 GAG 420
DB 361 GAG 420
QY 421 GAG 480
DB 421 GAG 480
QY 481 CTGAG 540
DB 481 CTGAG 540
QY 541 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTCTTGAAG 660
DB 601 GTCTTGAAG 660
QY 661 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720


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Db 661 TGGCCTTATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGGAAT 720
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Db 721 ACCACTCTGACACTAGCTATCTATTAATGAATTAATTAATGAGCACTGCTTCT 780
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Db 1201 ATGTCTCAAGAACCAAAATTAATAGATGCTGATGAGAGGTTGAAGAAATGAAG 1260
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Db 1261 AAGCATGAAGATTAATGAGGATTAATGAGAAACCTGATTAATGCTGCTGCTGAC 1320
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Db 1321 AATGTGATATGATTAATCTCTCAAGAGAGAGCAACCTGAAATGCAATTT 1380
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Db 1381 CCTGACAGAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATGTTCTGACTA 1440
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Db 1441 AAAACAGATGCCAAAATATCTCTGTAATAAGCAACCAAGCACTTAAGCTGACA 1500
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Db 1501 TCAGAGAGAGAGTCAAAAAGCTTGAAGGCAAGTGAATGCGCAGCAGAGCTAGAA 1560
Qy 1561 TTTATGCTATTCGAAGAAATGAAGAGCAGGAATTCATGTCGATTTCCAGAAAAC 1620
Db 1561 TTTATGCTATTCGAAGAAATGAAGAGCAGGAATTCATGTCGATTTCCAGAAAAC 1620
Qy 1621 CTGACTAATGCTGCACTGCTGCAATGATGATGATGATTAATCTCTCAAGAGAGAC 1680
Db 1621 CTGACTAATGCTGCACTGCTGCAATGATGATGATGATTAATCTCTCAAGAGAGAC 1680
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Db 1681 AGAACAAGTGAAGAGCAATTTCTGCACTGAGAAATGAAGATGATCAAGTGCAG 1740
Qy 1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGACAGACACTGGAATATTAACGATGAG 1800
Db 1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGACAGACACTGGAATATTAACGATGAG 1800
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Db 1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGACAGACACTGGAATATTAACGATGAG 1800
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Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000
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US-09-924-400-302
; Sequence 302, Application US/09924400
; Patent No. US20020165371A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C12
; CURRENT APPLICATION NUMBER: US/09/924,400
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-924-400-302
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Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGTGTTGATGATGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGATTC 60
Qy 61 AGGACAGATGAGGCAAGTGTGCTGCGTGTCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGGACAGATGAGGCAAGTGTGCTGCGTGTCTTCCCTGCTGCAAGGAGCGGCAAG 120
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Db 181 ATGGCAAGTGTGCGGCACTTCCCTGCTGCAAGGAGAGTGGCAAGACAGT 240
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Db 241 GCGCTTCTGAGAGACAGACACTCTGTATGAAGACACTGAGAAACAAGTGGCAAG 300
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OY	301	TGTCCTCCTCAGCTGCTCCCTCCCTGCTGCAGGGGAGCCGACAGAGCAAGTGGGCGCTTGG	360
Db	301	TGTCCTCCTCAGCTGCTCCCTCCCTGCTGCAGGGGAGCCGAGAGCAAGTGGGCGCTTGG	360
OY	361	GGAGACTACGATGACAGTGCCTTCTCATGAGGCCAGGTATCCAGTCCCTGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCTCATGAGGCCAGGTATCCAGTCCCTGAGAAAGATCTG	420
OY	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTCATG	480
Db	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTCATG	480
OY	481	CTCAGGGGACACTGACGTGAAACAAGAAAGACAAGAAAGAGGACGTCTCATCTTGAGCC	540
Db	481	CTCAGGGGACACTGACGTGAAACAAGAAAGACAAGAAAGAGGACGTCTCATCTTGAGCC	540
OY	541	TCTGCGCAATGGGAATTCAGAAAGTAGTAATAACCTCGCTGAGCAGACGATGTCAACTTAT	600
Db	541	TCTGCGCAATGGGAATTCAGAAAGTAGTAATAACCTCGCTGAGCAGACGATGTCAACTTAT	600
OY	601	GTCCTTGACAAACAAAAGAGAGCAGCTCTGATAAAGGCCGTACAAATGCCAGAAAGTAA	660
Db	601	GTCCTTGACAAACAAAAGAGAGCAGCTCTGATAAAGGCCGTACAAATGCCAGAAAGTAA	660
OY	661	TGTGGCTTAATGTTGCTGGAAACATGGGACCTGATCCAAATATTCAGATGAGTAGTAAT	720
Db	661	TGTGGCTTAATGTTGCTGGAAACATGGGACCTGATCCAAATATTCAGATGAGTAGTAAT	720
OY	721	ACCACTCTGCACCTACGCTATCTATATATGAAGTAAATTAATGCCCAGAAAGCCTGCTTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTATATATGAAGTAAATTAATGCCCAGAAAGCCTGCTTTA	780
OY	781	TATGCTGCTGATATTCGAATCAAAAAACAAGATGGCTCACACCACTGTATCTTGGTGA	840
Db	781	TATGCTGCTGATATTCGAATCAAAAAACAAGATGGCTCACACCACTGTATCTTGGTGA	840
OY	841	CATAGGCAAAAAACAGCAAGCTGCTGAATTTTAAATCAGAAAAAAGCAATTTAAATGCA	900
Db	841	CATAGGCAAAAAACAGCAAGCTGCTGAATTTTAAATCAGAAAAAAGCAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGAGCTGCTCTCATACTGCTGATGTGTTGGATTCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGAGCTGCTCTCATACTGCTGATGTGTTGGATTCAGCAAGTATA	960
OY	961	GTCAGCCCTTCTACTTGAGCAAAATATGATGATCTTCAAGATCTATCTGCACAGCG	1020
Db	961	GTCAGCCCTTCTACTTGAGCAAAATATGATGATCTTCAAGATCTATCTGCACAGCG	1020
OY	1021	GCCAGAGAGTATGCTGTTCTAGTCATCATATGTAATTTCCAGTTACTTTCGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTCTAGTCATCATATGTAATTTCCAGTTACTTTCGACTAC	1080
OY	1081	AAAGAAAAACGATGCTTAAAAATCCCTCTGAAAAACACATTCAGAACCAAGACTTAAAG	1140
Db	1081	AAAGAAAAACGATGCTTAAAAATCCCTCTGAAAAACACATTCAGAACCAAGACTTAAAG	1140
OY	1141	CTGACATCAGAGAGAGTGCACAAAGGTTCAAAGGCACTGAAAAATAGCCACAGAGAAA	1200
Db	1141	CTGACATCAGAGAGAGTGCACAAAGGTTCAAAGGCACTGAAAAATAGCCACAGAGAAA	1200
OY	1201	ATGTCTCAAGAACCCAGAAATTAATATAGATGTGTATAGAGGTTGAAGAAATGAAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATTAATATAGATGTGTATAGAGGTTGAAGAAATGAAG	1260
OY	1261	AAGCATGAAGATTAATATGTGGGAATTACTAGAAAAACCTGAATATGGGTGCTACGTGGC	1320
Db	1261	AAGCATGAAGATTAATATGTGGGAATTACTAGAAAAACCTGAATATGGGTGCTACGTGGC	1320
OY	1321	AATGTGATTAATGATTAATTTCTTCAAAGAGACAGACACTGAAAAATCAGCAATTT	1380
Db	1321	AATGTGATTAATGATTAATTTCTTCAAAGAGACAGACACTGAAAAATCAGCAATTT	1380
OY	1381	CCTGACAAACGAATGGAAGAGTATCACGAATTTGGCAATTAGTTTCTGACTACAAAGAA	1440

Db	1381	CTGACACGAAATGAAAGTATCACGAATTTGCGAATTAGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATACTCTTCTGAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATACTCTTCTGAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGATCACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT	1560
Db	1501	TCAGAGGAAGATCACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT	1560
Qy	1561	TTTATGGCTATCGAAGAAATGAAGAACAAGAAAGTCTCATGTGCGATTCCCGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAACAAGAAAGTCTCATGTGCGATTCCCGAAAC	1620
Qy	1621	CTGACTAATGATGGCCACTGCTGCGAATGATGATGATTAATTCCTCCAGGAAGAGC	1680
Db	1621	CTGACTAATGATGGCCACTGCTGCGAATGATGATGATTAATTCCTCCAGGAAGAGC	1680
Qy	1681	AGAACACCTGAAGCCAGCAATTTCTCGACACTGGAATGAAGATTCACAGTGACGAA	1740
Db	1681	AGAACACCTGAAGCCAGCAATTTCTCGACACTGGAATGAAGATTCACAGTGACGAA	1740
Qy	1741	CAAAATATCTCAGGAACAATTTTGGAAAGACAGAACTGGAATTTTACAGATGAG	1800
Db	1741	CAAAATATCTCAGGAACAATTTTGGAAAGACAGAACTGGAATTTTACAGATGAG	1800
Qy	1801	ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGTTGAAAAAATGAATTTGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGTTGAAAAAATGAATTTGAGCTTCT	1860
Qy	1861	CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAATAGTACGTTGCCGGAAGAAAT	1920
Db	1861	CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAATAGTACGTTGCCGGAAGAAAT	1920
Qy	1921	GCCATGCTAAGACTGAGGCTTGAACAAATGAAACATCAAGCCAGCTTAAAAAATTTT	1980
Db	1921	GCCATGCTAAGACTGAGGCTTGAACAAATGAAACATCAAGCCAGCTTAAAAAATTTT	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	

RESULT 8
 US-09-895-793-374
 ; Sequence 374, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, JIANGCHUN
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: JIANG, YUJUN
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Baesols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C2
 CURRENT APPLICATION NUMBER: US/09/895,793
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 374
 LENGTH: 2000
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-895-793-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTGAAGTTTCAATGCGGCTGCTCTTCTGTGAAGACATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTTTCAATGCGGCTGCTCTTCTGTGAAGACATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTGCTTCCCTGTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTGCTTCCCTGTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAACAACAAGCACTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAACAACAAGCACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAATGTGCGCCGCCACTGCTTCCCTGCTGCAAGGAGGATGGCAAGACGTC 240
DB 181 ATGGGCAATGTGCGCCGCCACTGCTTCCCTGCTGCAAGGAGGATGGCAAGACGTC 240
QY 241 GGGCGTTCTGAGAACCAACAAGCACTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
DB 241 GGGCGTTCTGAGAACCAACAAGCACTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGCAAGAGTGGCGCTTGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGCAAGAGTGGCGCTTGG 360
QY 361 GGAAGATTAAGATGACAGTGTGCTTCAATGAGGCCAGGTACCAAGTGTGAGAAATCTG 420
DB 361 GGAAGATTAAGATGACAGTGTGCTTCAATGAGGCCAGGTACCAAGTGTGAGAAATCTG 420
QY 421 GACAACTCCACAGAGTGTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAACTCCACAGAGTGTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTGAGGAGCACTGACGTGAACAAGAAAGACAAAGCAAGAGAGTCTCTTACATCTGGCC 540
DB 481 CTGAGGAGCACTGACGTGAACAAGAAAGACAAAGCAAGAGAGTCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGAACAAGATGTCACCTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGAACAAGATGTCACCTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGGCGGTACATGCGAGAAATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGGCGGTACATGCGAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAATATTCAGATGATGAAAT 720
QY 721 ACCACTCTGCACTAAGCTATCTTAATGAAGATTAATTAAGCCAAAGCATGCTCTTA 780
DB 721 ACCACTCTGCACTAAGCTATCTTAATGAAGATTAATTAAGCCAAAGCATGCTCTTA 780
QY 781 TATGTGCTGATATCGAATCAAAAACAGATGGCTCACACCACTGTTACTTGGATGA 840
DB 781 TATGTGCTGATATCGAATCAAAAACAGATGGCTCACACCACTGTTACTTGGATGA 840
QY 841 CATGACAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTTAAATGCA 900

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DB 841 CATGACAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTTAAATGCA 900
QY 901 CTGGATTAAGTATGGAAGAGCTGCTCTCATACTCTGCTGATATGTTGGATACACCAAGTAA 960
DB 901 CTGGATTAAGTATGGAAGAGCTGCTCTCATACTCTGCTGATATGTTGGATACACCAAGTAA 960
QY 961 GTGACGCTTCTACTGAGCAAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGACG 1020
DB 961 GTGACGCTTCTACTGAGCAAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGACG 1020
QY 1021 GCCAAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTTCTGACTAC 1080
DB 1021 GCCAAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATGCTAAAATCTCTGTAACACAGAAATCCAGAACAAACCTTAAAG 1140
DB 1081 AAAAGAAAACAGATGCTAAAATCTCTGTAACACAGAAATCCAGAACAAACCTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCATGTAATTAAGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCATGTAATTAAGCCAGCCAGAGAA 1200
QY 1201 ATGCTCAAGAACCAAGAAATTAAGATGAGTATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACCAAGAAATTAAGATGAGTATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGATTTACTGAAAACCTGACTAAATGTTGTCATCTGGCC 1320
DB 1261 AAGCATGAAAGTAAATATGTTGGATTTACTGAAAACCTGACTAAATGTTGTCATCTGGCC 1320
QY 1321 AATGTTGATATGATTAATTTCTCAAGAAAGACAGAACACTGAAAATGACAAATTT 1380
DB 1321 AATGTTGATATGATTAATTTCTCAAGAAAGACAGAACACTGAAAATGACAAATTT 1380
QY 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGGGAAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGGGAAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCCAAAATATCTCTTCTGAAAACACCAACCCAGAACCAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCCAAAATATCTCTTCTGAAAACACCAACCCAGAACCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAAAAAGCTTGAAGGCACTGAAAATGAGCCAGAGCTAGAAAAT 1560
DB 1501 TCAGAGGAAGAGTCAAAAAGCTTGAAGGCACTGAAAATGAGCCAGAGCTAGAAAAT 1560
QY 1561 TTTATGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGCGAATTTCCAGAAAAAC 1620
DB 1561 TTTATGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGCGAATTTCCAGAAAAAC 1620
QY 1621 CTGACCTAATGGGCCACTGCTGGCAATGCTGATGATTAATTTCTTCCAGAGAAAGAC 1680
DB 1621 CTGACCTAATGGGCCACTGCTGGCAATGCTGATGATTAATTTCTTCCAGAGAAAGAC 1680
QY 1681 AAGAACCTGAAAGCAGCAATTTTCTGCACTGAGAAATGAAGATACAGTGAAGAA 1740
DB 1681 AAGAACCTGAAAGCAGCAATTTTCTGCACTGAGAAATGAAGATACAGTGAAGAA 1740
QY 1741 CAAAATGATACTCAGAAAGATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
DB 1741 CAAAATGATACTCAGAAAGATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
QY 1801 ATTTGATTTCAAGAAAGAAAGAGATGAGAGTGTGGAAGAAATGAAATCTGAGCTTTCT 1860
DB 1801 ATTTGATTTCAAGAAAGAAAGAGATGAGAGTGTGGAAGAAATGAAATCTGAGCTTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAATAGTACGTTGGGGAAGAAATTT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAATAGTACGTTGGGGAAGAAATTT 1920
QY 1921 GCCATGCTTAAGACTGAGCTTGAACAATGAACATCAGAGCCAGCTTAAATTAATTAATTA 1980
DB 1921 GCCATGCTTAAGACTGAGCTTGAACAATGAACATCAGAGCCAGCTTAAATTAATTAATTA 1980

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QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 9
US-09-895-814-374
Sequence 374, Application US/09895814
Publication No. US0020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Heppler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basbols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTGAGGTGATTCATGCGGCTCTTCTGTGAAGCAATTTGGTCTC 60
Db 1 ATGTGTGTGAGGTGATTCATGCGGCTCTTCTGTGAAGCAATTTGGTCTC 60

QY 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120

QY 121 AGCAACGTGGGCACTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAAGAGCAAG 180

QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240

QY 241 GGCGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAAGAAAGATGGGCAAG 300
Db 241 GGCGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAAGAAAGATGGGCAAG 300

QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360

QY 361 GGAGACTACGATGACAGTCCCTTCAATGAGAGCCAGAGTACCACTCCGTGGAAGATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCAATGAGAGCCAGAGTACCACTCCGTGGAAGATCTG 420

QY 421 GACAAGCTCCAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTGCTCATG 480
Db 421 GACAAGCTCCAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTGCTCATG 480

QY 481 CTCAGGAGCACTGACGTGAAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
Db 481 CTCAGGAGCACTGACGTGAAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540

QY 541 TCTGCAATGGGAATTCAGAAATAGTAAATCTCTGCTGCAAGACAGATGTCACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAATAGTAAATCTCTGCTGCAAGACAGATGTCACTTAAT 600

QY 601 GTCTTGAACAACAAAGAGAGCAGCTCTGATTAAGGCGGTACAAATGGCAGGAAGATGAA 660
Db 601 GTCTTGAACAACAAAGAGAGCAGCTCTGATTAAGGCGGTACAAATGGCAGGAAGATGAA 660

QY 661 TGTGCTTAATGTGCTGGAACATGGAATGCAATTAATTCAGATGATGGAAT 720
Db 661 TGTGCTTAATGTGCTGGAACATGGAATGCAATTAATTCAGATGATGGAAT 720

QY 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780

QY 781 TATGTGTGATGATGATGATCAAAAGCAAGTGGCTCAGCCACTGATCTGCTGTA 840
Db 781 TATGTGTGATGATGATGATCAAAAGCAAGTGGCTCAGCCACTGATCTGCTGTA 840

QY 841 CATGACAAACACAGAGCTGTAATTTTAAATCAAGAAAGAGCAATTTAAATGCA 900
Db 841 CATGACAAACACAGAGCTGTAATTTTAAATCAAGAAAGAGCAATTTAAATGCA 900

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Db 901 CTGATTAATGATGAAAGACTGCTCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960

QY 961 GTGAGCTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGAGCAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGAGCAGAG 1020

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Db 1081 AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACTTAAG 1140

QY 1141 CTGATATCAAGAGAGATCAAAAGTTTCAAGGCAATGAAATATGCCAGGCAAGAA 1200
Db 1141 CTGATATCAAGAGAGATCAAAAGTTTCAAGGCAATGAAATATGCCAGGCAAGAA 1200

QY 1201 ATGTCTCAAGAACAGAAATAAATAAGATGTTAGAGAGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATAAATAAGATGTTAGAGAGTGAAGAAATGAAG 1260

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Db 1261 AAGCATGAAGATTAATGTGGATTACTAGAAAAGCTGACTAATGTGTCTGCTGCGC 1320

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Db 1321 AATGTGATTAATGATTAATCTTCAAGAGAGCAAGCAACCTGAAATTAAGAAATTT 1380

QY 1381 CTTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440

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QY 1441 AACAGATGCCAAATACTCTTCTGAAAAAGCAAGCCAGAAACAGACTTAAAGCTGACA 1500
DB 1441 AACAGATGCCAAATACTCTTCTGAAAAAGCAAGCCAGAAACAGACTTAAAGCTGACA 1500
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DB 1501 TCAGAGAAAGATCAAAAGGCTTGAAGGCACTGAAAATGCGCAGCAGAGCTAGAAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAAGACAGAAAGTACTGATGCGGATTTCCAGAAAAC 1620
DB 1561 TTTATGCTATCGAAGAAATGAAAGACAGAAAGTACTGATGCGGATTTCCAGAAAAC 1620
QY 1621 CTGACTAATGATGCGCACTGCGCAATGATGATGATTAATTCCTCCAGAGAGAGC 1680
DB 1621 CTGACTAATGATGCGCACTGCGCAATGATGATGATTAATTCCTCCAGAGAGAGC 1680
QY 1681 AGAAGCCTGAAAGCCAGCAATTTCTGACACTGAAATGAAAGATATCAAGTACGAA 1740
DB 1681 AGAAGCCTGAAAGCCAGCAATTTCTGACACTGAAATGAAAGATATCAAGTACGAA 1740
QY 1741 CAAATGATATCTGAAAGCAATTTTGTGAAGACAGAACTGGATATTTACAGATGAG 1800
DB 1741 CAAATGATATCTGAAAGCAATTTTGTGAAGACAGAACTGGATATTTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAAGAAAGCAGATAGAAAGTGTGAAATTAATTCGAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAAGAAAGCAGATAGAAAGTGTGAAATTAATTCGAGCTTTCT 1860
QY 1861 CTTAGTGTGAAAGAAAGAAAGCAGATCTTGCAATTAATGTAAGTGTGCGGAAAGAAAT 1920
DB 1861 CTTAGTGTGAAAGAAAGAAAGCAGATCTTGCAATTAATGTAAGTGTGCGGAAAGAAAT 1920
QY 1921 GCCATGCTAGAGCTGAGCTAGACATGAAATCATGAGCCAGCTTAAATTAATTAATTA 1980
DB 1921 GCCATGCTAGAGCTGAGCTAGACATGAAATCATGAGCCAGCTTAAATTAATTAATTA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-10-012-896-374
; Sequence 374, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retzer, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yaelir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlotca
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mestababe, Yoshinhiro
; APPLICANT: Mescher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27

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; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-374

Query Match      100.0%; Score 2000; DB 5; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGTTGAGTTGATTCATAGCGGCTGCTCTTCTGTAAGAGCATTTGCTTC 60
DB 1 ATGGGTGTTGAGTTGATTCATAGCGGCTGCTCTTCTGTAAGAGCATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
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DB 121 AGCAACGTGGGCACTTTGAGAGCAAGCAAGCTCTGTATGAAAGCACTCAGAGCAAG 180
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DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCTTG 240
QY 241 GCGGCTTCTGAGACCAAGCAAGCTCTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GCGGCTTCTGAGACCAAGCAAGCTCTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGTGGCAAGTGGCAAG 360
DB 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGTGGCAAGTGGCAAG 360
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DB 361 GGAGACTAGAGTGAAGAGTCCCTCATGAGCCAGGTACAGCTCCGTGGAATAATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAACTCCACAGAGCTGCTGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
DB 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCCGTGCAAGAGATGTAATCTTAT 600
DB 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCCGTGCAAGAGATGTAATCTTAT 600
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DB 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGGCGGTCAATGCCAGAGATGAA 660
QY 661 TGTGCGTTATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGCACTAGCTATCTATATGAAAGTAAATTAATGCCAAAGCACTGCTCTTA 780
DB 721 ACCACTGCACTAGCTATCTATATGAAAGTAAATTAATGCCAAAGCACTGCTCTTA 780
QY 781 TATGCTGCTATGATGAATCAAAAACAGATGCGCTCAACCACTGTTACTTGATGTA 840
DB 781 TATGCTGCTATGATGAATCAAAAACAGATGCGCTCAACCACTGTTACTTGATGTA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900

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QY	901	CTGGAATAATATGGAAGACATGCTCTCTACTTCTGCTGTAATGTTGGATCAAGCAAGTTA	960
Db	901	CTGGATTAATATGGAAGACATGCTCTCTACTTCTGCTGTAATGTTGGATCAAGCAAGTTA	960
QY	961	GTCAAGCTTCTAATCTTGAGCAAAATATTATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
Db	961	GTCAAGCTTCTAATCTTGAGCAAAATATTATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
QY	1021	GCCAGAGATATGCTGTTTCTTAGTCATCATCATGTAATTTGGCAGTTACTTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTTAGTCATCATCATGTAATTTGGCAGTTACTTTCTGACTAC	1080
QY	1081	AAAGAAAAACGATGCTAAAAATCTCTTCTGAAAAACACATCCAGAACAAAGACTTAAAG	1140
Db	1081	AAAGAAAAACGATGCTAAAAATCTCTTCTGAAAAACACATCCAGAACAAAGACTTAAAG	1140
QY	1141	CTGACATCAGAGAAAGTCACAAAGTTCAAAGCAGTGAATAATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGAAAGTCACAAAGTTCAAAGCAGTGAATAATAGCCAGCCAGAGAA	1200
QY	1201	ATGTCCTCAAGAACCGAAATTAATTAAGATGCTGATAGAGGCTTGAAGAAATAG	1260
Db	1201	ATGTCCTCAAGAACCGAAATTAATTAAGATGCTGATAGAGGCTTGAAGAAATAG	1260
QY	1261	AAGCATGAAGATTAATATGCGGATTAATAGAAAACTGAATATGGTCACTGCTGGC	1320
Db	1261	AAGCATGAAGATTAATATGCGGATTAATAGAAAACTGAATATGGTCACTGCTGGC	1320
QY	1321	AATGGTGAATATAGTAAATTCCTTCAAAGAAAGCAGAACACCTGAATAACCAATTT	1380
Db	1321	AATGGTGAATATAGTAAATTCCTTCAAAGAAAGCAGAACACCTGAATAACCAATTT	1380
QY	1381	CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGCGAATTAGTTTCTGAATAAGAA	1440
Db	1381	CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGCGAATTAGTTTCTGAATAAGAA	1440
QY	1441	AAACGATGCAAAATTAATCTTCTGAAAAACAGCAACCAAGAACAAAGCTTAAACCTGACA	1500
Db	1441	AAACGATGCAAAATTAATCTTCTGAAAAACAGCAACCAAGAACAAAGCTTAAACCTGACA	1500
QY	1501	TCAGAGGAAGTCACAAAGCTTGAAGGCGCTGTAATAATGGCCAGCCAGACTTGAAAT	1560
Db	1501	TCAGAGGAAGTCACAAAGCTTGAAGGCGCTGTAATAATGGCCAGCCAGACTTGAAAT	1560
QY	1561	TTTATGGCTATCGAAAGATGTAAGAAAGACGGAAGTACTCATGTCCGATTCGCCAATAAC	1620
Db	1561	TTTATGGCTATCGAAAGATGTAAGAAAGACGGAAGTACTCATGTCCGATTCGCCAATAAC	1620
QY	1621	CTGACTAATGCTGCCACTGCTGGCAATGATGATGATGATTAATTTCTCCAAAGAAAGC	1680
Db	1621	CTGACTAATGCTGCCACTGCTGGCAATGATGATGATGATTAATTTCTCCAAAGAAAGC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCCCTGCAACTGAGATGAAGAGTATCAACATGACGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCCCTGCAACTGAGATGAAGAGTATCAACATGACGAA	1740
QY	1741	CAAAATGATCTCAGAAACCAATTTTGTGTAAGAACGAAACTGGAATATTACAAGATGAG	1800
Db	1741	CAAAATGATCTCAGAAACCAATTTTGTGTAAGAACGAAACTGGAATATTACAAGATGAG	1800
QY	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGGTTGAATAATGAATTTCTGACCTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGGTTGAATAATGAATTTCTGACCTTCT	1860
QY	1861	CTTAGTGTAAAGAAAGAAAGACATCTTGATGAATAATAGTTCGGGAGGAAGAAAT	1920
Db	1861	CTTAGTGTAAAGAAAGAAAGACATCTTGATGAATAATAGTTCGGGAGGAAGAAAT	1920
QY	1921	GCCATGCTAAGCTGAGCTAGACCAATGAACATCAGACCAGCTAAAAAATAAAAA	1980
Db	1921	GCCATGCTAAGCTGAGCTAGACCAATGAACATCAGACCAGCTAAAAAATAAAAA	1980

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CY      1981  AAAAAAAAAAAAAAAAAAAAAA  2000
        |||||||||||||||||||
Db      1981  AAAAAAAAAAAAAAAAAAAAAA  2000
        |||||||||||||||||||

RESULT 11
US-10-010-940-374
/ Sequence 374, Application US/10010940
/ Publication No. US2003008062A1
GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Hitchcock, Jennifer L.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Jiang Yuxin
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Kalos, Michael
/ APPLICANT: Fanger, Gary
/ APPLICANT: Retter, Mark
/ APPLICANT: Solk, John
/ APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FOR THE TREATMENT OF PROSTATE
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
/ FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
/ SOFTWARE: FASTSEQ for Windows Version 3.0.
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-010-940-374

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Cy      1981 AAAAAAAAAAAAAAAAAA 2000
        |||||||
Db      1981 AAAAAAAAAAAAAAA 2000

RESULT 11
US-10-010-940-374
; Sequence 374, Application US/10010940
; Publication No. US20030088062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: JIANG YuguI
APPLICANT: Reed, Steven G.
APPLICANT: Kaios, Michael
APPLICANT: Fanger, Gary
APPLICANT: Recter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010.940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-10-010-940-374
```

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QY 541 TCGCAATGGGAATTCAGAAAGTAAAACTCTGCTGGACAGCATGTCAACTTAAT 600
DB 541 TCGCAATGGGAATTCAGAAAGTAAAACTCTGCTGGACAGCATGTCAACTTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGAGCAGCTGTATTAAGCCGTACATGCCAGGAAGATGA 660
DB 601 GTCTCTTGACAAACAAAAGAGAGCAGCTGTATTAAGCCGTACATGCCAGGAAGATGA 660
QY 661 TGGGCGTTAATGTTGGTGGAAACAATGGCACTGATCCCAATATTCCAATAGATGAAT 720
DB 661 TGGGCGTTAATGTTGGTGGAAACAATGGCACTGATCCCAATATTCCAATAGATGAAT 720
QY 721 ACCACTGCTGACACTACGCTATCTTAATGAAGATTAATTAAGGCCAAGACCTGCTTA 780
DB 721 ACCACTGCTGACACTACGCTATCTTAATGAAGATTAATTAAGGCCAAGACCTGCTTA 780
QY 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCTCACACACTGTTACTTGGTGA 840
DB 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCTCACACACTGTTACTTGGTGA 840
QY 841 CATGACCAAAAAACAGCAAGCTCGTGAATTTTAAATCAAGAAAAAACGGAATTTAAATGA 900
DB 841 CATGACCAAAAAACAGCAAGCTCGTGAATTTTAAATCAAGAAAAAACGGAATTTAAATGA 900
QY 901 CTGGATAGATATGGAAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGTATA 960
QY 961 GTGACGCTTCTACTTGAGCAAAATATGATGTAATCTTCAAGATCTATCTGGACAGACG 1020
DB 961 GTGACGCTTCTACTTGAGCAAAATATGATGTAATCTTCAAGATCTATCTGGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACAGCAATCAGAACAGACTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACAGCAATCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGAGTGAATAATGACCAAGCAAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGAGTGAATAATGACCAAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATATATATGTTGGAATTAAGAAAACCTGACTAATGCTGCTGAC 1320
DB 1261 AAGCATGAAGATATATATGTTGGAATTAAGAAAACCTGACTAATGCTGCTGAC 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGACCACTGAAATCAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGACCACTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCAAAATATCTCTTGAAAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500
DB 1441 AAAACAGATGCAAAATATCTCTTGAAAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTCAACAAAGCTTGAAGGAGTGAATGCGCAGGCAAGAGCTAGAAAT 1560
DB 1501 TCAGAGAAAGAGTCAACAAAGCTTGAAGGAGTGAATGCGCAGGCAAGAGCTAGAAAT 1560
QY 1561 TTTATGCTATTCGAAGAAATGAAGAGCAGGAAGTACTATGCGAATTTCCAGAAAC 1620
DB 1561 TTTATGCTATTCGAAGAAATGAAGAGCAGGAAGTACTATGCGAATTTCCAGAAAC 1620

```

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QY 1621 CTGACATATGTTGGCCACTGCTGCAATGGTGAATGATTAATTCCTCAAGAGAGAC 1680
DB 1621 CTGACATATGTTGGCCACTGCTGCAATGGTGAATGATTAATTCCTCAAGAGAGAC 1680
QY 1681 AGAACAACCTGAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCAGATGCGAA 1740
DB 1681 AGAACAACCTGAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCAGATGCGAA 1740
QY 1741 CAAAATGATATCTCAGAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACCATGAG 1800
DB 1741 CAAAATGATATCTCAGAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACCATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAAAGTGTGAAAAAATGAATTCAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAAAGTGTGAAAAAATGAATTCAGCTTTCT 1860
QY 1861 CTTAGTTGTGAAGAAAAAGAAAGACATCTTGACATGAATAATGATACGTTGCGGGAAGAAAT 1920
DB 1861 CTTAGTTGTGAAGAAAAAGAAAGACATCTTGACATGAATAATGATACGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAATGAAGCCAGCTTAATTAATTAATTA 1980
DB 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAATGAAGCCAGCTTAATTAATTAATTA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

```

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RESULT 12
US-10-212-679-302
; Sequence 302, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, David
; APPLICANT: Roy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-302

```

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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGATGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
DB 1 ATGTGTTGATGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
QY 61 AGGAGCAGATGGGCAAGTGTGCTGCGTTCCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAGATGGGCAAGTGTGCTGCGTTCCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGAGACAGACGACTGTGATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGAGACAGACGACTGTGATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAACG 240
DB 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAACG 240

```


QY 241 GGGGCTTTGGAGACCAAGCACTCTGCTATGAAAGCACTCAAGAACAAAGATGGGCAAG 300
DB 241 GGGGCTTTGGAGACCAAGCACTCTGCTATGAAAGCACTCAAGAACAAAGATGGGCAAG 300
QY 301 TGGTGCTGCACTGCTTCCCTCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
DB 301 TGGTGCTGCACTGCTTCCCTCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
QY 361 GAGAGCTACGATGACAGTGCCTTCAATGAGCCCAAGTACCAAGTCCGCTGAGAAAGTCTG 420
DB 361 GAGAGCTACGATGACAGTGCCTTCAATGAGCCCAAGTACCAAGTCCGCTGAGAAAGTCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGGAACACTGACGGAACAAAGAGGACAAAGAGGAGGAGTGCCTCTCAATCTGGCC 540
DB 481 CTCAGGGAACACTGACGGAACAAAGAGGACAAAGAGGAGGAGTGCCTCTCAATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAATGATTAACCTCTGCTGACAGAGATGCTCACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAATGATTAACCTCTGCTGACAGAGATGCTCACTTAAT 600
QY 601 GTCTCTGACAAACAAAGAGGACAGCTCTGATTAAGGCGCTCAATGCGCAAGAAATGAA 660
DB 601 GTCTCTGACAAACAAAGAGGACAGCTCTGATTAAGGCGCTCAATGCGCAAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATTTCTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATTTCTCAGATGATGGAAT 720
QY 721 ACCACTCTGACCTACGCTATCTAATTAATGAAATTAATTAATGAGCAAGCACTGCTTAA 780
DB 721 ACCACTCTGACCTACGCTATCTAATTAATGAAATTAATTAATGAGCAAGCACTGCTTAA 780
QY 781 TATGCTGCTGATATCGAATCAAAAACAGCATGCGCTCAACCATCTGTTACTTGGTGA 840
DB 781 TATGCTGCTGATATCGAATCAAAAACAGCATGCGCTCAACCATCTGTTACTTGGTGA 840
QY 841 CATGACCAAAAACAGCATGCGTGAATTTTAAATCAAGAAAGGAAATTTAAATGCA 900
DB 841 CATGACCAAAAACAGCATGCGTGAATTTTAAATCAAGAAAGGAAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGGAGCTGCTCTCATCTTCTGATATGTTGATGATGATGATGAT 960
DB 901 CTGATAGATATGGAAGGAGCTGCTCTCATCTTCTGATATGTTGATGATGATGATGAT 960
QY 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCAAGTAACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCAAGTAACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAGAAACAGCAATCAGAAACAAAGCTTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAGAAACAGCAATCAGAAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGGAGCTGAATAATGCGCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGGAGCTGAATAATGCGCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 AAGCATGAAGATTAATGATGAGATTAAGTGAAGAAACCTGATTAATGATGATGATGATGAT 1320
DB 1261 AAGCATGAAGATTAATGATGAGATTAAGTGAAGAAACCTGATTAATGATGATGATGATGAT 1320

QY 1321 AATGATTAATGATTAATTTCTCAAGAAAGAGCAAGAACCTGAAAAATCAGCAATTT 1380
DB 1321 AATGATTAATGATTAATTTCTCAAGAAAGAGCAAGAACCTGAAAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTTGGCAATTTAGTTCTGACTCAAGAA 1440
DB 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTTGGCAATTTAGTTCTGACTCAAGAA 1440
QY 1441 AAACAGATGCAAAATTAATCTTCTGAAAAACAGCAACCAAGAACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCAAAATTAATCTTCTGAAAAACAGCAACCAAGAACTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATCAAAAGGCTTGAAGGCAAGTAAATGAGCCAGCAAGCTTAAGAAAT 1560
DB 1501 TCAGAGAAAGATCAAAAGGCTTGAAGGCAAGTAAATGAGCCAGCAAGCTTAAGAAAT 1560
QY 1561 TTTATGCTATGCAAGAAATGAAAGAGCAAGAAATGCTCATGCGGATTTCCAGAAAC 1620
DB 1561 TTTATGCTATGCAAGAAATGAAAGAGCAAGAAATGCTCATGCGGATTTCCAGAAAC 1620
QY 1621 CTGACTTAATGCTGCACTGCTGCAATGATGATGATTAATTTCTCCAGAGAGAGC 1680
DB 1621 CTGACTTAATGCTGCACTGCTGCAATGATGATGATTAATTTCTCCAGAGAGAGC 1680
QY 1681 AGAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAAGATATCAAGTGAAGAA 1740
DB 1681 AGAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAAGATATCAAGTGAAGAA 1740
QY 1741 CAAAAATGATCTCAGAAAGCAATTTTGAAGAACAGAACCTGGAATTAATTAACGATGAG 1800
DB 1741 CAAAAATGATCTCAGAAAGCAATTTTGAAGAACAGAACCTGGAATTAATTAACGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGATGAAAGTGTGAAATAATGAAATTCAGCTTCTT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATGAAAGTGTGAAATAATGAAATTCAGCTTCTT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAATATGTCGTTGGGAGAAATTT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAATATGTCGTTGGGAGAAATTT 1920
QY 1921 GCCATGCTAAGCTGAGGCTGACCAATGAAACATCAAGCAGCTAAATTAATTAATTA 1980
DB 1921 GCCATGCTAAGCTGAGGCTGACCAATGAAACATCAAGCAGCTAAATTAATTAATTA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 13
US-10-144-678A-374
; Sequence 374, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

```
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals Y de Bassole, Carlota
/ APPLICANT: Roy, Teresa M.
/ APPLICANT: Matanabe, Yoshihiro
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C28
/ CURRENT APPLICATION NUMBER: US/10/144,678A
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-144-678A-374

Query Match      100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGTTGAGGTTGATTCATGCGGCTCTTCTGTGAAGAGCCATTGCTTC 60
DB      1 ATGTGTTGAGGTTGATTCATGCGGCTCTTCTGTGAAGAGCCATTGCTTC 60

QY      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGAGGAGAGCGGCAAG 120
DB      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGAGGAGAGCGGCAAG 120

QY      121 AGCAAGTGGGCACTTCTGAGACACAGACACTGCTATGAAGACACTCAGAGCAAG 180
DB      121 AGCAAGTGGGCACTTCTGAGACACAGACACTGCTATGAAGACACTCAGAGCAAG 180

QY      181 ATGAGGCAAGTGTGCGGCGCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGACGTC 240
DB      181 ATGAGGCAAGTGTGCGGCGCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGACGTC 240

QY      241 GGGCTTCTGAGAGACACAGACACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
DB      241 GGGCTTCTGAGAGACACAGACACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300

QY      301 TGTGCTGCGCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGTGGGCGCTTGG 360
DB      301 TGTGCTGCGCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGTGGGCGCTTGG 360

QY      361 GGAAGACTACGATGACAGTGTCTTCAATGAGCCAGGTACCACTGCTGAGAGATCTG 420
DB      361 GGAAGACTACGATGACAGTGTCTTCAATGAGCCAGGTACCACTGCTGAGAGATCTG 420

QY      421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480
DB      421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480

QY      481 CTGAGGAGACCTGACGTGAACAAAGAGCAAGCAAAAGAGACTGCTCTTCAATCTGGCC 540
DB      481 CTGAGGAGACCTGACGTGAACAAAGAGCAAGCAAAAGAGACTGCTCTTCAATCTGGCC 540

QY      541 TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGAGACAGACGATGTCACTTAAT 600
DB      541 TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGAGACAGACGATGTCACTTAAT 600

QY      601 GTCTTGAACAACAAAAGAGAGACAGCTGTAATAAGGCGTAACTAGCCAGAGAGATGAA 660
DB      601 GTCTTGAACAACAAAAGAGAGACAGCTGTAATAAGGCGTAACTAGCCAGAGAGATGAA 660

QY      661 TGTGCTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAGAAAT 720
DB      661 TGTGCTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAGAAAT 720

QY      721 ACCACTCTGACCTACGCTATCTAATATGAAGATTAATTAAGCCAAAGACATGCTTTA 780
DB      721 ACCACTCTGACCTACGCTATCTAATATGAAGATTAATTAAGCCAAAGACATGCTTTA 780
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QY      781 TATGTGCTGATATGGAATCAAAAAACAAGATGGCTTCACACACTGTTACTGTGTGA 840
DB      781 TATGTGCTGATATGGAATCAAAAAACAAGATGGCTTCACACACTGTTACTGTGTGA 840

QY      841 CATGAGCAAAAAACAGAGTCTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB      841 CATGAGCAAAAAACAGAGTCTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900

QY      901 CTGATATGATATGAAGAGCTGCTCATCTTGTCTGTATGTTGTGATCAGCAAGTATA 960
DB      901 CTGATATGATATGAAGAGCTGCTCATCTTGTCTGTATGTTGTGATCAGCAAGTATA 960

QY      961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGAG 1020
DB      961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGAG 1020

QY      1021 GCCAGAGATATGCTGTTCTAGTCATCATCTAATTTGCGAGTTACTTCTGACTAC 1080
DB      1021 GCCAGAGATATGCTGTTCTAGTCATCATCTAATTTGCGAGTTACTTCTGACTAC 1080

QY      1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
DB      1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140

QY      1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAGTAAATAGCCAGCAGAGAA 1200
DB      1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAGTAAATAGCCAGCAGAGAA 1200

QY      1201 ATGTCTCAAGAACAGAAATTAATAGATGTGTATGAGAGTTGAAGAAATGAAG 1260
DB      1201 ATGTCTCAAGAACAGAAATTAATAGATGTGTATGAGAGTTGAAGAAATGAAG 1260

QY      1261 AAGCATGAAGATTAATATGTGGATTTACTGAAAACTGACCTAATGTGTCTACTGTGGC 1320
DB      1261 AAGCATGAAGATTAATATGTGGATTTACTGAAAACTGACCTAATGTGTCTACTGTGGC 1320

QY      1321 AATGTGATTAATGATTAATTTCTCAAAAGAGAGAGAAACCTGAAATCAGCAATTT 1380
DB      1321 AATGTGATTAATGATTAATTTCTCAAAAGAGAGAGAAACCTGAAATCAGCAATTT 1380

QY      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTAATGTTCTGACTACAAAGAA 1440
DB      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTAATGTTCTGACTACAAAGAA 1440

QY      1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGAACCCAGAACAAAGCTTAAAGCTGACA 1500
DB      1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGAACCCAGAACAAAGCTTAAAGCTGACA 1500

QY      1501 TCAGAGAAAGATCAAAAAGCTTGAAGGCAAGTGAATAATGGCAGACAGAGCTAGAAAT 1560
DB      1501 TCAGAGAAAGATCAAAAAGCTTGAAGGCAAGTGAATAATGGCAGACAGAGCTAGAAAT 1560

QY      1561 TTTATGCTATGAAAGAAATGAAGAGCAAGAGTACTCATGTGGATTTCCAGAAAAAC 1620
DB      1561 TTTATGCTATGAAAGAAATGAAGAGCAAGAGTACTCATGTGGATTTCCAGAAAAAC 1620

QY      1621 CTGACTAATGTGTGCACTGCTGCAATGTGTATGATTAATTTCTTCCAGAGAAAGAC 1680
DB      1621 CTGACTAATGTGTGCACTGCTGCAATGTGTATGATTAATTTCTTCCAGAGAAAGAC 1680

QY      1681 AGAACACCTGAAAGCAGCAATTTTCTGACACTGAGAAATGAAGAGATCAGAGTACGAA 1740
DB      1681 AGAACACCTGAAAGCAGCAATTTTCTGACACTGAGAAATGAAGAGATCAGAGTACGAA 1740

QY      1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
DB      1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800

QY      1801 ATTCTGATTCATGAAGAAAGCAGATAGAGGTGTTGAAAAATGAATTTGAGCTTTCT 1860
DB      1801 ATTCTGATTCATGAAGAAAGCAGATAGAGGTGTTGAAAAATGAATTTGAGCTTTCT 1860
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Accession	Sequence	Length
OY	CTGTGGTTAAGAAAGAAAAGACACTCTGTGATGAAAATAGTACGTCGGGGAAGAATT	1920
Db	1861 CTGTGGTTAAGAAAGAAAAGACACTCTGTGATGAAAATAGTACGTCGGGGAAGAATT	1920
OY	1921 GCCATGCTAAGACCTGAGAGCTAGACACATGATAACATCAGAGCCAGCTAAAAA	1980
Db	1921 GCCATGCTAAGACCTGAGAGCTAGACACATGATAACATCAGAGCCAGCTAAAAA	1980
OY	1981 AAAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981 AAAAAAAAAAAAAAAAAAAAAA 2000	

RESULT 14
US-10-033-527-6

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? Sequence 6 Application US/10033527
? Publication No. US20030170631A1
? GENERAL INFORMATION:
? APPLICANT: Houghton, Raymond L.
? APPLICANT: Dillon, Davin C.
? APPLICANT: Molesh, David A.
? APPLICANT: Xu, Jiangchun
? APPLICANT: Zehentner, Barbara
? APPLICANT: Persing, David H.
? TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
? FILE OF INVENTION: 210121.513C1
? CURRENT APPLICATION NUMBER: US/10/033,527
? CURRENT FILING DATE: 2001-10-27
? NUMBER OF SEQ ID NOS: 77
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 6
? LENGTH: 2000
? TYPE: DNA
? ORGANISM: Homo sapien
? US-10-033-527-6

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Query Match	100.0%;	Score 2000;	DB 6;	Length 2000;
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Db	1	ATGGTGGTTGAGGTGATTCCATGCGCGGCTGCTCTTCGTGGAAGAACAACGCATTGGTCTC	60
QY	61	AGAGCAAGATGCGCAAGTGTGTGTCGCCGTGCTTCCCTGCTGCAGGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGCGGCAAGTGTGTGTCGCCGTGCTTCCCTGCTGCAGGGAGAGCGGCAAG	120
QY	121	AGCAACGTGGGCATTCTTGAGAGCCAGACGACTCTGCTATGAGAGCACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCATTCTTGAGAGCCAGACGACTCTGCTATGAGAGCACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGGGAGTGGAAAGCAACGTG	240
Db	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGGGAGTGGCAAGCAACGTG	240
QY	241	GGCGCTTCTGAGAGCAACGACGACTCTGCTATGAAAGCACTCAGGAACAAGTGGGCAAG	300
Db	241	GGCGCTTCTGAGAGCAACGACGACTCTGCTATGAAAGCACTCAGGAACAAGTGGGCAAG	300
QY	301	TGGTGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAAACGGCAAGCAAGTGGGCGCTTGG	360
Db	301	TGGTGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAAACGGCAAGCAAGTGGGCGCTTGG	360
QY	361	GGAGCTACGATGACAGTGCCTTCACTGAGAGCCCAAGTACCAAGTCCGTGAGAAAGTCTG	420
Db	361	GGAGCTACGATGACAGTGCCTTCACTGAGAGCCCAAGTACCAAGTCCGTGAGAAAGTCTG	420
QY	421	GACCAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGGATCTCATGCTCATG	480
Db	421	GACCAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGGATCTCATGCTCATG	480

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Db	4481	CTCAGGCACTGTAACGTGAAACAABAAGACACAGCAAAAAGAGACTGCTCTACATCTGACC	540
OY	5441	TCGCGCAATGGGAATTCCAGAGTGTGTAAATCTCCGCTGGGACAGACGATGCACTTAAAT	600
Db	5441	TCGCGCAATGGGAATTCCAGAGTGTGTAAATCTCCGCTGGGACAGACGATGCACTTAAAT	600
OY	601	GTCCTTGCAACAATAAAGAGACAGCTCTGATAAAGCCGTACAAATGCACGAAGATGAA	660
Db	601	GTCCTTGCAACAATAAAGAGACAGCTCTGATAAAGCCGTACAAATGCACGAAGATGAA	660
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Db	661	TGTGCGTTAAATGTTGCTGGAACATGCGACTGATCTCAATATTTCCAGATGAGATGAAAT	720
OY	721	ACCACTCTGCACCTACGCTATCTAATAAGAGAATAAATTAATGGAACAAGCATCTCTTA	780
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Db	781	TATGGTGTGATATCGAATCAAAAAAACAAGCATGCGCTCACACCACTGTTACTTGATGTA	840
OY	841	CATGAGCAAAAACAGCAAGTCGTGAAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGGACCTGCTCTCATCTTGCCTGATAGTTGTGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGGACCTGCTCTCATCTTGCCTGATAGTTGTGATCAGCAAGTATA	960
OY	961	GTCAGCCCTTCACTTGGAGCAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGACG	1020
Db	961	GTCAGCCCTTCACTTGGAGCAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGACG	1020
OY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC	1080
OY	1081	AAAGAAAAACGAGTCTTAAAAATCTCTTGTGAAAACAGCAATCCAGAACAAAGATTAAAG	1140
Db	1081	AAAGAAAAACGAGTCTTAAAAATCTCTTGTGAAAACAGCAATCCAGAACAAAGATTAAAG	1140
OY	1141	CTGACATCAGAGGAAAGTCACAAAAGGTTCAAGAGCAGTGAATAATAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAAAGTCACAAAAGGTTCAAGAGCAGTGAATAATAGCCAGAGAAA	1200
OY	1201	ATGTCCTAGAACCCAGAAATTAATATAGATGCTGATAGAGGTTGAAAGAAATGAAAG	1260
Db	1201	ATGTCCTAGAACCCAGAAATTAATATAGATGCTGATAGAGGTTGAAAGAAATGAAAG	1260
OY	1261	AAGCATGAAGTAAATATGTTGGATTTCTGAAAACTGACTAATGTTGATCAGCTGCGC	1320
Db	1261	AAGCATGAAGTAAATATGTTGGATTTCTGAAAACTGACTAATGTTGATCAGCTGCGC	1320
OY	1321	AATGCTGATATGATTAATTCCTCAAGAGAAAGAGCAACCTGTAATATCAGCAATTT	1380
Db	1321	AATGCTGATATGATTAATTCCTCAAGAGAAAGAGCAACCTGTAATATCAGCAATTT	1380
OY	1381	CCTGACAAACGAAAGTGAAGATATCAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAAGTGAAGATATCAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA	1440
OY	1441	AAAACAGATGCCAAAATCTCTTCTGAAAAACGCAACCCAGAAACAAAGACTTAAAGCTACA	1500
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OY	1501	TCAGAGGAAGTCACAAAAGGCTTGAAGGACGTGAAATATGCGACGACGAGCTTGAATAT	1560
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OY	1561	TTTATGCGCTATCGAAGAAATGAAGAACACGAAAGTACTGATGCGATTTCCAGAAAC	1620

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Db 1561 TTATGGCTATCGAAGAAATGAGAAAGACGGAAGTACTCATGTCCGATTCCCAAGAAAC 1620
QY 1621 CTGACCTAAATGGTCCCTGCTGGCAATGGTGAATGATTAATTCCTCCAGAGAAAGC 1680
Db 1621 CTGACCTAAATGGTCCCTGCTGGCAATGGTGAATGATTAATTCCTCCAGAGAAAGC 1680
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Db 1681 AGAACAACCTGAAAGCCAGCAATTTCTGCACTGAGATGAATGAAGTATCACTATGACGA 1740
QY 1741 CAAATGATATCTAGAAAGCAATTTTGTAAAGAACAGAACCTGGAATATTACAGATGAG 1800
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QY 1801 ATTCTGATTCATGAAGAAAGCAGATGAGATGGTTGAAATTTGAAATTTCTGACTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATGAGATGGTTGAAATTTGAAATTTCTGACTTTCT 1860
QY 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATTTGACGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATTTGACGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAAATCATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAAATCATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 15
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; Sequence 374, Application US/10294025
; Publication No. US2003018530A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Skolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-374

Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCGGTTGGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTTGAGAACAGAGCACTTGTATGAAGACATCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTTGAGAACAGAGCACTTGTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGAGCAAGCG 240
Db 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGAGCAAGCG 240

QY 241 GCGCTTCTGAGAGCAACAGCACTCTGCTATGAAGACATCAGGAAACAAGATGGGCAAG 300
Db 241 GCGCTTCTGAGAGCAACAGCACTCTGCTATGAAGACATCAGGAAACAAGATGGGCAAG 300
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Db 301 TGGTCTGCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
QY 361 GGAAGCTACAGTACAGTGCCTTCATGAGGCCAGGTATCAGTCCGTGGAGAAATCG 420
Db 361 GGAAGCTACAGTACAGTGCCTTCATGAGGCCAGGTATCAGTCCGTGGAGAAATCG 420
QY 421 GACAACTCCACAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
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Qy 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGCAATGAAATATAGTACGTTGGCGGAAGAAAT 1920
Db 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGCAATGAAATATAGTACGTTGGCGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGGCTAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGGCTAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000
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Job time : 1634.23 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:12:24 ; Search time 243.564 Seconds
(without alignment)
4025.047 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atggtggtggtggtggtc.....aaaaaaaaaaaaaaaa 2000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.New:*
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2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170.6	8.5	1041	US-10-131-826A-21	Sequence 21, App1
2	84.6	4.2	14770	US-10-821-234-268	Sequence 268, App1
3	71.4	3.6	1870	US-10-750-185-34429	Sequence 34429, A
4	66	3.3	2048	US-10-955-054A-16	Sequence 16, App1
5	61	3.0	3343	US-11-108-172-795	Sequence 795, App1
6	60.2	3.0	4270	US-10-714-781A-54	Sequence 54, App1
7	60.2	3.0	5004	US-10-714-781A-77	Sequence 77, App1
8	58.8	2.9	6928	US-10-714-781A-60	Sequence 60, App1
9	56	2.8	2505	US-11-186-283-9	Sequence 9, App1
10	56	2.8	3026	US-11-186-283-7	Sequence 7, App1
11	52	2.6	6549	US-11-186-284-92	Sequence 92, App1
12	50.6	2.5	5054	US-10-821-234-123	Sequence 123, App1
13	50.4	2.5	2505	US-11-186-283-3	Sequence 3, App1
14	50.4	2.5	3025	US-11-186-283-1	Sequence 1, App1
15	50	2.5	2487	US-10-689-742-165	Sequence 165, App1
16	49.8	2.5	1790	US-11-080-463-671	Sequence 671, App1
17	49.4	2.5	1196	US-10-750-185-55958	Sequence 55958, A
18	46.4	2.3	1108	US-10-689-742-209	Sequence 209, App1
19	45	2.2	2658	US-10-131-826A-511	Sequence 511, App1
20	44.4	2.2	3819	US-10-131-826A-405	Sequence 405, App1
21	44	2.2	496	US-10-131-826A-533	Sequence 533, App1
22	43.8	2.2	2036	US-10-996-217A-8	Sequence 8, App1
23	43.6	2.2	755	US-10-131-826A-153	Sequence 153, App1

24	43	2.1	398	7	US-11-123-896-262	Sequence 262, App
25	42.8	2.1	1524	6	US-10-131-826A-181	Sequence 181, App
26	42.8	2.1	2392	7	US-11-045-802-4	Sequence 4, App1
27	42.8	2.1	2476	6	US-10-131-826A-489	Sequence 489, App1
28	42.8	2.1	2778	7	US-11-080-991-75	Sequence 75, App1
29	42.8	2.1	4339	6	US-10-909-125-801	Sequence 801, App1
30	42.8	2.1	28524	6	US-10-995-561-13292	Sequence 13292, A
31	42.6	2.1	1533	6	US-10-131-826A-217	Sequence 217, App
32	42.6	2.1	2533	6	US-10-131-826A-345	Sequence 345, App
33	42.4	2.1	373	6	US-10-986-501-106	Sequence 106, App
34	42.4	2.1	156297	7	US-11-121-086-65	Sequence 65, App1
35	42.2	2.1	1441	7	US-11-080-991-57	Sequence 57, App1
36	42.2	2.1	1658	7	US-11-102-240-59	Sequence 59, App1
37	42.2	2.1	1668	6	US-10-955-054A-113	Sequence 113, App
38	42.2	2.1	2463	7	US-11-108-528-3	Sequence 3, App1
39	42	2.1	1454	6	US-10-750-185-57501	Sequence 57501, A
40	42	2.1	1904	6	US-10-131-826A-99	Sequence 99, App1
41	41.8	2.1	693	6	US-10-131-826A-499	Sequence 499, App
42	41.8	2.1	1503	6	US-10-131-826A-363	Sequence 363, App
43	41.8	2.1	2846	7	US-11-102-240-37	Sequence 37, App1
44	41.8	2.1	34000	7	US-11-102-978-3	Sequence 3, App1
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ALIGNMENTS

RESULT 1
US-10-131-826A-21
Sequence 21, Application US/10131826A
Publication No. US20050245750A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 21
 ; LENGTH: 1041
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-131-826A-21

Query Match 8.5%; Score 170.6; DB 6; Length 1041;
 Best Local Similarity 63.7%; Pred. No. 4.7e-29;
 Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTCATGAGCCCGAGTACCGTCCGTGAGAAAGATGAGCAAGCTCCACAGAG 437
 DB 300 TGGCTTCGACATTTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCACAGAG 359
 QY 438 TGCCTGCTGGGTAAAGTCCCGAGAAAGATCTCATGCTGATGAGGACATGAGT 497
 DB 360 TGTCTTACATGTAACTAGAGAACTGAA--GTACCTTCTGCTCACGATATTATGACCG 416
 QY 498 GAAACAAG 557
 DB 417 CAAATAAG 476
 QY 558 AGAAGTAGTAAACTCTGCTGAGACAGATGTCACCTTAATGCTCTTGACAAAGAAA 617
 DB 477 GGAATATGTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
 QY 618 GAGACAGACTGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
 DB 537 CAGAGACACCTGTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
 QY 678 GGAACATGACAGTCAATTAATTCAGATGAGTATGAAATACCACTCTGACATACGC 737
 DB 597 GCAAAATGGCGCAATCAATTAATTAACGATTTCTTGAAGAGAGAGAGAGAGAGAG 656
 QY 738 TATCTATATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 797
 DB 657 TGTGTATTAATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 716
 QY 798 ATCAAAAAACAG 810
 DB 717 AGAATGCAGCAG 729

RESULT 2

US-10-821-234-268
 ; Sequence 268, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andertman, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; PRIOR FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 268
 ; LENGTH: 14770
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-821-234-268

Query Match 4.2%; Score 84.6; DB 6; Length 14770;
 Best Local Similarity 49.9%; Pred. No. 2.3e-09;
 Matches 213; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 511 AAGCAAAAG 570
 DB 1879 AAGAAAGATTTATCTCTCTTATGATGAGCAAGAAATATGAAAGCTTGAATGCCAAT 1938
 QY 571 CTCTGCTGAGACAGAGATGCAACTTAATGCTCTTGACAAAGAGAGAGAGAGAG 630
 DB 1939 CTCTGCTGAG 1998
 QY 631 ATAAAGCCGTACATATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
 DB 1999 CATGTAGCTGACATTAATCATATATCAAGAAAGAGAGAGAGAGAGAGAGAGAG 2058
 QY 691 GATCCAAATATTTCCAGATAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
 DB 2059 TCACCTCAG 2118
 QY 751 GATTAATTAATGAG 810
 DB 2119 CAGATGACATATGAG 2178
 QY 811 CATGCTCTACACACTGTTACTGTGTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
 DB 2179 CAG 2238
 QY 871 TTAATCAAG 930
 DB 2239 CTCTCTGAG 2298
 QY 931 CTGCTG 937
 DB 2299 TTGGCTG 2305

RESULT 3

US-10-185-34429
 ; Sequence 34429, Application US/10750185
 ; Publication No. US2005026063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: PANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 34429
 ; LENGTH: 1870
 ; TYPE: DNA
 ; ORGANISM: Bovine
 US-10-185-34429

Query Match 3.6%; Score 71.4; DB 6; Length 1870;
 Best Local Similarity 72.1%; Pred. No. 9.2e-07;
 Matches 93; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 916 AGAGCTGCTCTCATCTGCTGATGTTGTGATCAGCAAGTATGACGCTTCTACTT 975
 DB 1634 AGAAGAGCCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1693
 QY 976 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGAGAGAGAGAGAGAG 1035
 DB 1694 CAGCAAGGTGTTGACATCTTCTCAAGATGTTTGTGATGAGAGAGAGAGAGAGAG 1753
 QY 1036 GTTCTAGT 1044

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RESULT 5
US-11-108-172-795/C
; Sequence 795, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secretist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aljun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Panger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 2.0121.471C5
; CURRENT APPLICATION NUMBER: US/11/108.172
; PRIORITY FILING DATE: 2005-04-15
; PRIORITY APPLICATION NUMBER: US 10/025,380

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RESULT 6 - 781A-54
US-10-714-781A-54
? Sequence 54, Application US/10714781A
? Publication No. US20050255127A1
? GENERAL INFORMATION:
? APPLICANT: LOOSMORE, SHEENA MAY
? APPLICANT: MINKE, JULES MAARTEN
? TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
? FILE REFERENCE: 574313-3161.5
? CURRENT APPLICATION NUMBER: US/10/714,781A
? CURRENT FILING DATE: 2003-11-17
? PRIOR APPLICATION NUMBER: 10/679,520
? PRIOR FILING DATE: 2003-10-06
? PRIOR APPLICATION NUMBER: 10/374,953
? PRIOR FILING DATE: 2003-02-26
? PRIOR APPLICATION NUMBER: 10/116,298
? PRIOR FILING DATE: 2002-04-04
? PRIOR APPLICATION NUMBER: 60/281,923
? PRIOR FILING DATE: 2001-04-06
? PRIOR APPLICATION NUMBER: 10/676,502
? PRIOR FILING DATE: 2003-09-30
? PRIOR APPLICATION NUMBER: PCT/FR02/01200
? PRIOR FILING DATE: 2002-04-05
? NUMBER OF SEQ ID NOS: 85
? SOFTWARE: Patentin Ver. 3.2
? SEQ ID NO 54
? LENGTH: 4270
? TYPE: DNA

```

ORGANISM: West Nile virus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1760)..(3811)
 US-10-714-781A-54

Query Match 3.0%; Score 60.2; DB 6; Length 4270;
 Best Local Similarity 47.9%; Pred. No. 0.0041;
 Matches 173; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 524 CTGCTTACATCTGCGCTCTGCCAATGGGAATTGAGAATTGATAAATCTCTGCTGGACA 583
 DB |||||
 DB 977 CTGTCTGATGATGCGGTGTTGAGAGACGACTACAAATAGTGAAGATCTGTTGAAGA 1036
 QY 584 GACGATGCACTTATGTCCTTGAACAACAAAGAGACAGCTCGATTAAGGCCGTAC 643
 DB |||||
 DB 1037 ATTAATGATTAACAATGTTCTTTACAGCGAGGCTTTACTCTTTGTTGGACGCTT 1096
 QY 644 AATGCCAGAGATGAATGTCGTTAATGTTGCTGGACATGCACTGATCCAAATATTC 703
 DB |||||
 DB 1097 ACCTTAACAAAGTTAATTGTTAACTTCTAATGCTGATTCGGCGGATGATGATTT 1156
 QY 704 CAGATGATGATGAATATACCACTCTGCACTACGCTATCTTAATGATGAATTAATG 763
 DB |||||
 DB 1157 CAAGACGATCGGTTAACTCTCTACATATAGCCGTATCAATTAATAATTAACAATGG 1216
 QY 764 CCAAGACACTGCTTTATATGTCGTGATGATGAATCAAAAAACAAGCATGGCTCACAC 823
 DB |||||
 DB 1217 TTAACTTCTATTAAGCAAGGTCGATGATGACTGCTGTGATTAACATGGACGTACTC 1276
 QY 824 CACTGTACTTGTGTACATGAGCAAAAAACAGCAAGTCGTAATTTTAAATCAAGAAA 883
 DB |||||
 DB 1277 CTTTATGATGCTGCTGTACATCTGGAATATGGAATATGACACACTTAATAAAAA 1336
 QY 884 A 884
 DB 1337 A 1337

RESULT 7

US-10-714-781A-77
 Sequence 77, Application US/10714781A
 Publication No. US20050255127A1
 GENERAL INFORMATION:
 APPLICANT: LOOSMORE, SHEENA MAY
 APPLICANT: MINKS, JULES MAARTEN
 TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
 FILE REFERENCE: 574313-3161.5
 CURRENT APPLICATION NUMBER: US/10/714,781A
 CURRENT FILING DATE: 2003-11-17
 PRIOR APPLICATION NUMBER: 10/679,520
 PRIOR FILING DATE: 2003-10-06
 PRIOR APPLICATION NUMBER: 10/374,953
 PRIOR FILING DATE: 2003-02-26
 PRIOR APPLICATION NUMBER: 10/116,298
 PRIOR FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: 60/281,923
 PRIOR FILING DATE: 2001-04-06
 PRIOR APPLICATION NUMBER: 10/676,502
 PRIOR FILING DATE: 2003-09-30
 PRIOR APPLICATION NUMBER: PCT/FR02/01200
 PRIOR FILING DATE: 2002-04-05
 NUMBER OF SEQ ID NOS: 85
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 77
 LENGTH: 5004
 TYPE: DNA
 ORGANISM: Canaripox virus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1864)..(2187)
 US-10-714-781A-77

Query Match 3.0%; Score 60.2; DB 6; Length 5004;
 Best Local Similarity 47.9%; Pred. No. 0.0043;
 Matches 173; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 524 CTGCTTACATCTGCGCTCTGCCAATGGGAATTGAGAATTGATAAATCTCTGCTGGACA 583
 DB |||||
 DB 1304 CTGTCTGATGATGCGGTGTTGAGAGACGACTACAAATAGTGAAGATCTGTTGAAGA 1363
 QY 584 GACGATGCACTTATGTCCTTGAACAACAAAGAGACAGCTCGATTAAGGCCGTAC 643
 DB |||||
 DB 1364 ATTAATGATTAACAATGTTCTTTACAGCGAGGCTTTACTCTTTGTTGGACGCTT 1423
 QY 644 AATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTC 703
 DB |||||
 DB 1424 ACCTTAACAAAGTTAATTGTTAACTTCTAATGCTGATTCGGCGGATGATGATTT 1483
 QY 704 CAGATGATGATGAATATACCACTCTGCACTACGCTATCTTAATGATGAATTAATG 763
 DB |||||
 DB 1484 CAAGACGATCGGTTAACTCTCTACATATAGCCGTATCAATTAATAATTAACAATGG 1543
 QY 764 CCAAGACACTGCTTTATATGTCGTGATGATGAATCAAAAAACAAGCATGGCTCACAC 823
 DB |||||
 DB 1544 TTAACTTCTATTAAGCAAGGTCGATGATGACTGCTGTGATTAACATGGACGTACTC 1603
 QY 824 CACTGTACTTGTGTACATGAGCAAAAAACAGCAAGTCGTAATTTTAAATCAAGAAA 883
 DB |||||
 DB 1604 CTTTATGATGCTGCTGTACATCTGGAATATGGAATATGACACACTTAATAAAAA 1663
 QY 884 A 884
 DB 1664 A 1664

RESULT 8

US-10-714-781A-60
 Sequence 60, Application US/10714781A
 Publication No. US20050255127A1
 GENERAL INFORMATION:
 APPLICANT: LOOSMORE, SHEENA MAY
 APPLICANT: MINKS, JULES MAARTEN
 TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
 FILE REFERENCE: 574313-3161.5
 CURRENT APPLICATION NUMBER: US/10/714,781A
 CURRENT FILING DATE: 2003-11-17
 PRIOR APPLICATION NUMBER: 10/679,520
 PRIOR FILING DATE: 2003-10-06
 PRIOR APPLICATION NUMBER: 10/374,953
 PRIOR FILING DATE: 2003-02-26
 PRIOR APPLICATION NUMBER: 10/116,298
 PRIOR FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: 60/281,923
 PRIOR FILING DATE: 2001-04-06
 PRIOR APPLICATION NUMBER: 10/676,502
 PRIOR FILING DATE: 2003-09-30
 PRIOR APPLICATION NUMBER: PCT/FR02/01200
 PRIOR FILING DATE: 2002-04-05
 NUMBER OF SEQ ID NOS: 85
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 60
 LENGTH: 6928
 TYPE: DNA
 ORGANISM: West Nile virus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (2005)..(4059)
 US-10-714-781A-60

Query Match 2.9%; Score 58.8; DB 6; Length 6928;
 Best Local Similarity 47.0%; Pred. No. 0.001;
 Matches 217; Conservative 0; Mismatches 242; Indels 3; Gaps 1;
 QY 524 CTGCTTACATCTGCGCTCTGCCAATGGGAATTGAGAATTGATAAATCTCTGCTGGACA 583
 |||||

Db 1128 CTCCTTGGAATGGCTGTATGTTCAAGAAATCCGAGGCTATPAAAAATCTTGATGAGT 1187
QY 584 GACGATGTCAACTTAATGTCCTTGACAACAAAAAAGAGACAGCTGTGATAAGCCGTAC 643
Db 1188 ATGAGAGTAAACCTGTAGTACTGAATGACACA--ACTTCTGTCTGATGATGCGGTG 1244
QY 644 AATGACAGGAAGATGATGCGTTAATGTTGCTGGAACATGGACATGATCCAAATATTC 703
Db 1245 TGAAGAGCGACTCAAAAATAGTGAAGATCTGTGAAGAAATTAATGTAACAAATGTC 1304
QY 704 CAGATGATATGAAAATACCACTCTGCACTACGCTATCTAATGAAGATAAATTAATG 763
Db 1305 TTAAACGCGAGGCTTACTCCCTTGTGTGTTGGACGTTACCTTAACAAAGTAATTTG 1364
QY 764 CCAAGACATGCTCTTATATATGTCGTGATATCGAATCAAAAAACAAGATGCGCTCAC 823
Db 1365 TTTAACTCTATTGGCTCATTTGCGCGATGATGATATTTCAACAAGATGCTTAACTC 1424
QY 824 CACTGTACTTGTGTATCATAGACAAACAAGACAGCTGGAATTTTAAATCAAGAAA 883
Db 1425 CTCTACATATAGCCGTATCAAAATTAATTAACAATGTTAACTTATTAAGAACAG 1484
QY 884 AAGCGAATTTAAATGACATGATAGATGAAAGACTGCTCATACTTGTGTATGTT 943
Db 1485 GTGCTGATATGACTTGTGATGATTAACATGGAGTACTCTTTAATGATGCTGTACAT 1544
QY 944 GTGATTCAGCAAGTATAGTCAGCCTTCTACTGAGCAAAATA 985
Db 1545 CTGAAATATTTGAATATGTAGCACACTTAATAAAAAATA 1586

RESULT 9

US-11-186-283-9
; Sequence 9, Application US/1186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: NM1-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-9

Query Match 2.8%; Score 56; DB 7; Length 2505;
Best Local Similarity 46.3%; Pred. No. 0.0029;

Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;

QY 524 CTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTCGACA 583
Db 308 CAGCTCTGACCTGGCGCTTTACAAAGACAGCCGGAATTAATCACTTCACTGTTCACA 367
QY 584 GACGATGTCAACTTAATGTCCTTGACAACAAAAAAGAGCAGCTGTGATTAAGCCGTAC 643

Db 368 GCGAGACAGATGTTTCAGCAAGTGGATACGCTGCTCACAGCCCTCCACATAGCTGCA 427
QY 644 AATGACAGGAAGATGATGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTC 703
Db 428 TACCTGAGACACCAAGAGGCTGCAAGAGTGTCTGTACAAATGAGGCAATGTAAATTC 487
QY 704 CAGATGATATGAAAATACCACTCTGCACTACGCTATCTAATGAAGATAAATTAATG 763
Db 488 AATATCCGCTCTTTCACCCCACTGCAATTCACGCTTACTATGTGGCACAGAGTAA 547
QY 764 CCAAGACATGCTCTTATATATGTCGTGATATCGAATCAAAAAACAAGATGCGCTCAC 823
Db 548 CAGTGTCTTTTGAAGTTTGTGCTGATGTCAATGATAGCGGTAAATGTTGGAGAGGC 607
QY 824 CACTGTACTTGTGTATCATAGCAAAAAACAGACAGCTGGAATTTTAAATCA----- 878
Db 608 CTGTGACCTGGCTGTGCAAAAGGCTTCTTCAACTTGTGAATCTCTGTGAAGAAAG 667
QY 879 -GAAAAAGCGAATTTAAATGACATGATAGATATGAAAGACTGCTCTCATCTTGTG 937
Db 668 GAGCAAAACAGATGTGAACGCTCAGACAAATGAAACACACGTCCTGCACTTCTGTT 727
QY 938 TATGTTGTGATCAGCAAGTATAGTCAGCCTTCTACTTGAAGAAAATATGATATCTT 997
Db 728 CTGATTTGACACCAATATATGATGATCTGCTCCAGATGACTTAAGATCCAGC 787
QY 998 CTCAG 1003
Db 788 CTCAG 793

RESULT 10

US-11-186-283-7
; Sequence 7, Application US/1186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: NM1-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 3026
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(2565)
US-11-186-283-7

Query Match 2.8%; Score 56; DB 7; Length 3026;
Best Local Similarity 46.3%; Pred. No. 0.0011;

Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;

QY 524 CTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTCGACA 583
Db 368 CAGCTCTGACCTGGCGCTTTACAAAGACAGCCGGAATTAATCACTTCACTGTTCACA 427
QY 584 GACGATGTCAACTTAATGTCCTTGACAACAAAAAAGAGCAGCTGTGATTAAGCCGTAC 643

Db 428 GCGAGCAGATGTTGAGCAAGTGGATGAGTGGCTTCACAGCCCTCCACATAGCTGCAA 487
Qy 644 AATGCCAGAAATGAATGCGTTTAATGTTGCTGGAAATGACACTGATCCAAATATTC 703
Db 488 TAGCTGACACCCAGAGGCTGCAAGAGTCTGTCTACAAATGGGCAATGGAAATGTTT 547
Qy 704 CAGATGATGATGAAATACCACTGCTGACACTGCTATCTATATGAATGAATTAATGATG 763
Db 548 AAGATGCGCTCTTCTTCAACCCCACTGCAATGCAACCTACTATGGGCAAGAGCTAA 607
Qy 764 CCAAGCACTGCTCTTATATATGCTGATGATGATCAAAACCAAGATGCGCTTCAC 823
Db 608 CCAAGTCTCTTATGAAATGTTGGCTGATGATGATGATGATGATGATGATGATGATG 667
Qy 824 CACTGTACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
Db 668 CTCTGACCTGCTGCTTGCACAAAGGCTTCTTCAACATGTAAGAACTCTGTGTAAGAA 727
Qy 879 -GAAAAAGCGAATTTAAATGCACTGATGATGATGATGATGATGATGATGATGATG 937
Db 728 GAGGCAAGCAGATGTAAGAGCTGACAGACATGAAACACAGCTCCCTGCACTTCTGTT 787
Qy 938 TATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997
Db 788 CTGATTTGAGACCAACAATATATGATGATGATGATGATGATGATGATGATGATGATG 847
Qy 998 CTCAG 1003
Db 848 CTCAG 853

RESULT 11

US-11-186-284-92
; Sequence 92, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-0292RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 6549
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (240) ..(4904)
US-11-186-284-92

Query Match 2.6%; Score 52; DB 7; Length 6549;
Best Local Similarity 46.8%; Pred. No. 0.033;
Matches 163; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

Qy 491 CTGACGTGAACAAGAGCAAGCAAAAGAGGACTGCTTACATCTGGCCTTGCCAAATG 550
Db 2626 CTGCTGTGTGCGGGCAAAACAGAGAGGGTTCCACTTTTGTGTTGTGACAGCCGAG 2685
Qy 551 GGAATTCAGAAATGATTAATCTCTGTCGACAGATGTCACCTTAATGTCCTTGACA 610
Db 2686 GGCATTGGCAGATTGTAGACTGCTGTTGAAACGGGCTGTGTATGTGAACCTAAGTGACA 2745
Qy 611 ACAAAGAGGACACTCTGATTAAGCCGCTCAATGCCAGGAATGATATGTCGTTAA 670
Db 2746 AGCAAGGCGGAGCGCCCTCATGCTGCTGTGAAAGGACCTTGAGACCGTGAAT 2805
Qy 671 TGTTCGTGAACATGAGCACTGATCCAAATATTCAGATGATGATGATGATGATGATGAT 730
Db 2806 TCTCTCTTCAAAAGTGTGAGCCCTTCTTCTCTAGACAAAGAGGCTGTGTGACATTAA 2865
Qy 731 ACTACGCTATCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
Db 2866 GCTGGGCTGTGTGAAAGGTTCACAGGGCAGTGTCCAGATGCTGTTGAAAGAGAGCTG 2925
Qy 791 AATAGATCAAAAAAACAAGCATGGCTTCACACCACTGTTACTTGTG 838
Db 2926 CAATAGACCAGACAGACAAAGATGGCCGACACCCCTTGACCTGCTG 2973

RESULT 12

US-10-821-234-123
; Sequence 123, Application US/10821234
; Publication No. US2005025114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 123
; LENGTH: 5054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-123

Query Match 2.5%; Score 50.6; DB 6; Length 5054;
Best Local Similarity 44.4%; Pred. No. 0.061;
Matches 203; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

Qy 526 GCTTACATCTGGCCTTGCCAAATGGAAATTCAGAAATGTAATAAATCTGCTGACACAGA 585
Db 519 GCTTACATCTGGCCTTGCCAAATGGAAATTCAGAAATGTAATAAATCTGCTGACATCT 578
Qy 586 CGATGCACTTAATGTCCTTGAACAACAAAGAGAGAGCTGTGTAATAAGCCGTCACAA 645
Db 579 AATGCCAGCCGAAAGTGTGACAGCTCTGGGAAAAACAGCTTTACATTATCCAGCGCT 638
Qy 646 TGCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 705
Db 639 CAGGCTGCTTCAAGCTGTGCAAGTTCTGTGCAACACAAAGGCCCTTAACCTCAAA 698
Qy 706 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 765
Db 699 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 758
Qy 766 AAGACATGCTCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 825
Db 759 CACTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 818
Qy 826 CTGTTACTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 885

	Query Match	2.5%	Score 50.4;	DB 7;	Length 2505;
	Blast Local Similarity	44.0%;	Pred. No. 0.051;		
	MATCHES 213; Conservative	0;	Pred. Matches 271;	Indels 0;	Gaps 0;
QY	523 ACTGCTCAACCTGGCCCTCGCCAATGGGAATTGAGAAGTGTGTAATAACTCCTGCTGCAC				
Db	307 ACACGCTTGACATTGACAGTTTACAAGAGTAATGAGAAATGATCACTTCCTGCTTCAC				
QY	583 AGAGCATGTCAACTTAATGTCCCTTGACAACAAAAGAGGACAGCTCTGATTAAGGCCGTA				
Db	367 AGTAGAGTGTATPATCACAGAGTTGATACGCTGACCCTCACGCTCCATATTCCTACA				
QY	643 CAATGCCAGAAGATGATGTGCGCTTAATGTGTGCTGGAACATGAGCACTGATCCAATATT				
Db	427 ATAGCTGGCCACTTAGAGGCTGTGATGTGCTGTGGCAACATGAGAGCTPATATTCATATT				
QY	703 CCAGATAGTATGGAATAATACCACTGTGCATACGCTATCTTAATGAAGATTAATTAATG				
Db	487 CAAATGTAGATTTTTTTCACCTCCATGCAATATTCGACGGTACTATGACATBAACAGSTA				
QY	763 GCCAAAGACATGCTCTTATATGTGTCGTATATCGAATCAAAAAACAGATGSGCTTCACA				
Db	547 ACTGGCCCTCTTTTGAATTTTGTTGTCGTATGTAAATGTAAAGTGTGAAGTTGGAATAGA				
QY	823 CCACTGTTACTTGTGTGATCATGAGCAAAAAACGAAAGTCGTGAAATTTTAAATCAAGAA				
Db	607 CCCCTCCACCTAGCATCTGCAAAAAGATTCCTTGAAATTTGCAAAACCTCTGATGAGAGA				
QY	883 AAAGCAAATTTAAATGCACTGGATATGATATGGAAGAACTGCTCTCATACTTGCTGTATGT				

Query Match	2.5%;	Score 50.4;	DB 7;	Length 3025;
Best Local Similarity	44.0%;	Pred. No. 0.055;		
Matches 213;	Conservative	0;	Mismatches 271;	Indels 0;
			Gaps	0
Qy	523	ACTGCTCTACATCTGGCTCTGCCAATGGAAATTCAAGATGATGAAAATCTCTGCTGGAC	562	
Db	354	ACAGCCTTGCAATTTAGCAGTTTACAGAGATATATCAGAAATGATCACTTCTGCTTCAC	413	
Qy	583	AAGACATGTCACCTTAATATGTCCTTGACACAAAAAGAGACAGCTCTGATTAAGGCCGTA	642	
Db	414	AGTGAAGCTGGAATATCACAGAGTTGGATACGGTGCGCTCACTGCTTCATATTTGCTACA	473	
Qy	643	CAATGCGAAGAAAGATGAAATGTCGCTTAATGTTGCTGGAAACATGGCACTGATCCAAATATT	702	
Db	474	ATAGCTGGCAACTAGAGGCTGCTGAATGCTGTTGGAAACATGAGGTAATGTCAATATT	533	
Qy	703	CCAGATGATATGAGAAATACCACTCTGCGACACAGCTATCTATTAATGAAGTAAATTAATG	762	
Db	534	CAGATGACGTTTTTTTTTCACTCCATTTGATATTCACAGCTACTATGGAATGAAACAGTA	593	
Qy	763	GCCAAAGCACTGCTCTTATATGATGCTGATATGCATCAAAACAAAGCATGGCGCTCAC	822	
Db	594	ACTCGCTCTTTTGAATTTGGTGTGATTAATGTAAGTGTGAAGTTGGAGATAGA	653	
Qy	823	CCACTGTTACTTGATGATCATAGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAA	882	
Db	654	CCCTTCACCTAGCATCTGCAAAAAGATTTCTGAATTTTGCAAAACCTTTGATGGAAGAA	713	
Qy	883	AAAGCAATTTAATGACGTGATGATATGAAAGGACGTCTCATATCTGCTGATGT	942	

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Db      714 GCAGCAAGCAGTGTGATGCTCAAGTAATGAAGACCATGTCCTCCATTTCTGT 773
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QY      1003 GATC 1006
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RESULT 15

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; Sequence 165, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallee, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 165
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-742-165
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Query Match 2.5%; Score 50; DB 6; Length 2487;

Best Local Similarity 56.8%; Pred. No. 0.063;

Matches 92; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY      1899 TAGTACGTTGCGGAGAAATTTGCCATGCTAAAGACTGAGCTAGACACAATGAAACATCA 1958
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Search completed: December 18, 2005, 07:36:38
Job time : 246.564 secs

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Query March	55.2%; Score 1105; DB 4; Length 6098
Best Local Similarity	88.2%; Pred. No. 3,4e-255;

Matches 1243; Conservative 0; Mismatches 95; Indels 71; Gaps 1;			
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QY	61	AGGAGCAAGATGGGCAAGTGGTCCGTTGCTTCCCTGCTGCAAGGAGAGCGCAAG	120
Db	501	AGGAGCAAGATGGGCAAGTGGTTCACACCGCTTCCCTGCTGCAAGGAGAGCGCAAG	560
QY	121	AGCAAGTGGGCACTTCTGAGACACAGAGACTCTGTATGAAGACACTCAGAGCAAG	180
Db	561	AGCAAGTGGGCACTTCTGAGACACAGAGACTCTGTATGAAGATGCTCAGAGCAAG	620
QY	181	ATGGCAAGTGGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG	240
Db	621	ATGGCAAGTGGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG	680
QY	241	GGGCTTTCTGAGACCAAGCACTCTGTATGAAGACACTCAGAAACAAGTGGCAAG	300
Db	681	GGCACTTCTGAGACCAAGCACTCTGTATGAAGACACTCAGAAACAAGTGGCAAG	740
QY	301	TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGGGCTGG	360
Db	741	TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGGGCTGG	800
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Db	801	GGAGACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	860
QY	421	GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	480
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QY	481	CTCAGGGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	540
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QY	541	TCTGCAATGGGAATTCAGAGATGATGATGATGATGATGATGATGATGATGATGAT	600
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QY	601	GTCCTTGAACAAAAAG	660
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QY	661	TGTGCTTATGTTGCTGGAACATGATGATGATGATGATGATGATGATGATGATGAT	720
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QY	721	ACCACTCTGCACTAGCTATCTATTAATGAAGATTAATGAAGATTAATGAAGATTA	780
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QY	781	TATGCTGCTGATTCGAATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	840
Db	1221	TATGCTGCTGATTCGAATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1280
QY	841	CATGAGCAAAAAAG	900
Db	1281	CATGAGCAAAAAAG	1340
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QY	961	GTCAGCTTCTACTGAGCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1020
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QY	1321	AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1380
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QY	1381	CCTGACAAAG	1409
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ACCESSION			
BM763453			
VERSION			
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EST.			
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ORGANISM			
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo			
REFERENCE			
1 (bases 1 to 633)			
Oh,K.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,			
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and			
Kim,Y.S.			
21C Frontier Korean EST Project 2001			
UNPUBLISHED (2002)			
CONTACT: Kim YS			
Genome Research Center			
Korea Research Institute of Bioscience & Biotechnology			
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea			
Tel: +82-42-860-4470			
Fax: +82-42-860-4409			
Email: yongsung@mail.krdb.re.kr			
Plate: 16 row: A column: 11			
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(A) + RNA was dephosphorylated with bacterial alkaline			
phosphatase (BAP) and then deapped with tobacco acid			
pyrophosphatase (TAP). The deapped intact RNA was			
ligated with DNA-RNA linker including EcoR I site by			
treatment of T4 RNA ligase and the first strand cDNA was			
synthesized from oligo dt-selected mRNA by priming with			
dt-tailed vector. The dt-tailed vector was adjusted to			
have about 60nt. The cDNA vector was circularized with E.			

coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match	29.6%;	Score 592.4;	DB 3;	Length 633;
Best Local Similarity	96.7%;	Pred. No. 1e-131;		
Matches 616;	Conservative 0;	Mismatches 17;	Indels 4;	Gaps 1;

QY	510	CAAGCAAAAAGAGCATGCTCTTCACTATCTGGCCCTCTGCAATGGGAATTTCAGAAAGTATGTA	563
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QY	570	ACTCTGCTGGACAGACGATGTCACTTAATGTCTTTGACAACAAAAAAGAGCAGCTCT	629
Db	61	ACTCGTGTGGACAGACGATGTCACTTAATGTCTTTGACAACAAAAAAGAGCAGCTCT	120
QY	630	GATAAAGGCCGTATCAATGCGAGGAAAGATGATGTGCGTTAATGTGTCTGGAAATGCGAC	689
Db	121	GACAAAGGCCGTATCAATGCGAGGAAAGATGATGTGCGTTAATGTGTCTGGAAATGCGAC	180
QY	690	TGATCCAATATATTCAGATAGATAGTAAATPACATCTGGACATGACGTATCTTAATGTA	749
Db	181	TGATCCAATATATTCAGATAGATAGTAAATPACATCTTAATGTCTTCAATGTA	240
QY	750	AGATAAATTAATGCGCAAAAGCATGCTCTTATATGATGCTGATATCGAATCAAAAAA	809
Db	241	AGATAAATTAATGCGCAAAAGCATGCTCTTATATGATGCTGATATCGAATCAAAAAA	300
QY	810	GCATGGCCCTCACACATGTTACTTGGTGTCAATGAGCAAAAAACAGCAATGCTGAATT	869
Db	301	GCATGGCCCTCACACATGTTACTTGGTGTCAATGAGCAAAAAACAGCAATGCTGAATT	360
QY	870	TTTATATCAAGAAAAAGCGAATTTTAAATGACCTGATATGATAGGAAGAATGCTCTCAT	929
Db	361	TTTATATCAAGAAAAAGCGAATTTTAAATGACCTGATATGATAGGAABAATGCTCTCAT	420
QY	930	ACTTGCTGTATGTTGTGATCAGCAGATATATGTACGCTTCTACTTGACCAAAATATGGA	989
Db	421	ACTTGCTGTATGTTGTGATCAGCAGATATATGTACGCTTCTACTTGACCAAAATATGGA	480
QY	990	TGTATCTTCTCAAGATCTATCTGGAAGACGGCCAGAGATATGTCTTTCTAGTCATCA	1049
Db	481	TGTATCTTCTCAAG---ATCTGGAAGACGGCCAGAGATATGTCTTTCTAGTCATCA	536
QY	1050	TCATGTATTTTGCAGTTACTTTCTGACTACAAAGAAAAACAGATGCTTAAATCTCTTC	1109
Db	537	TCATGTATTTTGCAGTTACTTTCTGACTACAAAGAAAAACAGATGTTAAATCTCTTC	596
QY	1110	TGAAAACGCAATCCAGAACAAAGCTTAAAGCTGACA	1146
Db	597	TGAAAACGCAATCCAGAACAAAGCTTAAAGCTGACA	633

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
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		mRNA sequence.							
BM763942									
BM763942.1	GI:19093557								
EST.									
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						Homo sapiens			
						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
						Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
						Homnidae; Homo			
						1 (bases 1 to 621)			
						Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,			

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS

Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@mail.kribb.re.kr
Plate: 25 row: A column: 11
High quality sequence stop: 621

FEATURES

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1..621
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phosphatase (BAP) and then deapped with tobacco acid
pyrophosphatase (TAP). The deapped intact mRNA was
ligated with T4 RNA ligase including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-tailed vector by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10p by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."
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ORIGIN

Query Match	29.1%;	Score 581.4;	DB 3;	Length 621;
Best Local Similarity	96.8%;	Pred. No. 4.7e-129;		
Matches 605; Conservative	0;	Mismatches 16;	Indels 4;	Gaps 1;

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Db	1	CAAGCAAAAAGAAGCATGCTCTTACATCTGCGCTCTGCCAATGGGAATTCAGAAAGTAGTAA	60
Qy	570	ACTGCTGCTGAGCAGACGATGTCAACTTAATGTCTTGAACACAAAAGAAGGACAGCTCT	629
Db	61	ACTGCTGCTGAGCAGACGATGTCAACTTAATGTCTTGAACACAAAAGAAGGACAGCTCT	120
Qy	630	GATAAAGGCCGTACAAATGCGAGGAAGATGATGTGCGTTAATGTGTGTGGAACATGGCAC	689
Db	121	GACAAAGCCGTACAAATGCGAGGAAGATGATGTGCGTTAATGTGTGTGGAACATGGCAC	180
Qy	690	TGATCCAAATATTCAGATGAGTAGTGGAAATTACCACCTTGCACTAGCGTATCTTAATGA	749
Db	181	TGATCCAAATATTCAGATGAGTAGTGGAAATTACCACCTTGCACTAGCGTATCTTAATGA	240
Qy	750	AGATTAATTTAATGGCCAAAGCACATGCGCTTATATGGCGTGAATATGGAATCAAAAAACA	809
Db	241	AGATTAATTTAATGGCCAAAGCACATGCGCTTATATGGCGTGAATATGGAATCAAAAAACA	300
Qy	810	GCATGGCCTCACAACCATGTACTTGATGGTGTACATGACAAAAACAGCAACTCGTGAATT	869
Db	301	GCATGGCCTCACAACCATGTACTTGATGGTGTACATGACAAAAACAGCAACTCGTGAATT	360
Qy	870	TTTAAATCAAAAAAGCGAATTTAAATGACATGGATATGATATGGAAGACTGCTCAT	929
Db	361	TTTAAATCAAAAAAGCGAATTTAAATGCGATATGATATGGAAGACTGCTCAT	420

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DB 481 TGTATCTTCTCAAGATCTATCTGACAGACGGCCAGAGATAGTGTCTTGTATGATCA 536
QY 1050 TCAATGTAATTTGGCAGTACTTCTCTGATCAAAAGAAAAAGATGCTTAAATCTCTTC 1109
DB 537 TCAATGTAATTTGGCAGTACTTCTCTGATCAAAAGAAAAAGATGTAATTAATCTCTTC 596
QY 1110 TGAACACGCAATCCAGAACAGAC 1134
DB 597 TGAACACGCAATCCAGAACAGAC 621

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VERSION BU930826.1 GI:24119645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Issue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
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and 3' adaptor sequence:
5'-ATTCTAGAGCCAGGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN
Query Match 25.4%; Score 508; DB 5; Length 729;
Best Local Similarity 94.8%; Pred. No. 2.6e-111;
Matches 548; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
QY 579 GGCACAGCATGTCACTTAATGTCTTGACAAACAAAGAGACAGCTCTGATAAGG-- 636
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QY 637 -----GCCGTACAAAGCCAGGAAGTGAATGTCCTT 668
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DB 243 TGAATATGCAATCAAAAAACAGATGCGCTCACACACATGCTTACTTGTGTATGATGAGA 302
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DB 423 TCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGCGCAGAGA 482
QY 1029 GTATGCTGTTTCTAGTCATCATCATGATATTTGCCAGTTACTTCTGACTCAAGAAAA 1088
DB 483 GTATGCTGTTTCTAGTCATCATCATGATATTTGCCAGTTACTTCTGACTCAAGAAAA 542
QY 1089 ACAGATGCTAAATATCTCTTCTGAAAAACGCAATCCAG 1126
DB 543 ACAGATGCTAAATATCTCTTCTGAAAAACGCAATCCAG 580

RESULT 5
AL703938 544 bp mRNA linear EST 04-SEP-2003
LOCUS DKFP686E1728_r1 686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION DKFP686E1728 5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 544)
AUTHORS Olterswaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weill,B. and
Wiemann,S.
TITLE EST (Olterswaelder,B., Obermaier,B., Mewes,H.W., Weill,B. and
Wiemann,S.)
JOURNAL Unpublished (2001)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No 81 sequence
available.
This clone (DKFP686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..544
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

RESULT 6	Bf676987				
LOCUS	Bf676987				
DEFINITION	Bf676987	865 bp	mRNA	linear	EST 21-DEC-2000
	602084215f1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',				
	mRNA sequence.				
ACCESSION	Bf676987				
VERSION	Bf676987.1	GI:11950882			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
	1 (bases 1 to 865)				
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Unpublished (1999)				
JOURNAL	Contact: Robert Strausberg, Ph.D.				
COMMENT	Email: cgabbs-td@mail.nih.gov				

Qy	635	AGGCGTACATGCGACGAAAGATAAAGTGGTTAAAGTTGCTGGAAACATGGCACTGATC	694
Db	69	AGGCGTACATGCGACGAAAGATAAAGTGGTTAAAGTTGCTGGAAACATGGCACTGATC	128
Qy	695	CAAAATTTCCAGATGAGTATGGAATAATCCACTTGCACATACGCTATCTATATATGAGATAT	754
Db	129	CAAACTTTCCAGATGAGTATGGAATAATCCACTTGCACATACGCTATCTACATGAAATAT	188
Qy	755	AATTAATGGCCAAAGCACTGCTCTTATATGGTGTGATGTATGAAATCAAAAAACAAGCATG	814
Db	189	AATTAATGGCCAAAGCACTGCTCTTATATGGTGTGATGTATGAAATCAAAAAACAAGCATG	248
Qy	815	GCCTCACACCACTGTATCTTGGTGTACATGACGCAAAAACAGCAAGTCGTGAAATTTTAA	874
Db	249	GCCTCACACCACTGTACTTGGTGTACATGACGCAAAAACAGCAAGTCGTGAAATTTTAA	308
Qy	875	TCGAAGAAAAAGCAATTTTAAATGCACTGGATAGATATGGAAGGACCTGCTCATATCTTG	934
Db	309	TCGAAGAAAAAGCAATTTTAAATGCGTGGATATATGGAAGAACCTGCTCATATCTTG	368
Qy	935	CTGATGTTGTGATTCAGCAAGTATAGTCAGCCTTCTACTTGAGCAAAATTTGATGTAT	994
Db	369	CTGATGTTGTGATTCAGCAAGTATATGAGCCTTCTACTTGAGCAAAATTTGATGTAT	428
Qy	995	CTTCTCAAGATCTATCTTGGACAGACGGCCAGAGAGTATGCTGTTTCTAAGTATCATCATG	1054
Db	429	CTTCTCAAGATCTATCTTGGACAGACGGCCAGAGAGTATGCTGTTTCTAAGTATCATCATG	488
Qy	1055	TAAATTTGCCAGTACTTTCTGACATACAAAGAAAAACAGATGCTAAAAATCTCTCTGAAA	1114
Db	489	TAA-TTGCAGTATCTTTCTGACATACAAAGAAAAACAGATGCTAAAAATCTCTCTGAAA	547
Qy	1115	ACAGCATTCAGAACAGACTTAA	1138
Db	548	ACAGCATTCAGAAAAATGCTCA	571

RESULT 7
BX492731

LOCUS BX492731 505 bp mRNA linear EST 04-SEP-2003
 DEFINITION DKFZP781C0523 r1 781 (synonym: hlc4) Homo sapiens cDNA clone
 DKFZP781C0523 5', mRNA sequence.
 ACCESSION BX492731
 VERSION BX492731.1 GI:32004516
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo
 1 (bases 1 to 505)
 Bioecker, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., Oeanger, A.,
 Podo, G., Han, M., and Wiemann, S.
 EST (Bioecker, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., et al.)
 Unpublished (2003)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No s1 sequence available.
 This clone (DKFZP781C0523) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubneweg 6, 14059
 Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.
 Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZP781C0523"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="781 (synonym: hlc4)"
 /note="Vector: pSPORT1_sfl; Site_1: sflIA; Site_2: sflIB;
 cDNA-collection"

ORIGIN
 Query Match 18.8%; Score 376.4; DB 5; Length 505;
 Best Local Similarity 92.7%; Pred. No. 1.4e-79;
 Matches 395; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 325 TGCAGGGGAGCGGCAAGCAAGTGGCGCTTGGGAGACTACGATACAGTGCCTTC 384
 DB 80 TGGCTGGGAGCGGCAAGCAAGTGGCGCTTGGGAGACTACGAGCGGCTTC 139
 QY 385 ATGAGCCGAGGATACGATCGGTGGAGAAATCTGGAGAACTCCAGAGCTGCTGG 444
 DB 140 ATGAGCCGAGGATACGATCGGTGGAGAAATCTGGAGAACTCCAGAGCTGCTGG 199
 QY 445 TGGGTAAGTCCCGAGAAAGATCTCATGTCATGCTCAGGAGCACTGACGTGAACAAG 504
 DB 200 TGGGTAAGTCCCGAGAAAGATCTCATGTCATGCTCAGGAGCACTGACGTGAACAAG 259
 QY 505 AAGGACAGCAAAAGAGAGCTGCTCATCTGGGCTTGGCAATGGGAATTCAGAGTA 564
 DB 260 AAGGACAGCAAAAGAGAGCTGCTCATCTGGGCTTGGCAATGGGAATTCAGAGTA 319
 QY 565 GTTAAATCTGCTGGAGAGAGTGTCACTTAATGTCCTTGAACAACAAAAGAGAA 624
 DB 320 GTTAAATCTGCTGGAGAGAGTGTCACTTAATGTCCTTGAACAACAAAAGAGAA 379
 QY 625 GCTGTGATAAGGCGCTTGAACAAGTGTCACTTAATGTCCTTGAACAAGTGTGCTGAACAT 684
 DB 380 GCTGTGATAAGGCGCTTGAACAAGTGTCACTTAATGTCCTTGAACAAGTGTGCTGAACAT 439
 QY 685 GGCAGTGAATCAATATTCAGATGAGTATGAGAAATACCACTTGCATCGCTATCTAT 744
 DB 440 GGCAGTGAATCAATATTCAGATGAGTATGAGAAATACCACTTGCATCGCTATCTATC 499

RESULT 8
 BX437445
 LOCUS BX437445
 DEFINITION BX437445 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP006YL04
 5-PRIME, mRNA sequence.
 ACCESSION BX437445
 VERSION BX437445.2 GI:46959477
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 910)
 Li W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30771569.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5500.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0CAP006Df02QPlc=5500.r.
 Location/Qualifiers
 1..910
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0CAP006YL04"
 /issue_type="THYMUS"
 /clone_1ib="Homo sapiens THYMUS"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and EcoRV sites of the
 pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN
 Query Match 17.9%; Score 357.2; DB 5; Length 910;
 Best Local Similarity 69.6%; Pred. No. 6.7e-75;
 Matches 501; Conservative 1; Mismatches 209; Indels 9; Gaps 1;

QY 223 AGTGCAAGAGCAAGTGGGCGCTTCTGGAGACCAAGAGCTCTGTGAAGACATC 282
 DB 100 AGAGCCGAGAGCAATGAGTGTCTCTGAAGCCGAGTGGCTTGGCCATGAAGAGATT 159
 QY 283 AGGAACAAGATGGGAGAGTGTGCTGCCACTTCCCTGCTGCAAGGGGAGCGGCAAG 342
 DB 160 TTTAGTAAGAAAGGAGAGTGTGCTGCCACTTCCCTGCTGCAAGGGGAGCGGCAAGC 216
 QY 343 AGCAAGTGGGCGCTTGGGAGACTACGATGCAAGTGTCTTACATGAGGCCAGATGACAC 402
 DB 217 -----GGGGAGGGGGGGGCGAGCGGGGGAGGGGCGCTTACATGCAAGCCGCTTACAC 270
 QY 403 GTCCGTGAGAGAGATCTGGACAAGCTCCACAGAGCTGCTGATGGGGTAAAGTCCCAAG 462
 DB 271 GTCCGAGACCGAGATCTCGGCAAGATCCACAAGCTGCCAGCGGGGTATGTGGTGAAG 330
 QY 463 AAGATTCATCGTATGCTCAGGAGCACTGACGTGAACAAGAGCAAGCAAGAGAG 522

Db 331 GTGCAGCAGATCCTTTTGTCTCAGAGAAATGCTTGACGATAGACAAAGTGAACAGG 390
 QY 523 ACTGCTCTTCATCTGGCCCTCTGCGCAATGGGAATTCAGAAATGTAATACTCTGCTGAC 582
 Db 391 AGGGCTCTACATTTGGCCCTGCTGCGCAATGGTCAATCCAGAAATGTAATCTCTGCTGAC 450
 QY 583 AGACGATGCACTTAATGCTCTGCAACAAAGAAAGAGACGCTGTGAATGAAGCCGTA 642
 Db 451 AGAAATGCGAGCTCAATGCTGTGACAAAGAAAGAGACGCTGTGAATGAAGCCGTA 510
 QY 643 CAATGCGAGAAAGATGAATGCGTGAATGCTGTGAAATGCTGAAATGCTGAAATGCT 702
 Db 511 CAATGCGAGAAAGATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCT 570
 QY 703 CCAATGATATGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCT 762
 Db 571 GCGGATGCTCAATGCGCAACGCTGCTTCAATGCTGTGAAATGCTGTGAAATGCTGTGAA 630
 QY 763 GCCAAGCAGCTGCTTATATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAAT 822
 Db 631 GCAACAAAGCTGCTTGTATGATGCAAAATGTAAGCAAAAGAGATGACCTGAC 690
 QY 823 CCACTGTTACTTGTGTATGATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 882
 Db 691 CCACTTCTTCTGCAATGATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
 QY 883 AAGCGAATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 942
 Db 751 AAGCGAATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 810

RESULT 9
 AUI20666 843 bp mRNA linear EST 01-AUG-2002
 LOCUS AUI20666 HEMBB1 Homo sapiens cDNA clone HEMBB1001175 5', mRNA

DEFINITION sequence.
 ACCESSION AUI20666
 VERSION AUI20666
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 843)
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
 Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isogai,T.

REFERENCE
 AUTHORS HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source
 Location/Qualifiers
 1..843
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEMBB1001175"
 /cissue_type="whole embryo, mainly body"
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 /note="Vector: PME18SFL3"

ORIGIN

Query Match 17.4%; Score 348.8; DB 1; Length 843;
 Best Local Similarity 69.2%; Pred. No. 7, 1e-73;
 Matches 492; Conservative 0; Mismatches 210; Indels 9; Gaps 1;

QY 223 AGTGCAGAGAGCAAGTGGGCGCTTCTGAGACCAAGAGACTGCTATGAAAGACATC 282
 Db 119 AAGCGAG 178
 QY 283 AGGAACAGAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 342
 Db 179 TTATAGTAAAG 235
 QY 343 AGCAAGTGGGCGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 402
 Db 236 -----GCCGAGAGCGGGGCGAGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
 QY 403 GTCCGTGAGAGAGATCTGGAGCAAGCTCCAGAGCTCTGGTGGGGTAAAGTCCCGACA 462
 Db 290 GTCCGAG 349
 QY 463 AAGATCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCAT 522
 Db 350 GTGCAGCAGATCCTTTTGTCTCAGAGAAATGCTGTGAACGATAGAGCAAGATGAACAG 409
 QY 523 ACTGCTCTTCATCTGGCCCTCTGCGCAATGGGAATTCAGAAATGTAATACTCTGCTGAC 582
 Db 410 AGGGCTCTACATTTGGCCCTGCTGCGCAATGGTCAATCCAGAAATGTAATCTCTGCTGAC 469
 QY 583 AGACGATGCACTTAATGCTGTGACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 642
 Db 470 AGAAATGCGAGCTCAATGCTGTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 529
 QY 643 CAATGCGAGAAAGATGAATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAAT 702
 Db 530 CAATGCGAGAAAGATGAATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAAT 589
 QY 703 CCAATGATATGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCT 762
 Db 590 GCGGATGCTCAATGCGCAACGCTGCTTCAATGCTGTGAAATGCTGTGAAATGCTGTGAA 649
 QY 763 GCCAAGCAGCTGCTTATATGCTGTGAAATGCTGTGAAATGCTGTGAAATGCTGTGAAAT 822
 Db 650 GCAACAAAGCTGCTTGTATGATGCAAAATGTAAGCAAAAGAGATGACCTGAC 709
 QY 823 CCACTGTTACTTGTGTATGATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 882
 Db 710 CCACTTCTTCTGCAATGATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
 QY 883 AAGCGAATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 933
 Db 770 AAGCGAATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 820

RESULT 10
 CR860726 2677 bp mRNA linear HTC 12-NOV-2004
 LOCUS CR860726 Pongo pygmaeus mRNA; cDNA DKFZp459P0427 (from clone DKFZp459P0427).
 DEFINITION CR860726
 ACCESSION CR860726
 VERSION CR860726.1 GI:55732274
 KEYWORDS HTC.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Pongo.

REFERENCE
 AUTHORS Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Well,B., Amid,C.,
 Oeinger,A., Fodo,G., Han,M. and Wiemann,S.
 CONSRM The German cDNA Consortium
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuberberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
 sequenced by GSF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the CDNA sequencing consortium of the
 German Genome Project.
 This clone (DKFZp459F0427) is available at the RZPD Deutsches
 Ressourcezentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneID=DKFZp459F0427
 Further information about the clone and the sequencing project is
 available at http://mipe.gsf.de/projects/cdna/.

FEATURES

source

1..2677

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp459F0427"

/issue_type="cortex"

/clone_id="459 (synonym: pcor1). Vector pSport1_Sfi; host

DH10B; sites SfiI + SfiIb"

/dev_stage="adult"

/note="hypothetical protein (Homo sapiens), differentially

spliced"

1..2677

/gene="DKFZp459F0427"

176..973

/gene="DKFZp459F0427"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAH92841.1"

/db_xref="GI:55732275"

/translation="MGVRSFLAACRRMATWRKNRDKDPSNGSYRQKDLGMIHK
 LAIADVNLKLSILGLDNDVDRKNTALHACRPGVADLVARKRLMTD
 SNRTALIAVOCQEAIVCASILEHGADNVADMTGNTALHYAIDINENISMGKLLAY
 GADIRASGCGHTSLIAVNRKEEMVAELKKKPDTRAIDRGTALILAAKNSSTS
 VYQLQHNIDVFQCDISGWTBDAVAAASKFOATLKRDIRAKRA"

ORIGIN

Query Match 17.4%; Score 347.2; DB 4; Length 2677;

Best Local Similarity 69.4%; Pred. No. 2.3e-72;

Matches 472; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

378 TGCCTTCATGAGGCCAGGTACCACTCGGTGAGAAAGTCTTGACAACTCCACAGAC 437
 250 TGGCTTCTCAAAATTCGGGGTACCGAATCCGACAGAAAGATCTGGGATGATCCACAAAGC 309
 438 TGCCTGTGGGGTAAAGTCCCAAGAAAGATCTCAATCGTCATGCTTCAGGAGACATGACCT 497
 310 TCCCATCGCGGTGATGTAACCAAGCTGCTGAGAGACATCTTGCGGCTGAATGACGT 369
 498 GACACAGAGACACAGCAAAAGAGACTGCTCTACATCTGGCCTTGCCATGGGAATTC 557
 370 GAATGACAGGACCAAGAAAGACAGCTGCTCACTTTGGCGTGTGCCCATGGCCGCTCC 429
 558 AGAAGTAGTAAACCTCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACAACAAAA 617
 430 GGGAGTGTAGTGAATCTGTGGCCAGAAAATGCGCGCTTAACTCACTGACAGTGA AAA 489
 618 GAGGACAGCTGTATTAAGCCGTACAATGCCAGAAAGATGATGCTTAATGTTGCT 677
 490 CAGGACAGCTGTATTAAGCCGTACAATGTCAGAAAGAGTTTGATGATCAATCTGCT 549
 678 GGAACATGGCAGCTCAATATTTCCAGATGATGTAATAATACCACTTGACATGACCC 737
 550 GGAACATGGCGCGACCCAAATCTTAGAATATGATGCAACAGGCTCTGACATATGC 609
 738 TATCTAATTAAGATTAATTAATGCGCAAGACCTCTTATATATGCTGATATGCA 797
 610 CATTTGATTAAGAAATATATCAATGACAGAAAACCTGCTTGCATATGTCAGATTTGA 669
 798 ATCAAAAACAGACATGGCTCAGACCATCTTTACTTGGTATCATAGACAAAAACAGCA 857
 670 ACCAAGAAACCCAGGCTGACATGATCACTTTTACTCGCTGTAATAAGAAAAAGAGGA 729

QY 858 AGTCGTAAATTTTAACTCAAGAAAAAGCAATTTAAATGACATGATATGGAAG 917
 DB 730 AATGTGCAATTTTGTGTAAGAAAAACCAATTTAACTGCAATAGATATTTGGAG 789
 QY 918 GACTGCTCATACTTGGCTGTATGTTGGATGACCAAGATATGCAAGCTTCTACTGA 977
 DB 790 AACAGCCCTCACTTGGCTGTGCTGTAAGGATCAACAAAGTATGATCTACAGCTTCTCA 849
 QY 978 GCAAAATTTGATATGATCTTCTCAAGATCTATCTGACAGACAGCGCAAGATAGCTCT 1037
 DB 850 GCACATATGACGCTTTTGGCAAGATATATCTGATGACTGACGAAGACTGAC 909
 QY 1038 TTCTAGTCATCATCATGTAA 1057
 DB 910 TGCTTCTAAGTTTCAAGCA 929

RESULT 11

DQ053800

LOCUS

DEFINITION

Homo sapiens KIAA1074 gene, VIRTUAL TRANSCRIPT, partial sequence.

ACCESSION

DQ053800

VERSION

DQ053800.1

KEYWORDS

SSS.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominae; Homo.

REFERENCE

1 (bases 1 to 5130)

Nilsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,

Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,

White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and

Chimpanzees

(ex) PLOS Biol. 3 (6), E170 (2005)

JOURNAL

PUBMED

15869325

2 (bases 1 to 5130)

Nilsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,

Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,

White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

Direct Submisison

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering

them based on alignment. Translation starts at the beginning of

alignment.

FEATURES

source

1..5130

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="10"

<1..>5130

/gene="KIAA1074"

/locus_tag="HCL4399"

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 Best Local Similarity 71.4%; Pred. No. 5.8e-72;
 Matches 455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

281 TCAGAAACAAGATGGGCAAGATGCTGCTGCTTCCCTGCTGCAAGGGGAGAGCGCA 340
 2 TGAAGAAAGATTTTGTAAAGAGGCGAGTCCCTTGAGCTCTTGCGCGCGAGCGGA 61
 341 AGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACC 400
 62 GAGGACGCGCGGAGCGGCGGCGAGCGGAGGAGGCGCTTACTGCGAGCCGCTACC 121
 401 ACGTCGTGAGAAATCTGCAAGCTTCCACAGAGCTGCTGCTGGGTAAAGTCCCA 460

Query Match	17.2%	Score 343.4	DB 7	Length 909
Best local Similarity	69.3%	Pred. No. 1.4e-71		
Matches 500	Conservative 0	Mismatches 211	Indels 10	Gaps 2
Qy	223	AGTGGCAAGCAACGTCGGCGCTTCCTGGAGACCAAGACACTGCTATGAAACACTC	282	
Db	92	AGACCCGAGAGACATGAGGTGCTCTTGAGCCCGGTGCGCTGGGCGCATGAAACAGATT	151	
Qy	283	AGGAACAAGATGGGCAAGTGGTGTGCACATGCTTCCTTCCTGTCAGAGGGAGCGGAGG	342	
Db	152	TTTAGTAAGAAAGGCGAGTGCCTTCCTGGGCTCCTTCGCGGCGGCGAGGAGCAGC---	208	
Qy	343	AGCAAGTGGCGCTTGGGAGACATACAGACAGACAGTCCCTTCACATGAGGCCAGTACAC	402	
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ORIGIN

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 /lab_host="DH10B"
 /clone_idb="RZPD no. 9016"
 /note="Vector: pQE801SN_cloned; Site_1: SalI; Site_2: NotI;
 http://www.tropd.de/info/vectors/pQE801SN_cloned_pic.shtml
 ; 1st strand cDNA was prepared from mRNA obtained from
 human T-Lymphocytes with a NotI - oligo(dT) primer [5',
 GACATGCTCTTACGATTCGGACGCGCGCTTTTATTTTATTTT 3']
 Double-stranded cDNA was ligated to SalI adaptors,
 digested with NotI and cloned into the NotI and SalI sites
 of the pQE801SN_cloned vector"

Db	263	GTCCGAGACCGAGATCTGGCGAAGATCCAAAGAGTCCAGCGCGGGTAAATGTGGCGAAA	322
Qy	463	AAGGATCTCATCGTCATGCTCAGGGAACCTGACGTGAACAAAGAGGCAAGCAAAGAGG	522
Db	323	GTCGAGAGAGATCCCTTTTGGCTCAGGAMAAATGGCTTGGAACATAGAGCAAGATGAACAGG	382
Qy	523	ACTGCTTAATCTGGGCGCTCTGGCCAAATGGGAATTCAGAAATGATGAAAACCTCTGCTGAC	582
Db	383	ACGGCTTAATCTTTGGCGCTGTGGCCAAATGCTCATTCAGAAATGATGAACTCTCTGTGTGAC	442
Qy	583	AGACGATGTCAACTTAATGTCTCTTGACAACAAAAAGGACAAGCTGTGATPAAAGCCGTA	642
Db	443	AGAAAAATGCACAGCTCATATGTCGTGACAACGAAAAACAGGACAGCTGTGATGAAGGCTGTA	502
Qy	643	CAATGCCAGAAAGATGAAATGTGCGTTAAATGTGCTGGACATGGCACTGATCCAAATATT	702
Db	503	CAATGCCAGAAAGGAATGTGCAACTATTCGTGTAACAATGTGCTGATCCAAATCTT	562

QY 942 T 942

RESULT 13
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LOCUS
DEFINITION
BC063888 Homo sapiens CDNA IMAGE:30389199, with apparent retained intron.
ACCESSION
BC063888
VERSION
BC063888.1 GI:39645658
KEYWORDS
HTC
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 5483)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Cairnci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McKwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Murray, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
TITLE
2 (bases 1 to 5483)
12477932
JOURNAL
Strausberg, R.
PUBMED
Direct Submission
REFERENCE
Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
JOURNAL
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
REMARK
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
COMMENT
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Mason, Mike R. Mayo, Josh Moran, Ryan Morin, Tella Olson, Diana Palmquist, Anca Petrescu, Anna Lisa Prabh, Parvaneh Saeedi, JR Santos, Angeliq Scherch, Ursula Skalska, Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRK Plate: 141 Row: 0 Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein
This clone has the following problem: retained intron.
Location/Qualifiers
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/organism="Homo sapiens"

ORIGIN
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Best Local Similarity 91.7%; Pred. No. 6, 1e-67;
Matches 355; Conservative 0; Mismatches 30; Indels 2; Gaps 1;
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/note="Vector: pCMV-SPORT6.1"
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DB 1 CAGAAACCTGACTATGATGGTCACCTGCGGGAATGATGATGATTAATTCGCCAA 60
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QY 1673 GGAAGAGCAGAACACCTGGAAGCCAGCAATTCCTGACACTGAGATGAAGATACACA 1732
| | | | |
DB 61 GGAAGAGCAGAACACCTGGAAGCCAGCAATTCCTGACACTGAGATGAAGATACACA 120
| | | | |
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DB 121 GTGATGAACAAATGATCTCAGAACCAATTTTGGAGAACAGAACTGGAATTTAC 180
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QY 1793 AGATGAGATCTGATTCATGAGAAAGACATGAGATGAGTGGTGAATGAATTCG 1852
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DB 181 AGATGAGATCTGATTCATGAGAAAGACATGAGATGAGTGGTGAATGAATTCG 238
| | | | |
QY 1853 AGCTTCTCTTATTGTTGTAAGAAAGAAAGACATCTTGATGAAATAGTACGTCGCG 1912
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DB 239 AGCTTCTCTTATTGTTGTAAGAAAGAAAGACATCTTGATGAAATAGTACGTCGCG 298
| | | | |
QY 1913 AAGAAATTCCTGCTGCTAGACCTGAGCTGACATGAAATGAAATCAGAGCCGCTAAAA 1972
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DB 299 AAGAAATTCCTGCTGCTAGACCTGAGCTGACATGAAATGAAATCAGAGCCGCTAAAA 358
| | | | |
QY 1973 AAAAAAAAAAAAAAAAAAAAAAAAAA 1999
| | | | |
DB 359 AAAAAAAAAATTTGAGAGAAATTGAAA 385
| | | | |
RESULT 14
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LOCUS
CD358418
DEFINITION
AGENCOURT_14284867 NIH_MGC_180 Homo sapiens CDNA clone
IMAGE:30389199 5', mRNA sequence.
ACCESSION
CD358418
VERSION
CD358418.1 GI:31129853
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 874)
NIH-MGC <http://mgc.nci.nih.gov/>
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10N07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: NDA462 row: e column: 16
High quality sequence stop: 625.

FEATURES source

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:30389199"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: Score (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

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Best Local Similarity 91.7%; Pred. No. 6.9e-67;
Matches 354; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

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DB 1 AGAAAACTGACCTAATGTCCTGCTGCAATGGTATGATGATTAATCTCCCAAG 60

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QY 1734 TGAAGAACAAATGATCTGAGAACAAATTTGTGAAGACAGAACACTGATATTACA 1793
    |||
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QY 1794 CGATGAGATTCTGATTCATGAGAAAAAGAGATGAGAGTGTGAAAAATGAAATTCGA 1853
    |||
DB 181 AGATGAGATTCTGATTCATGAGAAAAAGAGATGAGAGTGTG--AAATGAAATTCGA 238

QY 1854 GCTTCTCTTACGTTTGAAGAAAAAGACATCTTGATGAAATTAATGCTGGGGA 1913
    |||
DB 239 GCTTCTCTTACGTTTGAAGAAAAAGACATCTTGATGAAATTAATGCTGGGGA 298

QY 1914 AGAAATTCGATCTGAGACTGAGAGTGAAGACATGAAACATCAGAGCAGCTAAAAAA 1973
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DB 299 AGAAATTCGATCTGAGACTGAGAGTGAAGACATGAAACATCAGAGCAGCTAAAGAA 358

QY 1974 AAAAAAAAAAAAAAAAAAAAAA 1999
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DB 359 AAAAAAAAAAAAAAAAAAAAAA 384

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RESULT 15.
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LOCUS AGENCOURT 6444673 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585453
DEFINITION 5', mRNA sequence.
ACCESSION BM469654
VERSION BM469654.1 GI:18518696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1020)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12351 row: m column: 06
High quality sequence stop: 680.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:5585453"
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/lab_host="DH10B (phage-resistant)"
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ORIGIN

Query Match 16.2%; Score 323.2; DB 3; Length 1020;
Best Local Similarity 74.6%; Pred. No. 1.1e-66;
Matches 406; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

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QY 459 CAGAAAGATCTCATGCTGATGCTGAGGACACTGACGTAACAAGAACAGAACAA 518
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DB 61 GAAAGTGCAGCAGATCTCTTTGCTCAGAGAAAGATGCTTGAACGATAGAGCAAGATGA 120

QY 519 GAGGACGCTCTACATCTGAGCTCTGCAATGGGAATTCAGAGTGAATTAATCTCTGCT 578
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DB 121 CAGGACGCTCTACATCTGAGCTCTGCAATGGGAATTCAGAGTGAATTAATCTCTGCT 180

QY 579 GAGCAGCAGATGTCATTAATGCTCTTGAACAACAAAAAGAGACAGCTCTGATAAGC 638
    |||
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QY 639 CGTACCAATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAA 698
    |||
DB 241 TGTACATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAA 300

QY 699 TATTCAGATGATGAGAAATACCACTGCACTAGCGTATCTATTAATGAAGATAATT 758
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QY 759 AATGGCCAAAGCAGCTGCTTTATATGCTGCTGATATGATCAAAAAACAGCATGCGCT 818
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DB 361 AATGGCCAAAGCAGCTGCTTTATATGCTGCTGATATGATCAAAAAACAGCATGCGCT 420

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DB 421 CACACCACTGTTACTTGGTGTGATCAGAGCAAAAAAGCAAGTCGTAATTTTATATCA 480

QY 879 GAAAAAGCGAATTTAATGCACTGATGATGATGAGAGAGCTGCTCTATCTGCTGT 938
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DB 481 GAAAAAGCGAATTTAATGCACTGATGATGATGAGAGAGCTGCTCTATCTGCTGT 540

QY 939 ATGT 942
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DB 541 ATAT 544

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Job time : 8066.4 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:05:29 ; Search time 10314.1 Seconds
(without alignments)
11242.903 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040
Sequence: 1 atggtggtgaggtgcatc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11752642

Minimum DB seq length: 10
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	6	BD242273
2	2040	100.0	2040	6	BD242273 Compound
3	2040	100.0	2040	6	AR278480 Sequence
4	2040	100.0	2040	6	AR350944 Sequence
5	2040	100.0	2040	6	AR367176 Sequence
6	2040	100.0	2040	6	AR371072 Sequence
7	2040	100.0	2040	6	AR400212 Sequence
8	2040	100.0	2040	6	AR405479 Sequence
9	2040	100.0	2040	6	AR433320 Sequence
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11	2040	100.0	2040	6	AR588845 Sequence
12	2040	100.0	2040	6	AR605665 Sequence
13	2040	100.0	2040	6	AR615064 Sequence
14	2040	100.0	2040	6	AR642106 Sequence
15	2040	100.0	2040	6	AR657004 Sequence
16	2040	100.0	2040	6	AX106594 Sequence
17	2040	100.0	2040	6	AX140885 Sequence
18	2040	100.0	2040	6	AX200745 Sequence
				6	AX267401 Sequence

19	2040	100.0	2040	6	AX282958
20	2040	100.0	2040	6	AX316966 Sequence
21	1551	76.0	2000	6	BD242272
22	1551	76.0	2000	6	AR278479 Sequence
23	1551	76.0	2000	6	AR350943 Sequence
24	1551	76.0	2000	6	AR367175 Sequence
25	1551	76.0	2000	6	AR371071 Sequence
26	1551	76.0	2000	6	AR400211 Sequence
27	1551	76.0	2000	6	AR405478 Sequence
28	1551	76.0	2000	6	AR433319 Sequence
29	1551	76.0	2000	6	AR563858 Sequence
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32	1551	76.0	2000	6	AR615063 Sequence
33	1551	76.0	2000	6	AR642105 Sequence
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ALIGNMENTS

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DEFINITION	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.				
ACCESSION	BD242273.1	GI:33052043			
VERSION	BD242273.1	GI:33052043			
KEYWORDS	JP 2002520054-A/360.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2040)				
AUTHORS	Dillon,D.C., Harlocker,S.L., Yugu,J., Xu,J. and Mitcham,J.L.				
TITLE	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use				
JOURNAL	Patent: JP 2002520054-A 360 09-JUL-2002;				
COMMENT	CORIXA CORP				
OS	Homo sapiens (human)				
PN	JP 2002520054-A/360				
PD	09-JUL-2002				
PF	14-JUL-1999 JP 2000560247				
PR	14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR				
PT	23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR				
15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR					
09-APR-1999 US 09/288946					
PI	DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUGU, PI				
JIANGCHUN XU, PI					
PI	JENNIFER LYNN MITCHAM				
PC	C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,				
PC	C12N5/10,				
PC	C12N21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,				
PC	A61K37/02,				
PC	C12N5/00				
CC	Compounds for immunotherapy and diagnosis of prostate cancer				
CC	and methods				
CC	for their use				
CC	Key				
FT	Location/Qualifiers				
FT	1. 2040				
FT	source				
FT	/organism='Homo sapiens (human)'				

FEATURES
Source Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ATGCTGTTGAGGTGATTCATCGCGCTGCTCTTCTGTGAAGACCATTGGTCTC 60
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121 AGCAACGTGGGCACTTCTGGAAGACACAGACCTCTGTATGAAGACCTCAGAGCAAG 180
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301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTG 420
361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTG 420
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481 CTCAGGACACTGACCTGAAACAAGAGCAAGCAAAAGAGAGCTGCTCAATCTGGCC 540
481 CTCAGGACACTGACCTGAAACAAGAGCAAGCAAAAGAGAGCTGCTCAATCTGGCC 540
541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGACGATGTCAATTAAT 600
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RESULT 2
AR278480 2040 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 375 from patent US 6512094.
DEFINITION AR278480
ACCESSION AR278480
VERSION AR278480.1 GI:29712726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
Unclassified.
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Recter,M.W., Stolk,J.A., Day,C.H.,
Vedvyck,T.S., Carter,D., Li,S.X., Wang,A., Skeily,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 375 28-JAN-2003;
Corixa Corporation; Seattle, WA
FEATURES
source 1. 2040
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
AR350944 AR350944 2040 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 303 from patent US 6586570.
DEFINITION AR350944
ACCESSION AR350944
VERSION AR350944.1 GI:33752584
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M. and Misher,L.
TITLES Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6586570-A 303 01-JUL-2003;
Corixa Corporation; Seattle, WA
FEATURES
source 1..2040
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No.0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
LOCUS AR367176 2040 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 375 from patent US 6339505.
ACCESSION AR367176
VERSION AR367176.1 GI:34600151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yudin,J.,
Reed,S.G., Kalos,M.D., Fanger,J.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6339505-A 375 11-DEC-2001;
FEATURES
source Corixa Corporation; Seattle, WA
1. 2040
/organism="Unknown"
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ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR371072 Sequence 375 from patent US 6395278.
DEFINITION AR371072
ACCESSION AR371072
VERSION AR371072.1 GI:34607965
KEYWORDS
SOURCE
ORGANISM

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REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L. and Yugu,J.
TITLE Prostate specific fusion protein compositions
JOURNAL Patent: US 6395278-A 375 28-MAY-2002;
Corixa Corporation; Seattle, WA

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RESULT 7
AR405479 2040 bp DNA linear PAT 18-DEC-2003
LOCUS AR405479
DEFINITION Sequence 375 from patent US 6630305.
ACCESSION AR405479
VERSION AR405479.1 GI:40154316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y., Kalos M.D., Fanger G.R., Reiter M.W., Stolk J.A., Day C.H., Vedick T.S., Carter D., Li S.X., Wang A., Skelky Y.A.W., Hepler W.T. and Henderson R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 375 07-OCT-2003;
Corixa Corporation; Seattle, WA;
BOX:

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source location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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AR433320 2040 bp DNA linear PAT 18-DEC-2003
LOCUS AR433320
DEFINITION Sequence 303 from patent US 6656480.
ACCESSION AR433320
VERSION AR433320.1 GI:40196102
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2040)
Rettner M.W. and Dillon, D.C.
TITLE
Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL
Patent: US 6656480-A 303 02-DEC-2003;
Corixa Corporation; Seattle, WA
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 9
AR563859
LOCUS AR563859 2040 bp DNA linear PART 08-OCT-2004
DEFINITION Sequence 375 from patent US 6759515.
ACCESSION AR563859
VERSION AR563859.1 GI:53978910
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kaleo,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,

Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: US 6759515-A 375 06-JUL-2004;
Corixa Corporation; Seattle, WA
Location/Qualifiers
1. .2040
/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 303 from patent US 6828431.
ACCESSION AR615064
VERSION AR615064.1 GI:56671468
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Frudek, T.N., Reed, S.G., Smith, J.M., Misher, L.E., Dillon, D.C.,
Retter, M.W., Wang, A., Skeiky, Y.A.W., and Harlocker, S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: US 6828431-A 303 07-DEC-2004;
Corixa Corporation; Seattle, WA
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Query Match 100.0%; Score 2040; DB 6; Length 2040;
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Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR642106
DEFINITION Sequence 303 from patent US 6861506.
ACCESSION AR642106
VERSION AR642106.1 GI:62778254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 2040)
AUTHORS Frudakis,T.N., Smith,J.M., Reed,S.G., Misher,L.E., Retter,M.W. and
Dillon,D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast
cancer
JOURNAL Patent: US 6861506-A 303 01-MAR-2005;
Corixa Corporation; Seattle, WA
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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2040)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Ketter,M.W., Stolk,J.A., Day,C.H., Vedvik,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepner,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: US 6894146-A 375 17-MAY-2005;
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 source Location/Qualifiers
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 /organism="Unknown"
 /mol_type="genomic DNA"
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGTGTGATGAGTGAATTCATGCGCGGCTCTTCGTGAAGCAATTTGGTCTC 60
 DB 1 ATGGTGTGATGAGTGAATTCATGCGCGGCTCTTCGTGAAGCAATTTGGTCTC 60
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 QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
 DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
 QY 181 ATGGGCAATGTTGCGCCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
 DB 181 ATGGGCAATGTTGCGCCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
 QY 241 GCGCTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
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 QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGCAAGTGGCGCTTGG 360
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 QY 361 GGAAGCTAGATGACAGTGTGCTTCAATGAGCCCAAGTACCAAGTCCGTGGAAGATCTG 420
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Search completed: December 19, 2005, 15:33:38
Job time : 10320.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: December 19, 2005, 01:50:48 ; Search time 1218.45 Seconds
(without alignments)
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Title: US-09-924-400-303

Perfect score: 2040

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9978348

Minimum DB seq length: 10

Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2040	100.0	2040	3 AAC81013	AAC81013 Human B11
2	2040	100.0	2040	4 AAH93716	AAH93716 Human pro
3	2040	100.0	2040	4 AA167213	AA167213 B305D iso
4	2040	100.0	2040	4 AA653809	AA653809 Human pro
5	2040	100.0	2040	4 AAH02781	AAH02781 Prostate
6	2040	100.0	2040	4 AAH85030	AAH85030 Human pro
7	2040	100.0	2040	5 ACA59617	ACA59617 Prostate
8	2040	100.0	2040	6 AB195178	AB195178 Human B30
9	2040	100.0	2040	6 AA999859	AA999859 Breast tu
10	2040	100.0	2040	8 ACC95344	ACC95344 Prostate
11	2040	100.0	2040	8 ADA11382	ADA11382 Human bre
12	2040	100.0	2040	10 ADG15355	ADG15355 Human bre
13	2040	100.0	2040	10 ADG26240	ADG26240 Human pro
14	2040	100.0	2040	10 ADG26241	ADG26241 Human pro
15	1989	97.5	2040	3 AAH06600	AAH06600 Human imm
16	1551	76.0	2000	3 AAC81012	AAC81012 Human B11
17	1551	76.0	2000	4 AAH93715	AAH93715 Human pro
18	1551	76.0	2000	4 AA167212	AA167212 B305D iso
19	1551	76.0	2000	4 AA653808	AA653808 Human pro

20	1551	76.0	2000	4 AAH02780	AAH02780 Prostate
21	1551	76.0	2000	4 AAH85029	AAH85029 Human pro
22	1551	76.0	2000	5 ACA59616	ACA59616 Prostate
23	1551	76.0	2000	6 AB195179	AB195179 Human B30
24	1551	76.0	2000	6 AA999858	AA999858 Breast tu
25	1551	76.0	2000	8 ACC95343	ACC95343 Prostate
26	1551	76.0	2000	8 ADA11381	ADA11381 Human bre
27	1551	76.0	2000	10 ADG15354	ADG15354 Human bre
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32	1128	55.3	1155	3 AAC81011	AAC81011 Human B11
33	1128	55.3	1155	4 AAH93714	AAH93714 Human pro
34	1128	55.3	1155	4 AA167211	AA167211 B305D iso
35	1128	55.3	1155	4 AA653807	AA653807 Human pro
36	1128	55.3	1155	4 AAH02779	AAH02779 Prostate
37	1128	55.3	1155	4 AAH85028	AAH85028 Human pro
38	1128	55.3	1155	5 ACA59615	ACA59615 Prostate
39	1128	55.3	1155	6 AB195178	AB195178 Human B30
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41	1128	55.3	1155	8 ACC95342	ACC95342 Prostate
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ALIGNMENTS

RESULT 1	
AAC81013	AAC81013 standard; cDNA; 2040 BP.
ID	
XX	AAC81013;
XX	
XX	13-FEB-2001 (first entry)
DE	Human B11A91 antigen splice isoform B11C-9-16 cDNA.
KW	Human; breast tumour-specific antigen; cytostatic; vaccine;
XX	breast cancer; B11A91; B11A91; B15A91; ss.
OS	Homo sapiens.
PN	WO200061753-A2.
XX	
PD	19-OCT-2000.
XX	
PF	07-APR-2000; 2000WO-US009312.
XX	
PR	09-APR-1999; 99US-00289198.
PR	28-OCT-1999; 99US-00429755.
PR	23-MAR-2000; 2000US-00534825.
XX	
PA	(COR1-) CORIXA CORP.
PI	
DR	Frudakis TN, Smith JM, Reed SG, Miesher LB, Retter MW, Dillon DC;
DR	WPI, 2000-628403/60.
XX	F-PDB; AA828630.
PT	An isolated polypeptide comprising an immunogenic portion of a breast
PT	tumor protein used for inhibiting the development of cancer, especially
XX	breast cancer, and monitoring cancer progression in a patient.
XX	
PS	Claim 4; Page 178; 187pp; English.
CC	The present sequence is given in a specification relating to compositions
CC	and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC	sequences that are preferentially expressed in breast tumor tissue, and
CC	the polypeptides encoded by such nucleotide sequences, are used in

CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
XX
XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCTTGAAGTTATTCATGACCGGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGTGCTTGAAGTTATTCATGACCGGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAAGACACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAAGCAAGACACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCGGCACTGCTCCCTGCTGAGGGGGAGTGGGCAAGCACTG 240
DB 181 ATGGGCAATGGTGGCGGCACTGCTCCCTGCTGAGGGGGAGTGGGCAAGCACTG 240
QY 241 GGGCTTCTGAGAGCAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGCTTCTGAGAGCAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGATAGAGTACAGTGTCTTCAATGAGCCCAAGTACCACTCCGTGGAAGATCTG 420
DB 361 GGAAGATAGAGTACAGTGTCTTCAATGAGCCCAAGTACCACTCCGTGGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGGTGAAGTCCCAAGAAAGATCTCATCGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGGTGAAGTCCCAAGAAAGATCTCATCGTCATG 480
QY 481 CTCAGGAGCACTGACGTGAACAAGAAAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGAGCACTGACGTGAACAAGAAAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
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DB 541 TCTGCCAATGGGAATTCAAGATGATTAATCTCTGCTGAGCAAGATGTCAACTTAAT 600
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DB 601 GTCTCTGACAAACAAAAGAGAGCAGCTGTGATTAAGGCGGTACATGCGAAGATGA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGACACCTATCTATAATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
DB 721 ACCACTGTGACACCTATCTATAATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
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DB 901 CTGGATTAATATGGAAGAGCTGCTCTCATCTGCTGTATGTTGGTATCAAGCAATTA 960
QY 961 GTCACTCTTCTACTGAGCAAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
DB 961 GTCACTCTTCTACTGAGCAAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
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DB 1381 CCTGACAAAGAAATGGAAGATATCAAGAAATTCGAAATTTGTTGACTTACAAAGAA 1440
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DB 1561 CAAGAACAGAAATTAATAGATGTGATAGAGCTGAGAAATTTTATGCTATCGAA 1620
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DB 1621 GAAATGAAGAACAGGAAGTACTATGTCGGAATTCCTCAAGAAACCTGACTAATGGTGC 1680
QY 1681 ACTGTGCAATGTGATGATGATTAATTCCTCAAGAAAGAGAGCAACCTGAAAGC 1740
DB 1681 ACTGTGCAATGTGATGATGATTAATTCCTCAAGAAAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAACAAATGATCTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAACAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATCAAGAGATCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATCAAGAGATCTGATTCATGAA 1860
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DB 1921 GAAAAAGCATCTTGCATGAAAAATGATGCTTGGGGAAGAAATTTGCCATGCTAAGACTG 1980

QY 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAGAGTACGACAAATGATCTCAG 1800
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Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAGAGTACGACAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGACGAAACACTGAAATATACAGATGAGATTCGATTCATGAA 1860
| | | | |
Db 1801 AAGCAATTTTGTGAAGACGAAACACTGAAATATACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAGACAGATGAGAGTGTGTTGAAAAATGAAATTCGAGCTTCTCTTAGTTGTAGAAA 1920
| | | | |
Db 1861 GAAAGACAGATGAGAGTGTGTTGAAAAATGAAATTCGAGCTTCTCTTAGTTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGATGATGAAATATAGTGTGCGGAGAAATTCCTGATTAACATG 1980
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Db 1921 GAAAAAGACATCTTGATGATGAAATATAGTGTGCGGAGAAATTCCTGATTAACATG 1980
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| | | | |
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040

RESULT 5
AAH02781

AAH02781 standard; cDNA; 2040 BP.

AAH02781;

14-JUN-2001 (first entry)

Prostate tumour antigen determined cDNA splice variant of B305D #10.

Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
prostate cancer; immunogenic; cytostatic; vaccine; ss.

Homo sapiens.

WO200125272-A2.

12-APR-2001.

04-OCT-2000; 2000WO-US027464.

04-OCT-1999; 99US-0157455P.

(CORI-) CORIXA CORP.

Xu J, Skelky YAM, Reed SG, Cheever MA;

WPI; 2001-245062/25.

P-PSDB; AAB74817.

Prostate specific protein and its encoding polynucleotide, useful for the
treatment and diagnosis of prostate cancer.

Claim 50; Page 233; 276pp; English.

The present invention describes an isolated polypeptide (I) comprising at
least an immunogenic portion of a prostate tumour antigen protein or its
variant. (I) have cytostatic activity and can be used in vaccine
production. (I), prostate tumour antigen polynucleotides, an antigen
presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
pharmaceutical composition containing (I) are useful for inhibiting the
development of cancer in a patient. Antibodies specific for prostate
specific proteins and oligonucleotides that hybridise to a polynucleotide
that encodes a prostate specific protein are useful for detecting the
presence or absence of a cancer or monitoring the progression of the
cancer. Progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
exemplification of the present invention

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match	100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 ATGTGTGTGAGTGAATTCATGCGGCTGCTCTTGTGTAAGAGCATTTGGTCTC 60	
Db 1 ATGTGTGTGAGTGAATTCATGCGGCTGCTCTTGTGTAAGAGCATTTGGTCTC 60	
QY 61 AGGACCAAGATGAGGCAAGTGTGCTGCCGTTTCCCTGTGCGAGGAGCGGCAAG 120	
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Db 181 ATGGCAAGTGTGCGCCCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGCAAGT 240	
QY 241 GCGGCTTGTGAGACCAAGCACTGTGCTATGAAGACATTCAGAGCAAGATGGCAAG 300	
Db 241 GCGGCTTGTGAGACCAAGCACTGTGCTATGAAGACATTCAGAGCAAGATGGCAAG 300	
QY 301 TGTGTGCTGCACTGCTTCCCTGTGCGAGGAGAGCGGCAAGAGCAAGTGGCGTTGG 360	
Db 301 TGTGTGCTGCACTGCTTCCCTGTGCGAGGAGAGCGGCAAGAGCAAGTGGCGTTGG 360	
QY 361 GGAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACAGTGCCTGTGAGAGATCTG 420	
Db 361 GGAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACAGTGCCTGTGAGAGATCTG 420	
QY 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480	
Db 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480	
QY 481 CTCAGGACACTGAGCTGTGAACAAAGACAAAGCAAGCAAGTCTTACATCTGGCC 540	
Db 481 CTCAGGACACTGAGCTGTGAACAAAGACAAAGCAAGCAAGTCTTACATCTGGCC 540	
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCCTGCTGAGCAGAGCATGTCAACTAAT 600	
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCCTGCTGAGCAGAGCATGTCAACTAAT 600	
QY 601 GTCTTGTGACCAACAAAGAGGACAGCTGTATGAAGCCGTACCAATGCCAGAAATGAA 660	
Db 601 GTCTTGTGACCAACAAAGAGGACAGCTGTATGAAGCCGTACCAATGCCAGAAATGAA 660	
QY 661 TGTGCTTAAATGTGTGAGACATGCTGTATCCAAATATTCAGATGATGGAAT 720	
Db 661 TGTGCTTAAATGTGTGAGACATGCTGTATCCAAATATTCAGATGATGGAAT 720	
QY 721 ACCACTGCACTAGGCTATCTATATGAAGTAAATTAATGCGCAAGCACTGCTCTTA 780	
Db 721 ACCACTGCACTAGGCTATCTATATGAAGTAAATTAATGCGCAAGCACTGCTCTTA 780	
QY 781 TATGTGTGATATGCAATCAAAAAAAGAGTGCCTCAACCACTGTACTTGGTGTGA 840	
Db 781 TATGTGTGATATGCAATCAAAAAAAGAGTGCCTCAACCACTGTACTTGGTGTGA 840	
QY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900	
Db 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900	
QY 901 CTGATATGATGAGAGAGTGTGCTCACTGTGATGATGATGATGATGATGATGATGAT 960	
Db 901 CTGATATGATGAGAGAGTGTGCTCACTGTGATGATGATGATGATGATGATGATGAT 960	
QY 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATGAGCAGAG 1020	
Db 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATGAGCAGAG 1020	
QY 1021 GCCAAGAGATATGCTGTTCTATGATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080	

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Db 1021 GCCAGAGATGATCTGTTCTAGTCATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAATAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAG 1140
Db 1081 AAGAGAAAAAGATGCTAAATAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCAGTGAATATGAGCCAGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCAGTGAATATGAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCAAGAAAGTAATTAATGAGGATTAATAGTAAACCTGATCTGCTGCTGCG 1320
Db 1261 AAGCAAGAAAGTAATTAATGAGGATTAATAGTAAACCTGATCTGCTGCTGCG 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGACCTGAAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACAAAGAA 1440
Db 1381 CCTGACACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACAAAGAA 1440
QY 1441 AAGCAATGCGCAAAATTAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAGCTGACA 1500
Db 1441 AAGCAATGCGCAAAATTAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAGAGGCTTGAGAGGAGTGAATATGAGCCAGAGAGAGAGATCT 1560
Db 1501 TCAGAGAGAGAGTCAAGAGGCTTGAGAGGAGTGAATATGAGCCAGAGAGAGAGATCT 1560
QY 1561 CAGAAACCGAAATTAATTAAGATGTGATAGAGCTGAGAAATTTTATGCTATCGAA 1620
Db 1561 CAGAAACCGAAATTAATTAAGATGTGATAGAGCTGAGAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAGACGGAAGTACTCATGTCGAAATTTCCAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAGACGGAAGTACTCATGTCGAAATTTCCAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCAAGAGAGAGAGAGACCTGAAAGC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCAAGAGAGAGAGAGACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGAAGAGAGAGAGTGAATTAATTAAGAGTGAATTTGATTTGATTAAGAA 1860
Db 1801 AAGCAATTTTGAAGAGAGAGAGTGAATTAATTAAGAGTGAATTTGATTTGATTAAGAA 1860
QY 1861 GAAAGCAGATAGAGTGTGTAAGAAATGAATTTCTGAGCTTTCTCTAGTTGTAAGAA 1920
Db 1861 GAAAGCAGATAGAGTGTGTAAGAAATGAATTTCTGAGCTTTCTCTAGTTGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGAATGAATTAATGATGCTTGGGAGAGAAATTTGCCATGCTAAGCTG 1980
Db 1921 GAAAAAGACATCTTGAATGAATTAATGATGCTTGGGAGAGAAATTTGCCATGCTAAGCTG 1980
QY 1981 GAGCTGAGACATGAAATCACTGAGAGCCAGCTAAATTAATTAATTAATTAATTAATTAAT 2040
Db 1981 GAGCTGAGACATGAAATCACTGAGAGCCAGCTAAATTAATTAATTAATTAATTAATTAAT 2040
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RESULT 6
AAH85030
ID AAH85030 standard; cDNA; 2040 BP.
XX
AC AAH85030;

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XX 25-SEP-2001 (first entry)
DT Human prostate-specific CDNA sequence B305D splice variant #10.
XX
DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US030904.
XX
PR 12-NOV-1999; 99US-00439313.
XX
PR 18-NOV-1999; 99US-00443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skealy YAW, Wang A,
XX WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX
PS Claim 31; Page 248; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712B, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGCTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGCTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
QY 61 AAGAGCAAGATGGGAGAGTGTGCTGCTGCTTCCCTGTGCGAGGAGCGGCAAG 120
Db 61 AAGAGCAAGATGGGAGAGTGTGCTGCTGCTTCCCTGTGCGAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGAGACAGAGACTCTGCTATGAAGACATCTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGACAGAGACTCTGCTATGAAGACATCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGCTTCTGAGAGACAGAGACTCTGCTATGAAGACATCTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGCTTCTGAGAGACAGAGACTCTGCTATGAAGACATCTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGCAAGTGGGCGCTTGG 360
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Db 301 TGTGTGCGCAGCTCTTCCCTGCTGCAAGGGGAGGGGCAAGAGCAAGGGGCGCTTGG 360
Qy 361 GAGAGTACGATACAGTGTCTTCATGAGGCCAGGATACCACTCCGTGGAAGAAATCTG 420
Db 361 GAGAGTACGATACAGTGTCTTCATGAGGCCAGGATACCACTCCGTGGAAGAAATCTG 420
Qy 421 GACAACTCCAGAGCTGCTGAGGATGAAAGTCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAACTCCAGAGCTGCTGAGGATGAAAGTCCCAAGAAAGATCTCATGTCATG 480
Qy 481 CTCAGGAGCACTGACCTGAAACAAGAGCAAGCAAAAGAGAGCTGCTCTACATCTGGCC 540
Db 481 CTCAGGAGCACTGACCTGAAACAAGAGCAAGCAAAAGAGAGCTGCTCTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGATGAAATCTCTGCTGGAAGAGAGTCAATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATGAAATCTCTGCTGGAAGAGAGTCAATTAAT 600
Qy 601 GTGCTTGAACAACAAAAGAGAGCAAGCTCTGATTAAGGCGCTACAAATGCGAAGATGAA 660
Db 601 GTGCTTGAACAACAAAAGAGAGCAAGCTCTGATTAAGGCGCTACAAATGCGAAGATGAA 660
Qy 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACTGTGCACTACGCTATCTAATTAAGAAATTAATGAGCAAGCACTGCTCTTA 780
Db 721 ACCACTGTGCACTACGCTATCTAATTAAGAAATTAATGAGCAAGCACTGCTCTTA 780
Qy 781 TATGAGTCTGATATCGAATCAAAAACAGCATGGCTCACACCACTGTTACTTGGTGA 840
Db 781 TATGAGTCTGATATCGAATCAAAAACAGCATGGCTCACACCACTGTTACTTGGTGA 840
Qy 841 CATGACCAAAAACAGCAAGCTGTAAGATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGACCAAAAACAGCAAGCTGTAAGATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGGATAGATAGGAAGAGCTGCTCATATCTTGTATGTTGTGATGATGCAAGATATA 960
Db 901 CTGGATAGATAGGAAGAGCTGCTCATATCTTGTATGTTGTGATGATGCAAGATATA 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAGATCTATCTGACGAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAGATCTATCTGACGAG 1020
Qy 1021 GGCAGAGATAGCTGTTTCTAGTCAATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GGCAGAGATAGCTGTTTCTAGTCAATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAATATCTCTTGAAAAACAGCATTCAGAACAGACTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAATATCTCTTGAAAAACAGCATTCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAAAGTCAAAAGTTCAAGGCAAGTGAATATGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAAAGTCAAAAGTTCAAGGCAAGTGAATATGCCAGCCAGAGAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAATAGATGATGAGAGGTGAAGAAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAATAGATGATGAGAGGTGAAGAAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGAGGATTAAGAAACCTGACTAATGATGCTGCTGCGC 1320
Db 1261 AAGCATGAAAGTAAATATGAGGATTAAGAAACCTGACTAATGATGCTGCTGCGC 1320
Qy 1321 AATGATGATTAATGATTAATCTCTCAAGAGAAAGCAAGCACTGAAATACGCAATTT 1380
Db 1321 AATGATGATTAATGATTAATCTCTCAAGAGAAAGCAAGCACTGAAATACGCAATTT 1380
Qy 1381 CCTGACACGAAGTAAAGATATCACAGAAATTTGGAATTAATTTCTGACTCAAGAA 1440
Db 1381 CCTGACACGAAGTAAAGATATCACAGAAATTTGGAATTAATTTCTGACTCAAGAA 1440

Db 1381 CCTGACACGAAGTAAAGATATCACAGAAATTTGGAATTAATTTCTGACTCAAGAA 1440
Qy 1441 AAAAGATGCCAAATATCTTCTGAAAAACAGAACCCAGAAACAGACTTAAAGTGA 1500
Db 1441 AAAAGATGCCAAATATCTTCTGAAAAACAGAACCCAGAAACAGACTTAAAGTGA 1500
Qy 1501 TCAGAGGAAGATCAAAAGGCTTGAGGAGCAGTGAATAATGGCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGGAAGATCAAAAGGCTTGAGGAGCAGTGAATAATGGCAGCAGAGAAAGATCT 1560
Qy 1561 CAAGAACCAAGATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 CAAGAACCAAGATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Qy 1621 GAAATGAAGACACGGAAGTACTCATGTCGATTCAGAAATCTGACTAATGATGCT 1680
Db 1621 GAAATGAAGACACGGAAGTACTCATGTCGATTCAGAAATCTGACTAATGATGCT 1680
Qy 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGATGATGATGATGATGATGATGAT 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGATGATGATGATGATGATGATGAT 1800
Qy 1801 AAGCAATTTTGAAGAACAGAACCTGGAATATTAACAGATGATGATGATGATGATGAT 1860
Db 1801 AAGCAATTTTGAAGAACAGAACCTGGAATATTAACAGATGATGATGATGATGATGAT 1860
Qy 1861 GAAAGCGATGAGAGTGTGAAAAATGAAATTCGAGCTTCTCTTGTGTAAGAA 1920
Db 1861 GAAAGCGATGAGAGTGTGAAAAATGAAATTCGAGCTTCTCTTGTGTAAGAA 1920
Qy 1921 GAAAAAGCATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 GAAAAAGCATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Qy 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAATGATGATGATGATGATGAT 2040
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAATGATGATGATGATGATGAT 2040

RESULT 7
ACAS9617
ID ACAS9617 standard; cDNA; 2040 BP.
XX
AC ACAS9617;
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #360.
XX
KW Prostate cancer; vaccine; gene therapy; cytosolic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMa; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALOS/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEIK/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
DR MPI; 2001-245062/25.
XX P-PSDB; ABU71670.
XX
XX
PS Example 11; SEQ ID NO 375; 85bp; English.
XX
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 3 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated CDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 5; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTGAATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTGAAGTGAATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGAAGCAAGTGGGCAAGTGTGCTGCTTCCCTGTGCGAGGAGAGACGGCGAAG 120
DB 61 AGAAGCAAGTGGGCAAGTGTGCTGCTTCCCTGTGCGAGGAGAGACGGCGAAG 120
QY 121 AGCAACGTGGGCACTTGTGAGACCAAGCACTGTGTAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTGTGAGACCAAGCACTGTGTAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGCAACGTG 240
QY 241 GGGGCTTTGGAGAACCAAGCACTGTGTAAGACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTTGGAGAACCAAGCACTGTGTAAGACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTTGGAGAACCAAGCACTGTGTAAGACACTCAGAGCAAGATGGGCAAG 300

QY 301 TGGTGTGCACTGCTCCCTGTGTCAGAGGGAGCGGCAAGGATGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTCCCTGTGTCAGAGGGAGCGGCAAGGATGGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGTCTTCATGAGGCCAAGTACACAGTCCGTGAGAGATCTTG 420
DB 361 GGAGACTAGATGACAGTGTCTTCATGAGGCCAAGTACACAGTCCGTGAGAGATCTTG 420
QY 421 GACAAGCTCCAGAGAGCTGGCGTGTGGGTAAAGTCCCGAAGAAAGATTCATCGTCATG 480
DB 421 GACAAGCTCCAGAGAGCTGGCGTGTGGGTAAAGTCCCGAAGAAAGATTCATCGTCATG 480
QY 481 CTCAGGGACACTGAGGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGAGCC 540
DB 481 CTCAGGGACACTGAGGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGAGCC 540
QY 541 TTGTCCAAATGGGAATTGAGAGTGAATAAATCTCTGTGTGACAGACAGATGTCACTTAAT 600
DB 541 TTGTCCAAATGGGAATTGAGAGTGAATAAATCTCTGTGTGACAGACAGATGTCACTTAAT 600
QY 601 GTCCCTTGACAAACAAAGAGAGCAGCTGTGATTAAGCCGTACATGCGCAAGAAATGAA 660
DB 601 GTCCCTTGACAAACAAAGAGAGCAGCTGTGATTAAGCCGTACATGCGCAAGAAATGAA 660
QY 661 TGTGCGTTAATGTGCTGGAAACATGACATGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTGCTGGAAACATGACATGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGACACTAGCTATCTATATATGAAATTAATTAAGCCAAAGACTGCTCTTA 780
DB 721 ACCACTGTGACACTAGCTATCTATATATGAAATTAATTAAGCCAAAGACTGCTCTTA 780
QY 781 TATGTGCTGATATGAAATCAAAACAAAGATGCGCTCAACACCTGTACTTGGTGA 840
DB 781 TATGTGCTGATATGAAATCAAAACAAAGATGCGCTCAACACCTGTACTTGGTGA 840
QY 841 CATGACAAACAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGAGCAATTTAAATGCA 900
DB 841 CATGACAAACAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGAGCAATTTAAATGCA 900
QY 901 CTGAGTATGATGAAAGAGCTGCTCATCTTGTGTAAGTGTGTGATGACCAAGTATA 960
DB 901 CTGAGTATGATGAAAGAGCTGCTCATCTTGTGTAAGTGTGTGATGACCAAGTATA 960
QY 961 GTGAGCTTCTAATGAGCAAAATTAATGATCTTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTAATGAGCAAAATTAATGATCTTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGGCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGGCAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATGTAATAATCTTCTGAAAACAGCAATCCAGAACCAAGCTTAAAG 1140
DB 1081 AAAAGAAAACAGATGTAATAATCTTCTGAAAACAGCAATCCAGAACCAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGATCAAAAGTTCAAAGGAGTGAATAATGCGACAGAGAAA 1200
DB 1141 CTGACATCAGAGAAAGATCAAAAGTTCAAAGGAGTGAATAATGCGACAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGATGGATTAATGAGAAACCTGAATATGATGTCACTGTGAC 1320
DB 1261 AAGCATGAAAGTAAATATGATGGATTAATGAGAAACCTGAATATGATGTCACTGTGAC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGAGCAACCTGAAATATGCAAAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGAGCAACCTGAAATATGCAAAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGATCAAAAGAA 1440

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Db      1381 CCGAGACAGGAAGTGAAGATTCACAGAAATTTGGAAATTTGATCTGACAAAGAA 1440
Qy      1441 AAAAGATGCCAAATATCTTCTTGTAAAAACAGAACCCAGAACAGATTAAAGCTGACA 1500
Db      1441 AAAAGATGCCAAATATCTTCTTGTAAAAACAGAACCCAGAACAGATTAAAGCTGACA 1500
Qy      1501 TCAGAGGAAGATCACAAGGCTTTGAGGAGGAGTGAATAATGGCCAGGAGAAAGATCT 1560
Db      1501 TCAGAGGAAGATCACAAGGCTTTGAGGAGGAGTGAATAATGGCCAGGAGAAAGATCT 1560
Qy      1561 CAGAGACAGAAATTAATTAAGATGATAGAGCTAGAAATTTTATGCTATCGAA 1620
Db      1561 CAGAGACAGAAATTAATTAAGATGATAGAGCTAGAAATTTTATGCTATCGAA 1620
Qy      1621 GAAATGAGAGACGAGAGTACTCATGTGGAATTCACAGAAACCTGAAATGATGTC 1680
Db      1621 GAAATGAGAGACGAGAGTACTCATGTGGAATTCACAGAAACCTGAAATGATGTC 1680
Qy      1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAGAGAGCACTGAAAGC 1740
Db      1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAGAGAGCACTGAAAGC 1740
Qy      1741 CAGCAATTTCTGACACTGAGATGAGAGATATCAGAGTACGAGAACAAATGATCTCAG 1800
Db      1741 CAGCAATTTCTGACACTGAGATGAGAGATATCAGAGTACGAGAACAAATGATCTCAG 1800
Qy      1801 AAGCAATTTTGTGAGAGACAGAACACTGGAATTAACAGATGATGATCTGATTCAGAA 1860
Db      1801 AAGCAATTTTGTGAGAGACAGAACACTGGAATTAACAGATGATGATCTGATTCAGAA 1860
Qy      1861 GAAAGACAGATAGAGTGGTTGAAAAAATGAATTCGAGCTTCTCTTATGTTAAGAA 1920
Db      1861 GAAAGACAGATAGAGTGGTTGAAAAAATGAATTCGAGCTTCTCTTATGTTAAGAA 1920
Qy      1921 GAAAAAGACATCTTGATGATGAAAAATAGATGCGGAGGAGAAATTCGATCAAGCTG 1980
Db      1921 GAAAAAGACATCTTGATGATGAAAAATAGATGCGGAGGAGAAATTCGATCAAGCTG 1980
Qy      1981 GAGCTAGACACATGAAATCAGACGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040
Db      1981 GAGCTAGACACATGAAATCAGACGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040

RESULT 8
ABL95180 standard; cDNA; 2040 BP.
XX      ABL95180;
AC      ABL95180;
XX      19-JUL-2002 (first entry)
DT      19-JUL-2002 (first entry)
XX      Human B305D splice variant cDNA sequence SEQ ID NO 375.
DE      Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX      gene therapy; gene; ss.
KM      Homo sapiens.
XX      OS
XX      US200202248-A1.
PN      21-FEB-2002.
XX      21-FEB-2002.
PD      12-JAN-2001; 2001US-00759143.
XX      12-JAN-2001; 2001US-00759143.
PF      25-FEB-1997; 97US-00806099.
XX      25-FEB-1997; 97US-00806099.
PR      01-AUG-1997; 97US-00904804.
XX      01-AUG-1997; 97US-00904804.
PR      10-FEB-1998; 98US-00020956.
XX      10-FEB-1998; 98US-00020956.
PR      25-FEB-1998; 98US-00030607.
XX      25-FEB-1998; 98US-00030607.
PR      14-JUL-1998; 98US-00115453.
XX      14-JUL-1998; 98US-00115453.
PR      23-SEP-1998; 98US-00159812.
XX      23-SEP-1998; 98US-00159812.
PR      15-JAN-1999; 99US-00232149.
XX      15-JAN-1999; 99US-00232149.
PR      09-APR-1999; 99US-00288946.
XX      09-APR-1999; 99US-00288946.

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PR      13-JUL-1999; 99US-00352616.
PR      12-NOV-1999; 99US-00439313.
PR      18-NOV-1999; 99US-00443686.
PR      14-JAN-2000; 2000US-00483672.
PR      27-MAR-2000; 2000US-00536857.
PR      09-MAY-2000; 2000US-00568100.
PR      12-MAY-2000; 2000US-00570737.
PR      13-JUN-2000; 2000US-00593793.
PR      27-JUN-2000; 2000US-00605783.
PR      10-AUG-2000; 2000US-00636215.
PR      29-AUG-2000; 2000US-00651236.
PR      06-SEP-2000; 2000US-00657279.
PR      02-OCT-2000; 2000US-00679426.
PR      10-OCT-2000; 2000US-00685166.
XX      (XUJ/) XU J.
PA      (DILL/) DILLON D C.
PA      (MITC/) MITCHAM J L.
PA      (HARL/) HARLOCKER S L.
PA      (JIAN/) JIANG Y.
PA      (KALO/) KALOS M D.
PA      (FANG/) FANGER G R.
PA      (RETT/) RETTER M W.
PA      (STOL/) STOLK J A.
PA      (DAYC/) DAY C H.
PA      (VEDV/) VEDVICK T S.
PA      (CART/) CARTER D.
PA      (LISX/) LI S X.
PA      (WANG/) WANG A.
PA      (SKER/) SKIRKY Y A W.
PA      (HEPL/) HEPLER W T.
PA      (HEND/) HENDERSON R A.
XX      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI      Li SX, Wang A, Skirky YAW, Hepler WT, Henderson RA;
XX      WPI; 2002-255649/30.
DR      WPI; 2002-255649/30.
XX      New prostate-specific polynucleotides for diagnosing and treating
PT      diseases, in particular prostate cancer, and as markers for the
PT      progression of cancer.
XX      Claim 1; SEQ ID NO 375; 87bp; English.
XX      The present invention provides prostate-specific coding sequences and
CC      their encoded proteins. These can be used in the diagnosis and treatment
CC      of cancers, particularly prostate cancer. The present sequence is a cDNA
CC      described in the invention
XX      SQ
XX      Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
XX      Query Match 100.0%; Score 2040; DB 6; Length 2040;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGGTGTGAGTGGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTC 60
Db      1 ATGGTGTGAGTGGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTC 60
Qy      61 AGAGCAGATGAGCAAGTGTGCTGCGGCTGCTCTTCCCTGCTGCAAGGAGCGCAAG 120
Db      61 AGAGCAGATGAGCAAGTGTGCTGCGGCTGCTCTTCCCTGCTGCAAGGAGCGCAAG 120
Qy      121 AGCAAGTGGGCACTTCTGAGACAGACAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db      121 AGCAAGTGGGCACTTCTGAGACAGACAGCACTGCTATGAAGCACTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGCGGCACTGCTCTGCTGCTGCAAGGAGAGTGGCAAGACGTG 240
Db      181 ATGGGCAAGTGTGCGGCACTGCTCTGCTGCTGCAAGGAGAGTGGCAAGACGTG 240
Qy      241 GGGCGTTCTGAGACAGACAGCACTCTGCTATGAAGCACTCAGAGCAAGATGGCAAG 300

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Db 241 GCGCGCTTGTGAGACGACGACTGTGCTATGTAAGACACTGAGAAACAATGGGCAAG 300
Qy 301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCGAAGACGAGTGGCGCTTGG 360
Db 301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCGAAGACGAGTGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGTGCCTTCATGAGAGCCAGGTACCAAGTCCGTGGAGAGATCTG 420
Db 361 GGAAGCTACGATGACAGTGCCTTCATGAGAGCCAGGTACCAAGTCCGTGGAGAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCTGCTGGGTAAGTCCCAAGAAAGATCTCATCTGATG 480
Db 421 GACAGCTCCACAGAGCTGCTGCTGGGTAAGTCCCAAGAAAGATCTCATCTGATG 480
Qy 481 CTCAGGGACACTGACGTGTAACAAGAGCAAGCAAAAGAGATCTGCTTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGTAACAAGAGCAAGCAAAAGAGATCTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAATAATCTCTGTGGAACAGATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAATAATCTCTGTGGAACAGATGTCACTTAAT 600
Qy 601 GTCTTGGACACAAAGAGAGACAGCTCTGATTAAGGCGGTACAATGCCAGAAAGATGA 660
Db 601 GTCTTGGACACAAAGAGAGACAGCTCTGATTAAGGCGGTACAATGCCAGAAAGATGA 660
Qy 661 TGTGGGTTATGTTGTGTAACAATGGCACTGATCCAAATATTCGAGATGATGGAAT 720
Db 661 TGTGGGTTATGTTGTGTAACAATGGCACTGATCCAAATATTCGAGATGATGGAAT 720
Qy 721 ACCACTGTGCACTACGCTATCTATAATGAAGATTAATATGAGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTGTGCACTACGCTATCTATAATGAAGATTAATATGAGCCAAAGCACTGCTCTTA 780
Qy 781 TATGTGCTGATATGCAATCAAAAAACAAGCATGCGCTCACACACTGTTACTTGGTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAAACAAGCATGCGCTCACACACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAATCGTGAATTTTAAATCAAGAAAAACGAAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAATCGTGAATTTTAAATCAAGAAAAACGAAATTTAAATGA 900
Qy 901 CTGAGATAGATGAGAGAGCTGCTCATACTTGTGTAATGTTGGATCAGCAAGTATA 960
Db 901 CTGAGATAGATGAGAGAGCTGCTCATACTTGTGTAATGTTGGATCAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTGAGCAAAATATGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
Qy 1021 GGCAGAGATAGTCTGTTCTAGTCAATCAATGTAATTTGCAAGTACTTCTGACTAC 1080
Db 1021 GGCAGAGATAGTCTGTTCTAGTCAATCAATGTAATTTGCAAGTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAAACAAGCTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAAACAAGCTTAAAG 1140
Qy 1141 CTGACATCAAGAGAGAGTCACAAGAGTTCAAGGAGTGAATTAAGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAAGAGAGAGTCACAAGAGTTCAAGGAGTGAATTAAGCCAGCCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAAATTAATAGATGTAATGAGAGTGAAGAGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATAGATGTAATGAGAGTGAAGAGTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGTAATATGAGGATTAAGTAAAGAACTGACTAATGATGCTGCTGAC 1320
Db 1261 AAGCATGAAGTAATATGAGGATTAAGTAAAGAACTGACTAATGATGCTGCTGAC 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACCTGAAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACCTGAAATCAGCAATTT 1380

Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACACTGAAATCAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
Qy 1441 AAAAGATGCGCAAAATTAATCTCTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
Db 1441 AAAAGATGCGCAAAATTAATCTCTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGTCACAAGAGCTTGAAGGCAAGTAAATGGCCAGCCAGAGAAAAAGTCT 1560
Db 1501 TCAGAGAAAGTCACAAGAGCTTGAAGGCAAGTAAATGGCCAGCCAGAGAAAAAGTCT 1560
Qy 1561 CAAGAACCAAGAAATTAATGAAGATGTAATGAGAGCTAGAAATTTTAATGGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATGAAGATGTAATGAGAGCTAGAAATTTTAATGGCTATCGAA 1620
Qy 1621 GAAATGAAGAGCAGAAAGTACTATGCGAATCCAGAAAACTGACTAATGATGCC 1680
Db 1621 GAAATGAAGAGCAGAAAGTACTATGCGAATCCAGAAAACTGACTAATGATGCC 1680
Qy 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCCAGAGAAAGAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCCAGAGAAAGAGCAACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACATGAGAAATGAAGATATCAAGTGAACAAATGAATCTGAG 1800
Db 1741 CAGCAATTTCTGACACATGAGAAATGAAGATATCAAGTGAACAAATGAATCTGAG 1800
Qy 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGATCTGATCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGATCTGATCATGAA 1860
Qy 1861 GAAAGCAGATGAGATGGTGAAGAAATGAATTTGAGCTTTCTTTAGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAGATGGTGAAGAAATGAATTTGAGCTTTCTTTAGTTGAAGAA 1920
Qy 1921 GAAAAAGCATCTTCATGAAAAATGTAACGTTGCGGAGAAATTTGCCATGCTTAAGACTG 1980
Db 1921 GAAAAAGCATCTTCATGAAAAATGTAACGTTGCGGAGAAATTTGCCATGCTTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAATCAAGAGCCAGCTTAAGAAAAAAGAAAAAAGAAAAA 2040
Db 1981 GAGCTAGACACATGAATCAAGAGCCAGCTTAAGAAAAAAGAAAAAAGAAAAA 2040

RESULT 9
AAS9859
ID AAS9859 standard; cDNA; 2040 BP.
XX
AC AAS9859;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11a1 splice variant B11C-9,16.
XX
KW Human; breast cancer; PCR primer; ss; cytosolic; immunostimulant;
XX
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN W0200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
XX
PR 08-JUN-2000; 2000US-00590583.
XX
PR 26-OCT-2000; 2000US-00699295.
XX
PR 16-MAR-2001; 2001US-00810936.
XX

(CORI-) CORIXA CORP.
XX Fundakie TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skeiky YAM, Harlocker SL, Day CH;
XX WPI; 2002-089919/12.
DR P-PSDB; AAU74379.
XX
PT New breast tumor proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response.
XX
PS Claim 1; Page 224-225; 245bp; English.
XX
CC The invention relates to novel breast tumor polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
CC represent novel human breast cancer protein coding sequences and PCR
CC primers of the invention
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGATGAGTTGATTCATGCGCGCTCTTCTGTGAAGAACATTTGGTCTC 60
DB 1 ATGTGTTGATGAGTTGATTCATGCGCGCTCTTCTGTGAAGAACATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTCCCTGCTGCAAGGAGACGGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTCCCTGCTGCAAGGAGACGGGCAAG 120
QY 121 AGCAAGTGGGCACTTTGAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTTGAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
QY 241 GGGGCTTTGGGAGACCAAGGACGACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTTGGGAGACCAAGGACGACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGTCTTATGAGAGCCAGGATACCAAGTCCGTGGAGAAATCTG 420
DB 361 GGAAGCTACGATGACAGTGTCTTATGAGAGCCAGGATACCAAGTCCGTGGAGAAATCTG 420
QY 421 GAAAGCTCCACAGAGCTGCTGTGGGAGTAAAGTCCCGAGAAAGATCTATCTGTCATG 480
DB 421 GAAAGCTCCACAGAGCTGCTGTGGGAGTAAAGTCCCGAGAAAGATCTATCTGTCATG 480
QY 481 CTGAGGAGACCTGACGATGAAAGAGCAAGCAAGCAAGAGAGAGTGTCTTCACTTGGCC 540
DB 481 CTGAGGAGACCTGACGATGAAAGAGCAAGCAAGCAAGAGAGTGTCTTCACTTGGCC 540
QY 541 TCTGCGAATGGGAATTCAGAAATGTAATAAATCTCTGTGAGACAGATGTAATTAAT 600
DB 541 TCTGCGAATGGGAATTCAGAAATGTAATAAATCTCTGTGAGACAGATGTAATTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGAA 660

DB 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGAA 660
QY 661 TGTGCGTAAATGTTGTGGAACAGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTAAATGTTGTGGAACAGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGACATACGCTATCTATTAAGAAATTAATGGCCAAAGACGCTCTTGA 780
DB 721 ACCACTCTGACATACGCTATCTATTAAGAAATTAATGGCCAAAGACGCTCTTGA 780
QY 781 TATGTGCTGATATGCAATCAAAAAAAGCATGGGCTCACACACTGTACTTGGTGA 840
DB 781 TATGTGCTGATATGCAATCAAAAAAAGCATGGGCTCACACACTGTACTTGGTGA 840
QY 841 CATGACAAAAACAGCAAGTCGTGAATTTTAAATCAGAAAAAAGCAATTTAAATGCA 900
DB 841 CATGACAAAAACAGCAAGTCGTGAATTTTAAATCAGAAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATGATATGGAAGAGACTGCTCTCATCTTCTGTATGTTGTGATCAGCAATATA 960
DB 901 CTGGATGATATGGAAGAGACTGCTCTCATCTTCTGTATGTTGTGATCAGCAATATA 960
QY 961 GTGAGCTTCTACTTGAAGAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTTGAAGAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTTAAATCTTTCTGAAAAACAGCAATCAGAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTTAAATCTTTCTGAAAAACAGCAATCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGGAGTAAGAAATGCGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGGAGTAAGAAATGCGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAAACAGAAATTAATAAGATGTGATAGAGAGTTGAAGAAATGAAAG 1260
DB 1201 ATGTCTCAAGAAACAGAAATTAATAAGATGTGATAGAGAGTTGAAGAAATGAAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTGGATTAATGAAAACTTAATCTATGCTGCTGCTG 1320
DB 1261 AAGCATGAAAGTAAATATGTGGATTAATGAAAACTTAATCTATGCTGCTGCTG 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGAGAGAAACCTGAATAATGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGAGAGAAACCTGAATAATGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGATATCACAAATTTTGGAAATTTAGTTCTGACTCAAGAA 1440
DB 1381 CCTGACAAAGAAAGTAAAGATATCACAAATTTTGGAAATTTAGTTCTGACTCAAGAA 1440
QY 1441 AAAAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACTTAAGCTGACA 1500
DB 1441 AAAAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCAAGTAAATGGCCAGCAAGAAATATCT 1560
DB 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCAAGTAAATGGCCAGCAAGAAATATCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAGAGACGGAAGTACTATGTCGATTTCCAGAAAACTTGAATTAATGCTGCC 1680
DB 1621 GAAATGAGAGACGGAAGTACTATGTCGATTTCCAGAAAACTTGAATTAATGCTGCC 1680
QY 1681 ACTGTGCGAATGGTATGATGATTAATTCCTCAAGAAAGAGCAAGCACTGAAAG 1740

Db 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCCAGAGAGACGAAACACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTACGAGAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTACGAGAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAGAGACGAACTGGAATATTAACAGATGAGATTTGATTCAGAA 1860
Db 1801 AAGCAATTTTGTGAGAGACGAACTGGAATATTAACAGATGAGATTTGATTCAGAA 1860
Qy 1861 GAAAGCAATGAAAGTGTGTAAGAAATGAATTTGAGCTTTCTTTAGTTGTAAGAA 1920
Db 1861 GAAAGCAATGAAAGTGTGTAAGAAATGAATTTGAGCTTTCTTTAGTTGTAAGAA 1920
Qy 1921 GAAAAAGCATCTTGATGATGAAATAGTACGTTGCGGAGAAATTCGCTAAGACTG 1980
Db 1921 GAAAAAGCATCTTGATGATGAAATAGTACGTTGCGGAGAAATTCGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAAATGAAATGAAATGAAATTCGAGCTTTCTTTAGTTGTAAGAA 2040
Db 1981 GAGCTAGACACATGAAATGAAATGAAATGAAATTCGAGCTTTCTTTAGTTGTAAGAA 2040
RESULT 10
ACC95344
ID ACC95344 standard; cDNA; 2040 BP.
XX ACC95344;
AC ACC95344;
DT 28-AUG-2003 (first entry)
XX Prostate tumour specific cDNA sequence SEQ ID 375.
DE Prostate tumour specific cDNA sequence SEQ ID 375.
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KM Immune response; prostate cancer; ss.
XX Homo sapiens.
OS WO200289747-A2.
PN 14-NOV-2002.
XX 09-MAY-2002; 2002WO-US014753.
PF 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kales MW, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAM, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolisC, Foy TM, Matanabe Y;
PI Deng T;
XX MPI; 2003-167130/16.
DR
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or creating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX Example 11; Page 416; 691pp; English.
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 8; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGTGGTTGAGGTTGATTCATGCGCGGCTGCTCTTGTAAGAACCATTTGGTCTC 60
Db 1 ATGGTGGTTGAGGTTGATTCATGCGCGGCTGCTCTTGTAAGAACCATTTGGTCTC 60
Qy 61 AGGAGCAAGTGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGGAGCAAGTGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Qy 121 AGCAAGTGGGCACTTCTGAGAGACGACGACTGCTGATGAGACACTGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGACGACGACTGCTGATGAGACACTGAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGACGTC 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGACGTC 240
Qy 241 GGGCGCTTCTGAGAGACGACGACTGCTGATGAGACACTGAGAGCAAGTGGGCAAG 300
Db 241 GGGCGCTTCTGAGAGACGACGACTGCTGATGAGACACTGAGAGCAAGTGGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGTGGGCGCTTGG 360
Qy 361 GGAAGCTAGATGACAGTGGCTTCAATGAGCCAGATACAGTCCGTTGAGAGATCTG 420
Db 361 GGAAGCTAGATGACAGTGGCTTCAATGAGCCAGATACAGTCCGTTGAGAGATCTG 420
Qy 421 GACCAAGCTTCCACAGAGCTGCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATG 480
Db 421 GACCAAGCTTCCACAGAGCTGCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATG 480
Qy 481 CTCAGGACACTGACGTTGCAAGAGGCAAGAGGCAAGAGGAGTCTTCAATCTGAGC 540
Db 481 CTCAGGACACTGACGTTGCAAGAGGCAAGAGGCAAGAGGAGTCTTCAATCTGAGC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGATGTCATCTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGATGTCATCTTAAT 600
Qy 601 GTCTTGGACACAAAGAGGACAGCTCTGATTAAGGCCGTACAAATGCCAGAAAGTGA 660
Db 601 GTCTTGGACACAAAGAGGACAGCTCTGATTAAGGCCGTACAAATGCCAGAAAGTGA 660
Qy 661 TGTGGCTTAATGTTGCTGGAACATGAGCACTGATCCAAATATTCGAGATGGAAT 720
Db 661 TGTGGCTTAATGTTGCTGGAACATGAGCACTGATCCAAATATTCGAGATGGAAT 720
Qy 721 ACCACTCTGACACTACGCTATCTAATAGAAATTAATGAGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTCTGACACTACGCTATCTAATAGAAATTAATGAGCCAAAGCACTGCTCTTA 780
Qy 781 TATGCTGCTGATATGATCAAAAAACAAGCATGCGCTCACACCTGTTACTTGGTGTGA 840
Db 781 TATGCTGCTGATATGATCAAAAAACAAGCATGCGCTCACACCTGTTACTTGGTGTGA 840
Qy 841 CATGAGCAAAAAACAGAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATATGATATGAGAGAGTGGCTCTCATCTGCTGATGTTGGATACAGCAAGTATA 960
Db 901 CTGATATGATATGAGAGAGTGGCTCTCATCTGCTGATGTTGGATACAGCAAGTATA 960
Qy 961 GTGACGCTTCTAATCTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGACGCTTCTAATCTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020

```

QY 1021 GCCAGAGATGTCGTTCTAGCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
    |||
Db 1021 GCCAGAGATGTCGTTCTAGCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
    |||
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCACAAAAGGTTCAAAGGCGAGTAAATAGCCAGAGAGAAA 1200
    |||
Db 1141 CTGACATCAGAGAGAGAGTCACAAAAGGTTCAAAGGCGAGTAAATAGCCAGAGAGAAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATTAAGAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
    |||
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAAGTAAATATGTTGAGTACTAGAAAACTGACTATGCTGCTGCG 1320
    |||
Db 1261 AAGCATGAAAAGTAAATATGTTGAGTACTAGAAAACTGACTATGCTGCTGCG 1320
QY 1321 AATGCTGATTAATGATTAATTTCTCTCAAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
    |||
Db 1321 AATGCTGATTAATGATTAATTTCTCTCAAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAGAGAGTATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
    |||
Db 1381 CCTGACAAAGAGAGAGTATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||
Db 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCACAAAAGGCTTGAAGGCGAGTGAATATGCGAGCCAGAGAAAGATCT 1560
    |||
Db 1501 TCAGAGAGAGAGTCACAAAAGGCTTGAAGGCGAGTGAATATGCGAGCCAGAGAAAGATCT 1560
QY 1561 CAAAGAACCGAATTAATTAAGATGCTGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620
    |||
Db 1561 CAAAGAACCGAATTAATTAAGATGCTGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCAATTCACGAAAAACCTGACTAATGCTGCC 1680
    |||
Db 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCAATTCACGAAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGATGATGATTAATTTCTCTCAAAGAGAGAGCAACCTGAAAGC 1740
    |||
Db 1681 ACTGCTGGCAATGATGATGATTAATTTCTCTCAAAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTCTGCACTGAGATGAAAGATATCAAGTGAAGAAATTAATGATCTCAG 1800
    |||
Db 1741 CAGCAATTTCTCTGCACTGAGATGAAAGATATCAAGTGAAGAAATTAATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAGATTCTGATTCATGAA 1860
    |||
Db 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAGATTCTGATTCATGAA 1860
QY 1861 GAAAGACAGATAGAACTGTTGAAAAATTAATTAATTTCTGAGTTTCTCTTATGTTGAAGAA 1920
    |||
Db 1861 GAAAGACAGATAGAACTGTTGAAAAATTAATTAATTTCTGAGTTTCTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACCTTGGGAGAGAAATTTGCCATGCTTAAAGCTG 1980
    |||
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACCTTGGGAGAGAAATTTGCCATGCTTAAAGCTG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCAGCTAAAAATTAATTAATTAATTAATTAATTAATTA 2040
    |||
Db 1981 GAGCTAGACACATGAAACATCAGAGCAGCTAAAAATTAATTAATTAATTAATTAATTAATTA 2040

```

RESULT 11
ADA11382
ID ADA11382 standard; cDNA; 2040 BP.

```

AC ADA11382:
XX
XX 06-NOV-2003 (first entry)
DT
XX
DE Human breast cancer specific cDNA B11C-9.16.
XX
XX ss; gene; human; breast cancer; cytosolic; tumour; gene therapy.
XX
XX Homo sapiens.
XX
XX US2002165371-A1.
XX
XX
XX 07-NOV-2002.
XX
XX
XX 07-AUG-2001; 2001US-00924400.
XX
XX
XX 11-JAN-1996; 96US-00585392.
XX 10-JAN-1997; 97MO-US000485.
XX 09-APR-1997; 97US-00838762.
XX 11-DEC-1997; 97US-00991789.
XX 17-APR-1998; 98US-00062451.
XX 09-APR-1999; 99US-00289198.
XX 28-OCT-1999; 99US-00429755.
XX 23-MAR-2000; 2000US-00534825.
XX 24-MAY-2000; 2000US-00577505.
XX 08-JUN-2000; 2000US-00590583.
XX 26-OCT-2000; 2000US-00699295.
XX 16-MAR-2001; 2001US-00810936.
XX
XX (PRUD/) FRUDAKIS T N.
XX (REED/) REED S G.
XX (SMIT/) SMITH J M.
XX (MISH/) MISHNER L E.
XX (DILL/) DILLON D C.
XX (RETT/) RETTER M W.
XX (WANG/) WANG A.
XX (SKET/) SKETKY Y A W.
XX (HARL/) HARLOCKER S L.
XX (DAYC/) DAY C H.
XX (LISX/) LI S X.
XX (DENG/) DENG T.
XX
XX Frudakis TM, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
XX Wang A, Skeiky YAM, Harlocker SL, Day CH, Li SX, Deng T,
XX P-PSDB; ADA11385.
XX
XX WPI; 2003-247262/24.
XX
XX New breast tumor proteins nucleic acids encoding such proteins, useful in
XX diagnosing, preventing and/or treating diseases such as cancer,
XX particularly breast cancer, and as markers for detecting the presence of
XX a cancer.
XX
XX Claim 1; Page 141; 190pp; English.
XX
XX The invention relates to a breast tumour polynucleotide selected from one
XX of the 275 fully defined nucleotide sequences (a) given in the
XX specification, including their complements, sequences consisting of at
XX least 20 contiguous residues of a sequence in (a), sequences that
XX hybridise to a sequence in (a) under moderately stringent conditions,
XX sequences having at least 75% or 90% identity to a sequence in (a), or
XX degenerate variants of a sequence in (a). Also included are an isolated
XX polypeptide (ii) (comprising an amino acid sequence selected from
XX sequences encoded by (a), sequences having at least 70% or 90% identity
XX to a sequence encoded by (a), sequences of 30 fully defined amino acid
XX sequences (c), and sequences having at least 70% or 90% identity to a
XX sequence in (c)), expression vectors comprising (a), a host cell
XX transformed or transfected with the expression vector, an isolated
XX antibody or its antigen-binding fragment that specifically binds to (ii),
XX a method for detecting the presence of a cancer in a patient, a fusion
XX protein comprising at least one polypeptide (ii), an oligonucleotide that
XX hybridises to (a), under moderately stringent conditions, a method for
XX stimulating and/or expanding T cells specific for a tumour protein (by

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CC contacting T cells with at least one component selected from (a), (ii)
CC and antigen-presenting cells that express (ii), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (ii), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosing,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a breast cancer specific cDNA of the
CC invention.

XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 8; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGCTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGACCATTTGCTTC 60
DB 1 ATGGTGCTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGACCATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGTGCTCCGTTGCTCCGTCGCAAGGAGCCGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGTGCTCCGTTGCTCCGTCGCAAGGAGCCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGTGATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGTGATGAAGACACTCAGAGCAAG 180
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGTGATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGTGATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GGGCTTCTGAGACACAGACGACTGTGATGAAGACACTCAGAGCAAGTGGGCAAG 300
DB 241 GGGCTTCTGAGACACAGACGACTGTGATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGGAGGAGGAGGAG 360
DB 301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGGAGGAGGAGGAG 360
QY 361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGAGAAAGTCTG 420
DB 361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGAGAAAGTCTG 420
QY 421 GACAAGCTCAGAGAGTGTGAGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
DB 421 GACAAGCTCAGAGAGTGTGAGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
QY 481 CTCAGGAGCACTGACGTGAAACAAGAAAGCAAGCAAAAGAGAGCTCTCTACATCTGGCC 540
DB 481 CTCAGGAGCACTGACGTGAAACAAGAAAGCAAGCAAAAGAGAGCTCTCTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAAGTCTCTCTGGAACAGAGTCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAAGTCTCTCTGGAACAGAGTCAACTTAAT 600
QY 601 GTCCTTGAACAACAAAAGAGAGAGAGCTGTGATTAAGGCGGTAAAGCCAGAGAAAGTGA 660
DB 601 GTCCTTGAACAACAAAAGAGAGAGAGCTGTGATTAAGGCGGTAAAGCCAGAGAAAGTGA 660
QY 661 TGTGCTTAATGTTGCTGAAACATGCACTGATCCAAATTTCCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGAAACATGCACTGATCCAAATTTCCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTAATTAAGAAATTAATGAGCAAGCACTGCTCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTAATTAAGAAATTAATGAGCAAGCACTGCTCTTA 780

QY 781 TATGGTCTGATATGGAATCAAAAACAGACATGGCTTCACACACTGTTAGTGATGA 840
DB 781 TATGGTCTGATATGGAATCAAAAACAGACATGGCTTCACACACTGTTAGTGATGA 840
QY 841 CATGAGCAAAAACAGACATGGCTTCAGAAATTTTAAATCAAGAAAAAGCCAAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGACATGGCTTCAGAAATTTTAAATCAAGAAAAAGCCAAATTTAAATGCA 900
QY 901 CTGATATGATGAAAGAGCTGCTCATCTTGTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATGAAAGAGCTGCTCATCTTGTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGTATGATGAAAGAGCTGCTCATCTTGTGATGTTGTGATCAGCAAGTATA 960
DB 961 GTGAGTATGATGAAAGAGCTGCTCATCTTGTGATGTTGTGATCAGCAAGTATA 960
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGCAATCCAGAACAGATTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGCAATCCAGAACAGATTAAAG 1140
QY 1141 CTGATATGAGAAAGAGTCAAAAAGTTCAAAAGCAAGTAAATAGCCAGCAGAGAA 1200
DB 1141 CTGATATGAGAAAGAGTCAAAAAGTTCAAAAGCAAGTAAATAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGAGGATTAATCTGAAAAACCTGACTAATGCTGCTGCTG 1320
DB 1261 AAGCATGAAAGTAAATATGAGGATTAATCTGAAAAACCTGACTAATGCTGCTGCTG 1320
QY 1321 AATGGTAAATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGGTAAATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCAATTTGCTGACTACAAAGAA 1440
DB 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCAATTTGCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAAAATCTCTGAAAAACAGCAACCCAGAAACAAAGCTTGAAGCTG 1500
DB 1441 AAACAGATGCCAAAAATCTCTGAAAAACAGCAACCCAGAAACAAAGCTTGAAGCTG 1500
QY 1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGAGTGAATATGCGCAGAGAGAGAGAGAGTCT 1560
DB 1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGAGTGAATATGCGCAGAGAGAGAGAGAGTCT 1560
QY 1561 CAAGAACAGAAATTAATAGATGCTGATAGAGAGTAAAGAAATTTTATGCTATCGAA 1620
DB 1561 CAAGAACAGAAATTAATAGATGCTGATAGAGAGTAAAGAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAGACAGAAAGTCTCATGTCGATTTCCAGAAAAACCTGATGATGCTG 1680
DB 1621 GAAATGAAGAGACAGAAAGTCTCATGTCGATTTCCAGAAAAACCTGATGATGCTG 1680
QY 1681 ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
DB 1681 ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1741 CAGCAATTTCTGACACTGAGATGATGATGATGATGATGATGATGATGATGATGATG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAAACCTGGAATATTAACAGATGATGATGATGATGAT 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAAACCTGGAATATTAACAGATGATGATGATGATGAT 1860

QY 1861 GAAAAGCAGATAGAGTGGTGGTAAAAATGATTTCTGAGCTTCTCTTAGTTAGTAA 1920
| | | | |
Db 1861 GAAAAGCAGATAGAGTGGTGGTAAAAATGATTTCTGAGCTTCTCTTAGTTAGTAA 1920
| | | | |
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTGCCATGCTAAGACTG 1980
| | | | |
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTGCCATGCTAAGACTG 1980
| | | | |
QY 1981 GAGCTAGACATGAAACATGACGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040
| | | | |
Db 1981 GAGCTAGACATGAAACATGACGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040
| | | | |
RESULT 12
ADCI5355
ID ADCI5355 standard; DNA; 2040 BP.
XX
AC ADCI5355;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human breast tumour protein DNA, SEQ ID 303.
XX
KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
XX ds.
OS Homo sapiens.
XX
PN WO2003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024917.
XX
PR 07-AUG-2001; 2001US-00924400.
XX 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
PA (CORI-) CORIXA CORP.
XX
XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
DR WPI; 2003-342398/32.
XX
PT New polynucleotide, useful for preparing a composition for diagnosing,
XX treating or preventing cancer.
PS
XX Example 1; SEQ ID NO 303; 308bp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which stimulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
| | | | |
QY 121 AGCAAGTGGGCACTTTCTGAGAGCAAGCACTCTGCTATGAAAGCACTCAGAGCAAG 180
| | | | |
Db 121 AGCAAGTGGGCACTTTCTGAGAGCAAGCAAGCACTCTGCTATGAAAGCACTCAGAGCAAG 180
| | | | |
QY 181 AAGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
| | | | |
Db 181 AAGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
| | | | |
QY 241 GCGGCTTCTGAGAGCAAGCAAGCACTCTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
| | | | |
Db 241 GCGGCTTCTGAGAGCAAGCAAGCACTCTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
| | | | |
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
| | | | |
Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
| | | | |
QY 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACACGTCCTGAGAGATCTG 420
| | | | |
Db 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACACGTCCTGAGAGATCTG 420
| | | | |
QY 421 GACAAAGCTCAGAGAGCTGCGTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCGTAA 480
| | | | |
Db 421 GACAAAGCTCAGAGAGCTGCGTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCGTAA 480
| | | | |
QY 481 CTCAGGGAACATGACGTGAAACAAGAGGCAAGCAAAAGAGAGCTCTTACATCTGCGC 540
| | | | |
Db 481 CTCAGGGAACATGACGTGAAACAAGAGGCAAGCAAAAGAGAGCTCTTACATCTGCGC 540
| | | | |
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGACGATGTCACTTAAT 600
| | | | |
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGACGATGTCACTTAAT 600
| | | | |
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGACGATGTCACTTAAT 600
| | | | |
QY 601 GTCTTGAACAACAAAAGAGAGCAGCTGATTAAGGCGGTCAATGCCAGGAAGTGA 660
| | | | |
Db 601 GTCTTGAACAACAAAAGAGAGCAGCTGATTAAGGCGGTCAATGCCAGGAAGTGA 660
| | | | |
QY 661 TGTGCGTTAATGTTCTGGAACATGGAACATGCCATCAATATTCAGATGATGAAAT 720
| | | | |
Db 661 TGTGCGTTAATGTTCTGGAACATGGAACATGCCATCAATATTCAGATGATGAAAT 720
| | | | |
QY 721 ACCACTCTGCACTACGCTATCTATATGAAAGTAAATTAATGCCAAGCACTGCTTAA 780
| | | | |
Db 721 ACCACTCTGCACTACGCTATCTATATGAAAGTAAATTAATGCCAAGCACTGCTTAA 780
| | | | |
QY 781 TATGCTGCTGATGATGAAATCAAAAACAAGATGCGCTCACACCACTGTTACTTGGTGA 840
| | | | |
Db 781 TATGCTGCTGATGATGAAATCAAAAACAAGATGCGCTCACACCACTGTTACTTGGTGA 840
| | | | |
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGCAATTTAAATGCA 900
| | | | |
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGCAATTTAAATGCA 900
| | | | |
QY 901 CTGATATGATGAAAGAGATGCTCTCAATCTTGTGATGTTGATCAGCAAGTATA 960
| | | | |
Db 901 CTGATATGATGAAAGAGATGCTCTCAATCTTGTGATGTTGATCAGCAAGTATA 960
| | | | |
QY 961 GTCAAGCTTCTTACCTGAGCAAAATTTGATGATTTCTCAAGATCTATCTGACAGAG 1020
| | | | |
Db 961 GTCAAGCTTCTTACCTGAGCAAAATTTGATGATTTCTCAAGATCTATCTGACAGAG 1020
| | | | |
QY 1021 GCCAGAGATATGCTGTTTCTGATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
| | | | |
Db 1021 GCCAGAGATATGCTGTTTCTGATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
| | | | |
QY 1081 AAAAGAAAACAGATCTTAAATCTCTTCTGAAAACAGCAATCCAGAACAACTTTAAAG 1140
| | | | |
Db 1081 AAAAGAAAACAGATCTTAAATCTCTTCTGAAAACAGCAATCCAGAACAACTTTAAAG 1140
| | | | |
QY 1141 CTGATCATGAGGAAGATGCAAAAGTTCAAAAGCAGTGAATATGACAGCAGAGAA 1200
| | | | |

Db 1141 CTGACATCAGAGGAGAGTCACAAAAGTTCAAAAGCATGAAAAATAGCCAGCCAGAGAAA 1200
 Qy 1201 ATGTCTCAAGAAACAGAAATTAATAGATGGATAGAGAGGTTGAAGAAATGAAG 1260
 Db 1201 ATGTCTCAAGAAACAGAAATTAATAGATGGATAGAGAGGTTGAAGAAATGAAG 1260
 Qy 1261 AAGCATGAAAGTAATATATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGAC 1320
 Db 1261 AAGCATGAAAGTAATATATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGAC 1320
 Qy 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACCTGAAAATACGCAATTT 1380
 Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACCTGAAAATACGCAATTT 1380
 Qy 1381 CCTGACAAAGAAAGTAAGATATCAAGAAATTTGGCAATTTGTTCTGACTACAAAGAA 1440
 Db 1381 CCTGACAAAGAAAGTAAGATATCAAGAAATTTGGCAATTTGTTCTGACTACAAAGAA 1440
 Qy 1441 AAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
 Db 1441 AAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
 Qy 1501 TCAGAGAAAGAGTCACAAAAGCTTTGAGGCGATGAAAAATGGCCAGCCAGAGAAAAGATT 1560
 Db 1501 TCAGAGAAAGAGTCACAAAAGCTTTGAGGCGATGAAAAATGGCCAGCCAGAGAAAAGATT 1560
 Qy 1561 CAAGAAACAGAAATTAATAGAGATGGTATAGAGAGCTAGAAAATTTTATGGCTATCGAA 1620
 Db 1561 CAAGAAACAGAAATTAATAGAGATGGTATAGAGAGCTAGAAAATTTTATGGCTATCGAA 1620
 Qy 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCGAATTTCCAGAAAACCTGACTAATGTGTGC 1680
 Db 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCGAATTTCCAGAAAACCTGACTAATGTGTGC 1680
 Qy 1681 ACTGCTGGCAATGTGTATATGATTAATTTCTCCAGAGAAAGCAACCTGAAAGC 1740
 Db 1681 ACTGCTGGCAATGTGTATATGATTAATTTCTCCAGAGAAAGCAACCTGAAAGC 1740
 Qy 1741 CAGCAATTTCTGACATGAGATGAAGAGTATCACAGTACGAAACAAATATATCTGAG 1800
 Db 1741 CAGCAATTTCTGACATGAGATGAAGAGTATCACAGTACGAAACAAATATATCTGAG 1800
 Qy 1801 AAGCAATTTTGTGAAGACAGAAACATGGAATATTAACAGATGAGATTGATTATGAA 1860
 Db 1801 AAGCAATTTTGTGAAGACAGAAACATGGAATATTAACAGATGAGATTGATTATGAA 1860
 Qy 1861 GAAAGACATATGAAAGTGTGAAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
 Db 1861 GAAAGACATATGAAAGTGTGAAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
 Qy 1921 GAAAAAGACATCTGATGAAAAATAGTAGTGGCGGAGAAATGGCCATGCTAAGACTG 1980
 Db 1921 GAAAAAGACATCTGATGAAAAATAGTAGTGGCGGAGAAATGGCCATGCTAAGACTG 1980
 Qy 1981 GAGCTAGACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040
 Db 1981 GAGCTAGACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040
 RESULT 13
 ADB13825
 ID ADB13825 standard; cDNA; 2040 BP.
 XX
 AC ADB13825;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human prostate specific cDNA B305 splice variant #10.
 XX
 KW Human; ss; prostate specific cDNA; cytosolic; immunostimulant;
 KW gene therapy; cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell.

XX Homo sapiens.
 OS
 XX
 PN US2003185830-A1.
 XX
 PD 02-OCT-2003.
 PF 12-NOV-2002; 2002US-00294025.
 PR 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00232149.
 PR 15-JAN-1999; 99US-00288946.
 PR 09-APR-1999; 99US-00352616.
 PR 13-JUL-1999; 99US-00439313.
 PR 12-NOV-1999; 99US-00443686.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00570737.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605763.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 PR 09-MAY-2002; 2002US-00144678.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Kalos MD;
 DR MPI: 2003-756193/71.
 DR P-PsDB; ADB13830.
 XX
 PT New isolated polypeptide for use in a vaccine for stimulating an immune
 PT response, or for treating or diagnosis cancer, preferably prostate
 PT cancer.
 XX
 PS Example 11; Page; 101pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising no more than
 CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
 CC peptides comprise a fragment ADB13563 of that contain naturally processed
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
 CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
 CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
 CC encoding the proteins and peptides, expression vectors, a host cell
 CC transformed with the vector, an isolated antibody (or antigen binding
 CC fragment) that specifically binds to the protein or peptide, detecting
 CC the presence of a cancer in a patient (comprising contacting a patient
 CC sample with a binding agent that binds to the peptides or a polypeptide
 CC appearing as ADB13563, detecting the amount of polypeptide that binds to
 CC the agent and comparing the amount of polypeptide to a predetermined cut-
 CC off value to determine the presence of cancer), a fusion protein
 CC comprising the peptides or proteins, stimulating or expanding T cells
 CC specific for a tumour protein comprising contacting T cells with the
 CC peptides or the isolated T cell population, treating prostate cancer in a
 CC patient comprising administering a composition comprising the peptides,
 CC nucleic acids, antibodies or compounds, determining the presence of a
 CC cancer in a patient and treating prostate cancer in a patient comprising
 CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocId=20030185830.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTTGATTCATGCGCGTCCCTCTTCTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGTGAGGTTGATTCATGCGCGTCCCTCTTCTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGTGGGCAAGTGTCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
DB 61 AGGAGCAAGTGGGCAAGTGTCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAAGCAAGCACTGCTATGAAGCACTGAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGTGAAGCAAGCACTGCTATGAAGCACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGTGTCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGTGTCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
QY 241 GGGGCTTCTGAGAGCAAGCACTGCTATGAAGCACTGAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGAGCAAGCACTGCTATGAAGCACTGAGAGCAAGTGGCAAG 300
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DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGGCAAGGAGTGGCGCTTGG 360
QY 361 GGAAGTACAGATGACAGTCTTCAATGAGCCAGGTACCACTGCGTGAAGATCTG 420
DB 361 GGAAGTACAGATGACAGTCTTCAATGAGCCAGGTACCACTGCGTGAAGATCTG 420
QY 421 GACAGCTTCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAGCTTCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
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DB 481 CTCAGGGAACAGTGAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
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DB 541 TCTGCAATGAGGAAATCAGAAAGTAAAGTCTCTGCTGCAAGCAAGTCTCAATTA 600
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DB 661 TGTGCTTATGTTGTGGAAGCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720
QY 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCT 780
DB 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCT 780

QY 781 TATGCTGTGATATGCAATCAAAAACAGACATGCTGACCACTGTTACTGTGTTA 840
DB 781 TATGCTGTGATATGCAATCAAAAACAGACATGCTGACCACTGTTACTGTGTTA 840
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DB 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAGCAATTTAAATGA 900
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DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCAAGTTACTTCTGACTAC 1080
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DB 1321 AATGTGATATGATTAATTTCTCAAGGAAGAGCAAGCACTGAAATATGACAAATTT 1380
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DB 1381 CCTGCAACGAAGGAAGATATCAAGAAATTTGCAATTTGATCTCAAGAAAGAA 1440
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DB 1501 TCAAGGAAGAGTCAAAAAGCTTGAAGGCAAGTAAATGSCCAGCCAGAGAAAAGATCT 1560
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DB 1681 ACTGCTGCAATGATGATGATTAATTTCTCAAGGAAGAGCAAGCACTGTAAGAC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAAAATATGACTGAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAAAATATGACTGAG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACACTGAAATATTAACAGATGATTTCTGATTAAGAA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACACTGAAATATTAACAGATGATTTCTGATTAAGAA 1860


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QY 1861 GAAACAGATAGAGTGTGTAAGAAAAATGAAATTCAGCTTCTCTAGTTGTAGAAA 1920
DB 1861 GAAACAGATAGAGTGTGTAAGAAAAATGAAATTCAGCTTCTCTAGTTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTCCGGGAGAAATTCGCACTGAAGCTG 1980
DB 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTCCGGGAGAAATTCGCACTGAAGCTG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTT 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTT 2040

RESULT 14
ADG26241
ID ADG26241 standard; cDNA; 2040 BP.
XX
AC ADG26241;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human prostate-specific CDNA #360.
XX
KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;
KM cytostatic.
XX
OS Homo sapiens.
XX
PN US2003157089-A1.
XX
PD 21-AUG-2003.
XX
PF 09-MAY-2002; 2002US-00144678.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00433913.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA,
PI Kalos MD, Fanger GR, Ratter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Basolisc, Foy TM, Watanabe Y;
PI Meagher MJ, Deng T;
XX
XX MPI; 2003-777973/73.
DR P-PSDB; ADG26246.
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XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
PS Example 11; SEQ ID NO 375; 99pp; English.
XX
CC The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGGTGTTGAGAGTTGATTCATGCCGGCTGCTCTTCTGTAGAAGACATTTGCTTC 60
DB 1 ATGGTGTTGAGAGTTGATTCATGCCGGCTGCTCTTCTGTAGAAGACATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 ACCAAGTGGGCACTTTGTGAGACCAAGCACTGTCTATGAAGACATTCAGAGCAAG 180
DB 121 ACCAAGTGGGCACTTTGTGAGACCAAGCACTGTCTATGAAGACATTCAGAGCAAG 180
QY 181 ATGGGCAATGTGTCGCCGCACTGCTTCCCTGCTCTCAAGGAGAGTGGCAAGCACTG 240
DB 181 ATGGGCAATGTGTCGCCGCACTGCTTCCCTGCTCTCAAGGAGAGTGGCAAGCACTG 240
QY 241 GCGGCTTGTGAGACCAAGCACTGTCTATGAAGACATTCAGAGCAAGTGGGCAAG 300
DB 241 GCGGCTTGTGAGACCAAGCACTGTCTATGAAGACATTCAGAGCAAGTGGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGTGCTGCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
QY 361 GAGACACTAGTGAAGTGTGCTTCAATGAGAGCCAGGTATCACTGCTGTGAAGATCTG 420
DB 361 GAGACACTAGTGAAGTGTGCTTCAATGAGAGCCAGGTATCACTGCTGTGAAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCGAAGAAAGATCTCATCGCATG 480
DB 421 GACAAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCGAAGAAAGATCTCATCGCATG 480
QY 481 CTCAGGAGACATGAGCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540
DB 481 CTCAGGAGACATGAGCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540
QY 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGTGACAGAGATGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGTGACAGAGATGTCACTTAAT 600
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DB 601 GTCTTGAACAACAAAAGAGAGCAGCTGTATTAAGGCGGTCAATGCCAGGAAGTGA 660
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DB 661 TGTGCTTAATGTTCTGTGAACATGGCACTGATCCAAATATTCAGATGATGTAAT 720
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Db 961 GTGAGGCTTCTACTTGAAGCAAAATATGATGATCTTTCACAAATCTATCTGACAGAGC 1020
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Db 1981 GAGCTAGACACATGAAATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040
RESULT 15
AAA06600 standard; cDNA; 2040 BP.
ID AAA06600;
AC AAA06600;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:375.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX immunogenic; cytostatic; vaccine; ss.
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JUN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
XX
PR 14-JUL-1998; 98US-00116134.
XX
PR 23-SEP-1998; 98US-00159812.
XX
PR 23-SEP-1998; 98US-00159822.
XX
PR 15-JAN-1999; 99US-00232149.
XX
PR 15-JAN-1999; 99US-00232880.
XX
PR 09-APR-1999; 99US-00288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
DR New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 50; Page 223-224; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PRP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idiotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AA082000 to AA082020 represent sequences used in the exemplification of
CC the present invention
XX
XX Sequence 2040 BP; 716 A; 393 C; 500 G; 431 T; 0 U; 0 Other;

Query Match 97.5%; Score 1989; DB 3; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ATGGTGGTGAAGTATTCATGCGCGCTCTCTTGTGAGAAAGCAATTTGGTCTC 60
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DB 61 AGGAGCAATAGGCGAAAGTGTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
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DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
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DB 241 GGGGCTTCTGAGACACAGACACTCTGTATGAAACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
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DB 361 GGAAGCTACGATGACAGTGTCTTATGAGACCCAGGTACCACTGCTGAGAAAGATCTG 420
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DB 601 GTCTTGAACAACAAAAGAGAGACGCTGTATAAAGCCGTACAAATGCGAGAAAGATGAA 660
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DB 661 TGTGCGTTAATGTTGCTGAAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
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DB 721 ACCACTGTGACACTGCTATCTAATTAAGATTAATTAATGCGCAAGCACTGCTTAA 780
QY 781 TATGCTGTGATATGAAATCAAAAACAGCAATGCGCTCACACACTGTAACTTGTATG 840
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	2040	100.0	2040	3	US-09-352-616A-375 Sequence 375, App
3	2040	100.0	2040	3	US-09-289-198-303 Sequence 303, App
4	2040	100.0	2040	3	US-09-636-215-375 Sequence 375, App
5	2040	100.0	2040	3	US-09-685-166A-375 Sequence 375, App
6	2040	100.0	2040	3	US-09-429-755-303 Sequence 303, App
7	2040	100.0	2040	3	US-09-679-426-375 Sequence 375, App
8	2040	100.0	2040	3	US-09-759-143-375 Sequence 375, App
9	2040	100.0	2040	3	US-09-651-236-375 Sequence 375, App
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12	2040	100.0	2040	3	US-09-657-279-375 Sequence 375, App
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ALIGNMENTS

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US-09-439-313-375
; Sequence 375, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Indels 0; Gaps 0;
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/ Sequence 375, Application US/09352616A
/ Patent No. 6395278
/ GENERAL INFORMATION:
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Liang, Yuxui
/ APPLICANT: Xu, Jianshun
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
/ TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.427C8
/ CURRENT APPLICATION NUMBER: US/09/352,616A
/ NUMBER OF SEQ ID NOS: 472
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Tue Dec 20 15:20:25 2005

us-09-924-400-303.011go.rn1

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1321 AATGTGATTAATGATTAATTTCTCAAGAGGAGAGCAACCTGAAAAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGGAGAGCAACCTGAAAAATCAGCAATTT 1380

QY 1381 CCGACCAAGAAAGTGAAGATATCAAGAAATTTGGCAATTTGTTCTGATCAAAAGAA 1440
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Db 1381 CCGACCAAGAAAGTGAAGATATCAAGAAATTTGGCAATTTGTTCTGATCAAAAGAA 1440

QY 1441 AAACAGATCCAAATATCTTCTGTAAGAACAGAACCCAGAACCAAGACTTAAGCTGACA 1500
1441 AAACAGATCCAAATATCTTCTGTAAGAACAGAACCCAGAACCAAGACTTAAGCTGACA 1500
Db 1441 AAACAGATCCAAATATCTTCTGTAAGAACAGAACCCAGAACCAAGACTTAAGCTGACA 1500

QY 1501 TCAAGGAAAGATCACAAAGCTTGAAGGCAAGTGAATTTGCGCAGAGAAAGATCT 1560
1501 TCAAGGAAAGATCACAAAGCTTGAAGGCAAGTGAATTTGCGCAGAGAAAGATCT 1560
Db 1501 TCAAGGAAAGATCACAAAGCTTGAAGGCAAGTGAATTTGCGCAGAGAAAGATCT 1560

QY 1561 CAAGAACCAAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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QY 1621 GAAATGAAGAACCAAGAGATCTCATGTCGATTTCCAGAAAACTGATTAATGTTGCTG 1680
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QY 1681 ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
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Db 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTTTACAGATGATGATGATGATGATGATGAT 1860

QY 1861 GAAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTTCTTATGTTGTAAGAAA 1920
1861 GAAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTTCTTATGTTGTAAGAAA 1920
Db 1861 GAAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTTCTTATGTTGTAAGAAA 1920

QY 1921 GAAAAAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
1921 GAAAAAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
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QY 1981 GAGCTAGACATGAGAAATCATGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAAATTT 2040
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Db 1981 GAGCTAGACATGAGAAATCATGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAAATTT 2040

RESULT 3
US-09-289-198-303
; Sequence 303, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
EARLIER FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 09/062,451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: PaeCSO for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 AGCAAGTGGGCACTTCTGGAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
121 AGCAAGTGGGCACTTCTGGAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
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481 CTCAGGAGCACTGAGCTGAACAAGAGGAGCAAGCAAGCAAGCAAGCTGCTTCACTG 540
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481 CTCAGGAGCACTGAGCTGAACAAGAGGAGCAAGCAAGCAAGCAAGCTGCTTCACTG 540
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1321 AATGCTGAATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAATGAGCAATTT 1380
1321 AATGCTGAATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAATGAGCAATTT 1380
1381 CCTGACAAAGAGTGAAGATATCAAGAAATTTGCAATTAATGTTCTGACTACAAAG 1440
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1441 AAGCATGAAAGTAAATGCTGGAATTAATGAAGAACTGAAATGCTGCTGAG 1500
1441 AAGCATGAAAGTAAATGCTGGAATTAATGAAGAACTGAAATGCTGCTGAG 1500
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1621 GAAATGAAGAGAGAGTCTATGCTGAGATTTCCAGAAACCTGATCTATGCTGTC 1680
1621 GAAATGAAGAGAGAGTCTATGCTGAGATTTCCAGAAACCTGATCTATGCTGTC 1680
1681 ACTGCTGGAATGATGATGATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAAGC 1740

D _b	1681	ACTGTGGCAATGGTGATGATGANTTAATTCCTCCAAAGGAAGACAGAACCTGGAAGC	1740
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D _b	1741	CAGCAATTTCCTGCACACTGAGAATGAAGATGATCACAGTGAAGCAACAATATGATCTAG	1800
O _y	1801	AAGCAATTTTGTGAAGAACAGACACTGGAATATTACCGATGAGATTCTGATTCATGAA	1860
D _b	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACCGATGAGATTCTGATTCATGAA	1860
O _y	1861	GAAAAGCAGATAGAGAAGTGGTGAAAAAATGSAATTCGTGACTTCTCTAGTTGTTAATGAA	1920
D _b	1861	GAAAAGCAGATAGAGAAGTGGTGAAAAAATGSAATTCGTGACTTCTCTAGTTGTTAATGAA	1920
O _y	1921	GA AAAAGACATCTTG CATG A AA ATAG T AC GT TG CG G GA AGA ATT GC CAT G CT A A G C TG	1980
D _b	1921	GA AAAAGACATCTTG CATG A AA ATAG T AC GT TG CG G GA AGA ATT GC CAT G CT A A G C TG	1980
O _y	1981	GAGCTAGACACATGAAACATCTGAGGCCAGTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
D _b	1981	GAGCTAGACACATGAAACATCTGAGGCCAGTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 4

```

US-09-636-215-375
Sequence 375, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yassir A. W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121, 42717C17
CURRENT APPLICATION NUMBER: US/09/636, 215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-636-215-375

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	Query March	100.0%	Score 2040;	DB 3;	Length 2040;
	Best Local Similarity	100.0%	Pred. No. 0;		
	March 2040; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY	1 ATGGTGCTTGAGGTGATTCCATGCGCGCTCCTCTTCTGTGAAGAAACCATTGGCTTC	60			
Db	1 ATGGTGCTTGAGGTGATTCCATGCGCGCTCCTCTTCTGTGAAGAAACCATTGGCTTC	60			
QY	61 AGGAGCAAGATGGGCAAGTGGTGCCTGCGCTTCCCTCTGCTCAGGAGAAAGGGCGAAG	120			
Db	61 AGGAGCAAGATGGGCAAGTGGTGCCTGCGCTTCCCTCTGCTCAGGAGAAAGGGCGAAG	120			
QY	121 AGCAACGTGGCACTTCTGAGAACCCAGACGACCTCTGATGAAGACACTCAGAGCGAAG	180			

Db	121	AGCAACGTGGCACTTCTTGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAG	180
OY	181	ATGGGCAAGTGGTCCCGCCACCTGCTCCCTCTGACAGGGGGAGTGGCAAGCAACGTG	240
Db	181	ATGGGCAAGTGGTCCCGCCACCTGCTCCCTGCTGACAGGGGGAGTGGCAAGCAACGTG	240
OY	241	GGCGCTTCTGGAGACACAGACGACTCTGCTATGAAGACCTCAGAACCAAGATGGGCAAG	300
Db	241	GGCGCTTCTGGAGACCAACGACGACTCTGCTATGAAGACCTCAGAACCAAGATGGGCAAG	300
OY	301	TGGTGCTGGCCACTGCTTCCCTGCTGACAGGGGGAGCGGCAAGACAGATGGGGCTTGG	360
Db	301	TGGTGCTGGCCACTGCTTCCCTGCTGACAGGGGGAGCGGCAAGACAGATGGGGCTTGG	360
OY	361	GGAGACTACGATGACAGTGCCTTCATGGAGCGCCAGGTACCAAGTCCGTGGAGAAATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGGAGCGCCAGGTACCAAGTCCGTGGAGAAATCTG	420
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OY	541	TCTGCGAATGGGAATTCAGAGTGTGTAAATCTCTGCTGACAGACGATGCACCTTAT	600
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OY	601	GTCCTTGACAACAAAAAGAGACAGCTCTGTAAAGGCGGTACAATGCCAGAAAGATGA	660
Db	601	GTCCTTGACAACAAAAAGAGACAGCTCTGTGTAAAGGCGGTACAATGCCAGAAAGATGA	660
OY	661	TGTGCGTTAATGTTGCTGGAAACATGGGCACTGATCCAAATATTCCAGATGATATGAAAT	720
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Db	841	CATAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCAATTTAATATCA	900
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Db	901	CTGATATGATATGGAAGGACTGCTCTAATCTTGTGTATGTTGTGATCGCAAGATTA	960
OY	961	GTCAGCCTTCTACCTTGAGCAAAATATGATATCTTCTCAAGATCTATCGGACAGCG	1020
Db	961	GTCAGCCTTCTACCTTGAGCAAAATATGATATCTTCTCAAGATCTATCGGACAGCG	1020
OY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTTACTTTCGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTTACTTTCGACTAC	1080
OY	1081	AAAGAAAAACGATGCTTAAAAATCTCTTGAAAAACGCAATCCAGAACAAAGACTTAAG	1140
Db	1081	AAAGAAAAACGATGCTTAAAAATCTCTTGAAAAACGCAATCCAGAACAAAGACTTAAG	1140
OY	1141	CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCCAGTGAATAATAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCCAGTGAATAATAGCCAGAGAAA	1200
OY	1201	ATGTCTCAGAACCAAGAAATTAATAGATGCTGATAGAGGTTGAAGAAATGAG	1260
Db	1201	ATGTCTCAGAACCAAGAAATTAATAGATGCTGATAGAGGTTGAAGAAATGAG	1260

QY 1261 AAGCATGAAAGTATATGTTGGGATTACTAGAAAACTGACTAATGGTGTCACTGCTGCGC 1320
DB 1261 AAGCATGAAAGTATATGTTGGGATTACTAGAAAACTGACTAATGGTGTCACTGCTGCGC 1320
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DB 1381 CCTGACAAAGAAAGTAAAGATGTCAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
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DB 1441 AAACAGATGCAAAATATCTCTTGTAAAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
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QY 1861 GAAAGCAGATGAGATGTTGAAAAATGAAATTTCTGAGCTTCTCTTATGTTGAAGAA 1920
DB 1861 GAAAGCAGATGAGATGTTGAAAAATGAAATTTCTGAGCTTCTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGTATGAAAAATGATGCTTGGGAGAGAAATTCCTATGCTAAGCTG 1980
DB 1921 GAAAAAGACATCTTGTATGAAAAATGATGCTTGGGAGAGAAATTCCTATGCTAAGCTG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAG 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAG 2040

RESULT 5
US-09-685-166A-375
Sequence 375, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Herlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-685-166A-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 CTCAGGGAACCTGACGTGAACAAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
DB 481 CTCAGGGAACCTGACGTGAACAAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
QY 541 TCTGCAATGGAATTTCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
DB 541 TCTGCAATGGAATTTCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
QY 601 GTCTTGAACAAACAAAGAGAGCAGCTGTATGAAGAGCGGTCAATTCAGAGAGATGA 660
DB 601 GTCTTGAACAAACAAAGAGAGCAGCTGTATGAAGAGCGGTCAATTCAGAGAGATGA 660
QY 661 TGTGCTTAATGTTCTGGAACATGCACTGATCAAAATTTCCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTCTGGAACATGCACTGATCAAAATTTCCAGATGATGGAAT 720
QY 721 ACCACTGCACTAAGCTATCTATATGAAGTAAATTAATTAATTAATTAATTAATTAAT 780
DB 721 ACCACTGCACTAAGCTATCTATATGAAGTAAATTAATTAATTAATTAATTAATTAAT 780
QY 781 TATGTGCTGATATGAATCAAAAAAAGAGATGAGCTTCAACCACTGTTACTGTGTGA 840

Db 781 TATGTCGATATGATCAATCAAAAACAGCATGGCTCAGACACATCTTACTTGGTGA 840
Qy 841 CATGACAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGACAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATAGATATGAGAGAGCTGCTCATCTTGTGATGTTGTGTGATCAGCAATATTA 960
Db 901 CTGATAGATATGAGAGAGCTGCTCATCTTGTGATGTTGTGTGATCAGCAATATTA 960
Qy 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGAGCAGC 1020
Db 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGAGCAGC 1020
Qy 1021 GCCAGAGATGCTGCTTTCTTACTGATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGCTGCTTTCTTACTGATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATATGCGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATATGCGCAGCAGAGAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGTTGGATTAATCAAGAAACCTGATATGCTGCTGCTG 1320
Db 1261 AAGCATGAAGATTAATATGTTGGATTAATCAAGAAACCTGATATGCTGCTGCTG 1320
Qy 1321 AATGTCATATGATTAATTAATCTTCAAGAGAGAGCAAGACCTGAATACGAATTT 1380
Db 1321 AATGTCATATGATTAATTAATCTTCAAGAGAGAGCAAGACCTGAATACGAATTT 1380
Qy 1381 CCTGACAAAGAGTGAAGATTAATCAAGAAATTTGCAATTTCTGATCAAGAA 1440
Db 1381 CCTGACAAAGAGTGAAGATTAATCAAGAAATTTGCAATTTCTGATCAAGAA 1440
Qy 1441 AAAACAGATCCCAAAATCTTCTTGAAGAACAGCAATCCAGAACAACTTAAGCTGAC 1500
Db 1441 AAAACAGATCCCAAAATCTTCTTGAAGAACAGCAATCCAGAACAACTTAAGCTGAC 1500
Qy 1501 TCAGAGAGAGAGTCACAAAGGCTTGAGGGAGTGAATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGAGTCACAAAGGCTTGAGGGAGTGAATGGCCAGCAGAGAAAGATCT 1560
Qy 1561 CAAGAACCAAGAAATTAAGATGATGATGAGAGCTGAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAAGATGATGATGAGAGCTGAATTTTATGCTATCGAA 1620
Qy 1621 GAAATTAAGAGAGAGAGTCAATGTCGATTTCCAGAAAACTGACTTAATGCTGCC 1680
Db 1621 GAAATTAAGAGAGAGAGTCAATGTCGATTTCCAGAAAACTGACTTAATGCTGCC 1680
Qy 1681 ACTGTCGCAATGTCATGATGATTAATTTCTCCAGAGAGAGAGCACTGAAAGC 1740
Db 1681 ACTGTCGCAATGTCATGATGATTAATTTCTCCAGAGAGAGAGCACTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACATGAGATGAAGATATCAAGTGAAGCAAAATGATATCTGAG 1800
Db 1741 CAGCAATTTCTGACATGAGATGAAGATATCAAGTGAAGCAAAATGATATCTGAG 1800
Qy 1801 AAGCAATTTTGTGAAGAGAGCACTGGAATTTTACAGATGAGATTTGATTTCTGAG 1860
Db 1801 AAGCAATTTTGTGAAGAGAGCACTGGAATTTTACAGATGAGATTTGATTTCTGAG 1860
Qy 1861 GAAAGCAGATAGAGATGTTGAAAAATGAATTTGAGCTTTCTGTTAGTTAAGAA 1920
Db 1861 GAAAGCAGATAGAGATGTTGAAAAATGAATTTGAGCTTTCTGTTAGTTAAGAA 1920

Db 1861 GAAAGCAGATAGAGATGTTGAAAAATGAATTTGAGCTTTCTGTTAGTTAAGAA 1920
Qy 1921 GAAAAAGACATCTTGATGATGATTAATGATGTTGCGGAGAGAAATTTGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGATGATGATTAATGATGTTGCGGAGAGAAATTTGCTAAGACTG 1980
Qy 1981 GAGCTAGACACAAATGAATATGAGAGCCAGCTGATTAATTAATTAATTAATTAATTA 2040
Db 1981 GAGCTAGACACAAATGAATGATGAGCCAGCTGATTAATTAATTAATTAATTAATTA 2040

RESULT 6
US-09-429-755-303
Sequence 303, Application US/09429755A
Patent No. 6656480
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John W.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCGTTGAGATGATTCATGCGCGCTGCTTCTGTAAGAGCAATTTGCTTC 60
Db 1 ATGTCGTTGAGATGATTCATGCGCGCTGCTTCTGTAAGAGCAATTTGCTTC 60
Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGAGCAAGCACTGCTGATGAAGCACTCAGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGCAAGCACTGCTGATGAAGCACTCAGAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCTG 240
Qy 241 GCGGCTTCTGAGAGCAAGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAG 300
Db 241 GCGGCTTCTGAGAGCAAGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAG 300
Qy 301 TGGTCGTCATGCTTCCCTGCTGCAAGGAGAGTGGCAAGGAGTGGCGCTTGG 360
Db 301 TGGTCGTCATGCTTCCCTGCTGCAAGGAGAGTGGCAAGGAGTGGCGCTTGG 360
Qy 361 GAGACATGATGATGATGCTTCTGATGAGAGCCAGATTAAGATGATGATGATGATG 420
Db 361 GAGACATGATGATGATGCTTCTGATGAGAGCCAGATTAAGATGATGATGATGATG 420
Qy 421 GACAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CTCAGGAGCACTGAGTGAAGAGAGCAAGAGAGCAAGAGAGAGAGAGAGAGAGAGAG 540
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Db 481 CTCAGGACACTGACGCTGAAACAAGAGACAAGCAAAAGAGACTGCTCTACATCTGGCC 540
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Db 601 GTCTTTGACAAACAAAAGAGAGACAGCTCTGATTAAGCCGTACAAATGACAGAAAGATGA 660
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Db 661 TGTGCTTATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGTAAT 720
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Db 721 ACCACTCTGACACGCTATCTATATGAAGATTAATTAAGCCCAAGACCTGCTCTTA 780
Qy 781 TATGCTGATATCGAATCAAAAAACAAGATGGCTCACACACTGTTACTTGGTGA 840
Db 781 TATGCTGATATCGAATCAAAAAACAAGATGGCTCACACACTGTTACTTGGTGA 840
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Db 841 CATGACCAAAAACAGCAAGTCTGAAATTTTATATCAAGAAAAAGCGAATTTAAATGA 900
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Db 901 CTGGATGATATGGAAGACCTGCTCATCTGCTGATATGTTGGATACAGCAAGTATA 960
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Db 961 GTGACGCTTCTACTTGGAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1081 AAGAAGAAACAGATGCTAAATCTCTGAAAAACAGCAATCCAGAACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAAAGCAGTGAATAATAGCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAAAGCAGTGAATAATAGCAGCAGAGAAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAATGAATGATGATGAAGGTTGAAGAAGATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAATGAATGATGATGAAGGTTGAAGAAGATGAAG 1260
Qy 1261 AAGCATGAAGTATTAATGAGGATTAAGTAAAGAACTGAATTAAGTGTGCTGCTGGC 1320
Db 1261 AAGCATGAAGTATTAATGAGGATTAAGTAAAGAACTGAATTAAGTGTGCTGCTGGC 1320
Qy 1321 AATGCTATTAATGATTAATCTTCAAGAGAGAGCAGAACTGAATAATGACAAATTT 1380
Db 1321 AATGCTATTAATGATTAATCTTCAAGAGAGAGCAGAACTGAATAATGACAAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAAGTTCTGACTACAAAGAA 1440
Qy 1441 AAAAGATGCGCAAAATTAATCTTCTGAAAACAGCAACCCAGAACTTAAGCTGANA 1500
Db 1441 AAAAGATGCGCAAAATTAATCTTCTGAAAACAGCAACCCAGAACTTAAGCTGANA 1500
Qy 1501 TCAGAGGAAGAGTCAAAAGGCTTTGAGGCACTGAAATATGCGCAGCAGAGAAAAGATCT 1560
Db 1501 TCAGAGGAAGAGTCAAAAGGCTTTGAGGCACTGAAATATGCGCAGCAGAGAAAAGATCT 1560
Qy 1561 CAAGAACCAAGAAATTAATGAATGATGATGAAGATGTAAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATGAATGATGATGAAGATGTAAGAAATTTTATGCTATCGAA 1620

Qy 1621 GAATGAAGAACACAGGAATTAATCTATGTCGATTCCTCAGAAAACCTGACTAATGTCGC 1680
Db 1621 GAATGAAGAACACAGGAATTAATCTATGTCGATTCCTCAGAAAACCTGACTAATGTCGC 1680
Qy 1681 ACTGCTGCAATGATGATGATGATTAATTTCTTCAAGAGAAAGAGAAACCTGAAAAC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTTCTTCAAGAGAAAGAGAAACCTGAAAAC 1740
Qy 1741 CAGCAATTTCTGACACATGAGATGAAGATATCAAGTACGAAACAAATGATATCTCAG 1800
Db 1741 CAGCAATTTCTGACACATGAGATGAAGATATCAAGTACGAAACAAATGATATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGAACAGAAACCTGAAATTAACAGATGATCTGATTAAGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAAACCTGAAATTAACAGATGATCTGATTAAGAA 1860
Qy 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Db 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Qy 1921 GAAAAAGCATCTTGCATGAATAATGTAAGTTGCGGAAAGAAATTCCTTAAGACTG 1980
Db 1921 GAAAAAGCATCTTGCATGAATAATGTAAGTTGCGGAAAGAAATTCCTTAAGACTG 1980
Qy 1981 GAGCTGACACATGAATGAATCATGAGCCAGCTTAATTAATTAATTAATTAATTAAT 2040
Db 1981 GAGCTGACACATGAATGAATCATGAGCCAGCTTAATTAATTAATTAATTAATTAAT 2040

RESULT 7
US-09-679-426-375
Sequence 375, Application US/09679426
Patent No. 6759515
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Michman, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPES: DNA
ORGANISM: Homo sapien
US-09-679-426-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGATCTC 60
Db 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGATCTC 60

QY	61	AGAGCAAGATGAGCAATGAGCTGCGCGTGGCTTCCCTGCTGACAGGAGAGCGGCAAG	120
Db	61	AGAGCAAGATGAGCAATGAGCTGCGCGTGGCTTCCCTGCTGACAGGAGAGCGGCAAG	120
QY	121	AGCAACGTGGCACTTCTGAGAGCCACAGACGACTCTGCTATGAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGCACTTCTGAGAGCCACAGACGACTCTGCTATGAGACACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGGTGGCGGCACCTGCTTCCCCTGCTGACAGGGGAGTGGCAAGCACTG	240
Db	181	ATGGGCAAGTGGTGGCGGCACCTGCTTCCCCTGCTGACAGGGGAGTGGCAAGCACTG	240
QY	241	GGCGCTTCTGAGAGCACAGACGACTCTGCTATGAGACACTCAGAGCAAGTGGGCAAG	300
Db	241	GGCGCTTCTGAGAGCACAGACGACTCTGCTATGAGACACTCAGAGCAAGTGGGCAAG	300
QY	301	TGTTGCTGCCACTGCTCTTCCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
Db	301	TGTTGCTGCCACTGCTCTTCCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
QY	361	GGAGACTTCGATGACAGTGGCTTCACTGAGAGCCCAAGTTCACGTCCTGGAGAAATCTG	420
Db	361	GGAGACTTCGATGACAGTGGCTTCACTGAGAGCCCAAGTTCACGTCCTGGAGAAATCTG	420
QY	421	GACAAAGCTCCACAGAGCTGCGTGGGGGTTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
Db	421	GACAAAGCTCCACAGAGCTGCGTGGGGGTTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
QY	481	CTCAGGGACACTGACGCTGAAACAGAGAGCAAGCAAAAGAGGACTGCTCTACATGAGCC	540
Db	481	CTCAGGGACACTGACGCTGAAACAGAGAGCAAGCAAAAGAGGACTGCTCTACATGAGCC	540
QY	541	TCTGCCAAATGGGAATTCAGAAAGTAGTAAATCTCCTGCTGACAGACGATGTCAACTTAAT	600
Db	541	TCTGCCAAATGGGAATTCAGAAAGTAGTAAATCTCCTGCTGACAGACGATGTCAACTTAAT	600
QY	601	GTCCTTGAACAACAAAAGAGACAGCTCTGATTAAGGCGGTCACATGCGAAGATGAA	660
Db	601	GTCCTTGAACAACAAAAGAGACAGCTCTGATTAAGGCGGTCACATGCGAAGATGAA	660
QY	661	TGTGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATTTCCAGATGAGTAGTAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATTTCCAGATGAGTAGTAAT	720
QY	721	ACCACTGCACTACGCTATCTATTAATGAAGTAAATTAATGCGCAAGCACTGCTCTTA	780
Db	721	ACCACTGCACTACGCTATCTATTAATGAAGTAAATTAATGCGCAAGCACTGCTCTTA	780
QY	781	TATGTGTCTGATATTCGAATCAAAAAACAGCATGGCTTCACACCACTGTATCTTGGTGT	840
Db	781	TATGTGTCTGATATTCGAATCAAAAAACAGCATGGCTTCACACCACTGTATCTTGGTGT	840
QY	841	CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAGAAAAAGCAATTTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAGAAAAAGCAATTTTAAATGCA	900
QY	901	CTGATATGATATGAAAGAGACTGCTCTCACTTACTGCTGATGTTGGATTCAGCAAGTATA	960
Db	901	CTGATATGATATGAAAGAGACTGCTCTCACTTACTGCTGATGTTGGATTCAGCAAGTATA	960
QY	961	GTCAGCTCTTACTCTTGAGCAAAATTAATGATGATCTTCAAGATCTATCTTGACAGACG	1020
Db	961	GTCAGCTCTTACTCTTGAGCAAAATTAATGATGATCTTCAAGATCTATCTTGACAGACG	1020
QY	1021	GCCAGAGATATGCTGTTCTTAAGCATATCATATGTAATTTGCCAGTTACTTTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTCTTAAGCATATCATATGTAATTTGCCAGTTACTTTGACATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
QY	1141	CTGACATAGAGAAAGTCAACAAAGTTCAAAGGCACTGAATAATGCGCACGACAGAGAA	1200

D	b		1141	CTGCAATCAGAGGAAGGTCAACAAAGTTCCAAAGCGTGGAAAATTACCACGCCAGAGAA	1200
O	y		1201	ATGTCCTAAGAACCAGAAATTAATTAAGATGTGTATAGAGCGTTGAAGAAATGAG	1260
D	b		1201	ATGTCCTAAGAACCAGAAATTAATTAAGATGTGTATAGAGCGTTGAAGAAATGAG	1260
O	y		1261	AAGCATGAAAGTAATAATGTGGGATTCTTGAAAACTGTAAATGGTGTCTACTGTGC	1320
D	b		1261	AAGCATGAAAGTAATAATGTGGGATTCTTGAAAACTGTAAATGGTGTCTACTGTGC	1320
O	y		1321	AATGTGATATATGATTAATTTCTCAAGGAAGAGCAACCTGAAATTCAGCAATTT	1380
D	b		1321	AATGTGATATATGATTAATTTCTCAAGGAAGAGCAACCTGAAATTCAGCAATTT	1380
O	y		1381	CCTGACAACGAAAGTAGAGTATCACAGATTTGCAATTAGTTTCTGACTACAAAGAA	1440
D	b		1381	CCTGACAACGAAAGTAGAGTATCACAGATTTGCAATTAGTTTCTGACTACAAAGAA	1440
O	y		1441	AAACAGATGCCAAATATCTCTTCTTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
D	b		1441	AAACAGATGCCAAATATCTCTTCTTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
O	y		1501	TCAGAGGAAGTCACAAAGGCTTAGAGGAGTAGTAAATGGCCAGCAGAGAAAGACT	1560
D	b		1501	TCAGAGGAAGTCACAAAGGCTTAGAGGAGTAGTAAATGGCCAGCAGAGAAAGACT	1560
O	y		1561	CAAGAACAGAAATMAATMAAGATGTGATAGAGCTAGAAAAATTTATGCTATTCGAA	1620
D	b		1561	CAAGAACAGAAATMAATMAAGATGTGATAGAGCTAGAAAAATTTATGCTATTCGAA	1620
O	y		1621	GAAATGGAAGACACGGAAATATCTACTGTGGATTTCCAGAAAACTGTAAATGTGTGC	1680
D	b		1621	GAAATGGAAGACACGGAAATATCTACTGTGGATTTCCAGAAAACTGTAAATGTGTGC	1680
O	y		1681	ACTCTGGCAATGGTGTATGTGATTTAATTCCTCCAGAGGAAGCAGAAACCTCGTAAGC	1740
D	b		1681	ACTCTGGCAATGGTGTATGTGATTTAATTCCTCCAGAGGAAGCAGAAACCTCGTAAGC	1740
O	y		1741	CAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTACGAAACAAATGATACTCAG	1800
D	b		1741	CAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTACGAAACAAATGATACTCAG	1800
O	y		1801	AAGCAATTTTGTAGAAACAGAAACACTGTGAATTTACACATATGATTTCTGATTCATGAA	1860
D	b		1801	AAGCAATTTTGTAGAAACAGAAACACTGTGAATTTACACATATGATTTCTGATTCATGAA	1860
O	y		1861	GAAAGCAGATAGAGGTGTGAAAAAATGAATTTCTGAGCTTTCTCTTAACTGTAAAGAA	1920
D	b		1861	GAAAGCAGATAGAGGTGTGAAAAAATGAATTTCTGAGCTTTCTCTTAACTGTAAAGAA	1920
O	y		1921	GAAAAAGACATCTTGTGATGAAAAATAGTACGTTCGGGAGAAATTTGCCATGCTAAAGCTG	1980
D	b		1921	GAAAAAGACATCTTGTGATGAAAAATAGTACGTTCGGGAGAAATTTGCCATGCTAAAGCTG	1980
O	y		1981	GAGCTAACAATGAAACATCAGAGCCACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
D	b		1981	GAGCTAACAATGAAACATCAGAGCCACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 8
US-09-759-143-375

; Sequence 375, Application US/09759143

; Patent NO. 6800746
: GENERAL INFORMATION.

GENERAL INFORMATION:
APPLICANT: Xu, Jiamechun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

```
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hedler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTGATTCATGCGCGCTCCTCTTGTGTAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGGTGATTCATGCGCGCTCCTCTTGTGTAAGAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGCAAGCACTGCTGTAAGAACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGTGAGCAAGCACTGCTGTAAGAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
QY 241 GGGCTTTGTGAGACCAAGCACTGCTGTAAGAACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGCTTTGTGAGACCAAGCACTGCTGTAAGAACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCGACCTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
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DB 421 GACAAGCTCCAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGAGCACTGACGTGAAACAAGAGACAAAGAAAGAGAGCTGCTTCACTCTGCGC 540
DB 481 CTCAGAGCACTGACGTGAAACAAGAGACAAAGAAAGAGAGCTGCTTCACTCTGCGC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTGTGGAAGAGATGTCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTGTGGAAGAGATGTCAACTTAAT 600
QY 601 GTCTTTGACAAACAAAAGAGAGAGAGCTGTGATTAAGCCGTACATGCAAGAGATGAA 660
DB 601 GTCTTTGACAAACAAAAGAGAGAGAGCTGTGATTAAGCCGTACATGCAAGAGATGAA 660
QY 661 TGTGCGTTATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGTAAT 720
DB 661 TGTGCGTTATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGTAAT 720
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QY 721 ACCACTGCACTACGCTATCTATATGAAAGATTAATTAATGCCAAGACATGCTCTTA 780
DB 721 ACCACTGCACTACGCTATCTATATGAAAGATTAATTAATGCCAAGACATGCTCTTA 780
QY 781 TATGTGCTGATATGAAATCAAAAAAGAGCTGCGCTCACACACTGTTACTTGGTGTGA 840
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QY 841 CATGAGCAAAAAAGAGAGTGTGAAATTTTATCAAGAAAAAGCAATTTAATATGCA 900
DB 841 CATGAGCAAAAAAGAGAGTGTGAAATTTTATCAAGAAAAAGCAATTTAATATGCA 900
QY 901 CTGATATGATATGAAAGAGCTGCTCATCTGCTGATGTGTTGATGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAAAGAGCTGCTCATCTGCTGATGTGTTGATGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGACAGAGC 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATAGCTGTTCTAGATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
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DB 1081 AAGAAAAAAGAGATCTAAAAATCTCTTCTGAAAAAGCAATCCAGAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTAAATGCCAGCAAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTAAATGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGTGATGAGAGTGTGAAAGATGAAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGTGATGAGAGTGTGAAAGATGAAAG 1260
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DB 1261 AAGCATGAAAGTAAATATGTGGGATTAATCTAGAAAACTGACTAATGTGTCTGCG 1320
QY 1321 AATGTGATATGATTAATTTCTTCAAGAAAGAGAGCACTGTAATGATGATGATGAT 1380
DB 1321 AATGTGATATGATTAATTTCTTCAAGAAAGAGAGCACTGTAATGATGATGATGAT 1380
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DB 1381 CCTGACCAAGAAAGAGAGATATCAAGAAATTTGCGAATTTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCCAAATTAATCTCTGTAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
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QY 1681 ACTGTGCAATGTGATGATGATTAATTTCTTCAAGAGAGAGCAAGCAAGCAAGCAAG 1740
DB 1681 ACTGTGCAATGTGATGATGATTAATTTCTTCAAGAGAGAGCAAGCAAGCAAGCAAG 1740
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QY	1801	AAGCAATTTTGGAGAAACAGAACCTGGAAATTTTACACGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGGAGAAACAGAACCTGGAAATTTTACACGATGAGATTTCTGATTCATGAA	1860
QY	1861	GAAAAGCAGATGAGTGGTGGTGAATAAATGAAATTCCTGAGCTTCTCTTAGTTGTAAGAA	1920
Db	1861	GAAAAGCAGATGAGTGGTGGTGAATAAATGAAATTCCTGAGCTTCTCTTAGTTGTAAGAA	1920
QY	1921	GAATAAGACATCTTTCATGAAATTAAGTACGTTGCGGGAAGAAATTCATGCTAGACCTG	1980
Db	1921	GAATAAGACATCTTTCATGAAATTAAGTACGTTGCGGGAAGAAATTCATGCTAGACCTG	1980
QY	1961	GAGCTAGACACATGAAACATGACGCCAGCTAAAAAATTTGTAAGAAATTTGTAAGAA	2040
Db	1961	GAGCTAGACACATGAAACATGACGCCAGCTAAAAAATTTGTAAGAAATTTGTAAGAA	2040
RESULT 9			
US-09-651-236-375			
; Sequence 375, Application US/09651236			
; Patent No. 6818751			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuyui			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedrick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			
; APPLICANT: Hepler, William			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; FILE REFERENCE: 210121.42718C18			
; CURRENT APPLICATION NUMBER: US/09/651,236			
; CURRENT FILING DATE: 2000-08-29			
; NUMBER OF SEQ ID NOS: 865			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 375.			
; LENGTH: 2040			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-651-236-375			
Query Match 100.0%; Score 2040; DB 3; Length 2040;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	ATGGGTTGAGGTGATTCATGCGCGCTGCTCTTCTGTAAGAAAGCAATTTGGTCTC	60
QY	61	AGAGCAAGATGGGCAAGTGTGTCGCGTTGCTTCCCTCTGCAAGAGCGCAAG	120
Db	61	AGAGCAAGATGGGCAAGTGTGTCGCGTTGCTTCCCTCTGCAAGAGCGCGCAAG	120
QY	121	AGCAACGTGGGCACTTTCTGAGAACACACGACGACTCTGCTATGAAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTTCTGAGAACACACGACGACTCTGCTATGAAGACACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGTGTCGCGCACTGCTTCCCTCTGCAAGGGAAGTGGCAAGCAAGTGTG	240
Db	181	ATGGGCAAGTGTGTCGCGCACTGCTTCCCTCTGCAAGGGAAGTGGCAAGCAAGTGTG	240
QY	241	GCGCGTTCTGAGACACACGACACTCTGCTATGAAGACACTCAGGACAGATGGCGAAG	300

Db	241	GGCGCTTCGAGACACAGCACTCTGTATGAAACACTCAGAAACAAATGGGCAAG	300
Oy	301	TGGTGCTCCACTGCTTCCCTGCTGCAGGGGGAGCGGCAAGAGCAAGTGGGCTTGG	360
Db	301	TGGTGCTCCACTGCTTCCCTGCTGCAGGGGGAGCGGCAAGAGCAAGTGGGCTTGG	360
Oy	361	GGAGCTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTCCGTGGAGAACTCG	420
Db	361	GGAGCTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTCCGTGGAGAACTCG	420
Oy	421	GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAGAAAGATCTCATGTCATG	480
Db	421	GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAGAAAGATCTCATGTCATG	480
Oy	481	CTCAGGGGCACTGACGTGAACAABAAGACAAGAAAGAGCACTGCTACATCTGCC	540
Db	481	CTCAGGGGCACTGACGTGAACAABAAGACAAGAAAGAGCACTGCTACATCTGCC	540
Oy	541	TCTGCAATGAGGAATTCAGAGTGTAAATCTCTGCTGCACAGATGTCAACTTAT	600
Db	541	TCTGCAATGAGGAATTCAGAGTGTAAATCTCTGCTGCACAGATGTCAACTTAT	600
Oy	601	GTCCTTGCAACAATAAAGAGGACAGCTCTGATTAAGCCGTACAATGCAGGAAGATGA	660
Db	601	GTCCTTGCAACAATAAAGAGGACAGCTCTGATTAAGCCGTACAATGCAGGAAGATGA	660
Oy	661	TGTCGCTTAATGTTGCTGGGAACATGGCATCTCAATATTCAGATGATATGAAAT	720
Db	661	TGTCGCTTAATGTTGCTGGGAACATGGCATCTCAATATTCAGATGATATGAAAT	720
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Db	781	TATGGTGTGATTCGAATCAAAAAACAAGCATGCTCACACCACTGTTACTTGGTGA	840
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Db	841	CATAGGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGGAAATTTAAATGA	900
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Db	901	CTGATAGATATGGAAGGACTGCTCTCACTTCTGTATGTTGATTCAGCAAGTATA	960
Oy	961	GTCAGCCTTCTACTTGAACAAATATTGATGTATCTTCAAGATCTATCTGCACAGC	1020
Db	961	GTCAGCCTTCTACTTGAACAAATATTGATGTATCTTCAAGATCTATCTGCACAGC	1020
Oy	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCGACTAC	1080
Oy	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTGA AAAACGCAATCCAGAACAAAGCTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTGA AAAACGCAATCCAGAACAAAGCTTAAAG	1140
Oy	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAGTGAATAATAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAGTGAATAATAGCCAGAGAAA	1200
Oy	1201	ATGTCTCAAGAACCAAAATTAATAGATGTGTATGAGAGTTGAAGAAATATAG	1260
Db	1201	ATGTCTCAAGAACCAAAATTAATAGATGTGTATGAGAGTTGAAGAAATATAG	1260
Oy	1261	AAGCATGAATATATATGTGGATTTACTGA AAAACCTGACTAATGTGTCTGCTGGC	1320
Db	1261	AAGCATGAATATATATGTGGATTTACTGA AAAACCTGACTAATGTGTCTGCTGGC	1320
Oy	1321	AATGTGATTAATGATTAATTTCTCAAGGAAGCAACA CCTGAATAATCAGCAATTT	1380


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Db      1381 CCTGACAAAGAAAGTAAAGATTCACAGAAATTTGGAAATTTGTTCTGATCAAGAA 1440
QY      1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGAC 1500
Db      1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGAC 1500
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QY      1621 GAAATGAAAGAGACGGAAGTACTCATGTCCGATTCGCAAAAACCTGACTAATGGTGC 1680
Db      1621 GAAATGAAAGAGACGGAAGTACTCATGTCCGATTCGCAAAAACCTGACTAATGGTGC 1680
QY      1681 ACTGCTGGCAATGGTATGATGATGATTAATTTCTCCAGAGAGAGCAACCTGAAAC 1740
Db      1681 ACTGCTGGCAATGGTATGATGATGATTAATTTCTCCAGAGAGAGCAACCTGAAAC 1740
QY      1741 CAGCAATTTCTCTGACACTGAGAAATGAAGATCAGAGTGAAGCAAAATGATCTCAG 1800
Db      1741 CAGCAATTTCTCTGACACTGAGAAATGAAGATCAGAGTGAAGCAAAATGATCTCAG 1800
QY      1801 AAGCAATTTTGTGAGAGACGAACTGTGAATTTACAGATGAGATTCGATTCATGAA 1860
Db      1801 AAGCAATTTTGTGAGAGACGAACTGTGAATTTACAGATGAGATTCGATTCATGAA 1860
QY      1861 GAAACAGCATAGAGTGTGAAAAATGAATTCGAGCTTCTCTTGTGTAAAGAA 1920
Db      1861 GAAACAGCATAGAGTGTGAAAAATGAATTCGAGCTTCTCTTGTGTAAAGAA 1920
QY      1921 GAAAAAGACATCTTGCATGAAAAATGATGCTGGGAGAGAAATTCAGATGCTAAGCTG 1980
Db      1921 GAAAAAGACATCTTGCATGAAAAATGATGCTGGGAGAGAAATTCAGATGCTAAGCTG 1980
QY      1981 GAGCTAGACATGAAATCATGAGCCAGCTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 2040
Db      1981 GAGCTAGACATGAAATCATGAGCCAGCTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 2040

RESULT 10
US-09-699-295-303
; Sequence 303, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-303
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY      121 AGCAACGTGGGCACTTCTGAGAGACCAAGCACTCTGCTATGAAAGCACTCAGAGCAAG 180
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QY      181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTCG 240
Db      181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTCG 240
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Db      241 GGGCGCTTCTGAGACCAAGCACTCTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
QY      301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Db      301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
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Db      421 GACAAAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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Db      481 CTGAGGAGACATGAGGTGAAACAAAGAGCAAGCAAAAGAGAGCTGCTTCAATCTG 540
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Db      541 TCTGCAATGGGAATTCAGAAATAGTAAATCTGCTGAGACAGAGATGCTCAATCT 600
QY      601 GTCTTGAACAAACAAAGAGAGCAAGCTGATAAAGCCGTACAAATGCGAGAGATGAA 660
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QY      661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db      661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY      721 ACCACTCTGCACTAGCTATCTATATGAGATTAATTAATGCGCAAGCACTGCTTGA 780
Db      721 ACCACTCTGCACTAGCTATCTATATGAGATTAATTAATGCGCAAGCACTGCTTGA 780
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Db      781 TATGTTGCTGATATGAAATCAAAAAACAGCACTGCTCAGCCACTGTTACTTGGTGT 840
QY      841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
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Db	1561	CAAGAACACAGAAATTAATTAAGATGCTGATAGAGGCTAGAGAAATTTTATGCGCTATGAA	1620
QY	1621	GAAATGAGAGAGACCGAGAGTACTCATGTCCGATTCCTCCAGAAAACCTGACTAATGCTCC	1680
Db	1621	GAAATGAGAGAGACCGAGAGTACTCATGTCCGATTCCTCCAGAAAACCTGACTAATGCTCC	1680
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QY	1741	CAGCAATTTTCTGACACTGAGAAATGAAGATATCACAGTGCAGAACAAATGATACTCAG	1800
Db	1741	CAGCAATTTTCTGACACTGAGAAATGAAGATATCACAGTGCAGAACAAATGATACTCAG	1800
QY	1801	AAGCAATTTTGTAGAGAACAGAACACTGGAATATTAACATGATGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTAGAGAACAGAACACTGGAATATTAACATGATGATTTCTGATTCATGAA	1860
QY	1861	GAAAAAGCAGATAGAGTGTGAATAATGAAATTCAGCTTCTCTTAATGTTGTAAGAA	1920
Db	1861	GAAAAAGCAGATAGAGTGTGAATAATGAAATTCAGCTTCTCTTAATGTTGTAAGAA	1920
QY	1921	GAAAAAGCATCTTGACATGAATAATGATACGTTGCGGAGAAAGAAATTGCCATGTAAGCTG	1980
Db	1921	GAAAAAGCATCTTGACATGAATAATGATACGTTGCGGAGAAAGAAATTGCCATGTAAGCTG	1980
QY	1981	GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040

```

: GENERAL INFORMATION:
:
: APPLICANT: Prudakis, Tony N.
: APPLICANT: Smith, John M.
: APPLICANT: Reed, Steven G.
: APPLICANT: Misher, Lynda
: APPLICANT: Retter, Marc W.
: APPLICANT: Dillon, David C.
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TREATMENT AND DIAGNOSIS OF BREAST CANCER
:
: FILE REFERENCE: 210121.419C7
:
: CURRENT APPLICATION NUMBER: US/09/534,825A
:
: CURRENT FILING DATE: 2000-03-23
:
: NUMBER OF SEQ ID NOS: 317
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 303
:
: LENGTH: 2040
:
: TYPE: DNA
:
: ORGANISM: Homo sapien
:
: US-09-534-825A-303

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RESULT 11
US-09-534-825A-303
; Sequence 303, Application US/09534825A
; Patent No. 6861506

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Db      841 CATGAGCAAAAAACAGCATGCGTGAATTTTATATCAAGAAAAACGAAATTTAATGCA 900
Qy      901 CTGATATGATATGGAAGAGCTGCTCTCATATCTTGCTGTAATGTTGTGATCAGCAAGTATA 960
Db      901 CTGATATGATATGGAAGAGCTGCTCTCATATCTTGCTGTAATGTTGTGATCAGCAAGTATA 960
Qy      961 GTGAGCTTCTACTGAGCAAAAAATATGATATCTTCTCAAGATCTATCTGACAGAGC 1020
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Qy      1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCGAGTTACTTTCTGACTAC 1080
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Qy      1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTTAAG 1140
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Qy      1141 CTGACATGAGAGAAAGTCACAAAGGTCACAAAGGTCACAAAGGTCACAAAGGTCACAAAG 1200
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Qy      1201 ATGTCCTCAAGAACAGAAATTAATAGATGATGATAGAGAGGTTGAAGAAAGAAATGAAG 1260
Db      1201 ATGTCCTCAAGAACAGAAATTAATAGATGATGATAGAGAGGTTGAAGAAAGAAATGAAG 1260
Qy      1261 AAGCATGAAAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db      1261 AAGCATGAAAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Qy      1321 AATGTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db      1321 AATGTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy      1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
Db      1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
Qy      1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTTAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTTAAGCTGACA 1500
Qy      1501 TCAGAGGAAGATGTCACAAAGGCTTGAGGCGCATGAAAAATGCGCGCAGCAAGAAAAAGATCT 1560
Db      1501 TCAGAGGAAGATGTCACAAAGGCTTGAGGCGCATGAAAAATGCGCGCAGCAAGAAAAAGATCT 1560
Qy      1561 CAAGAACCCAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db      1561 CAAGAACCCAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy      1621 GAAATGAAGAGCAACGGAAGTACTATGTCGAAATTTCCAGAAAACTGTAATGATGATGATG 1680
Db      1621 GAAATGAAGAGCAACGGAAGTACTATGTCGAAATTTCCAGAAAACTGTAATGATGATGATGATG 1680
Qy      1681 ACTGTCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db      1681 ACTGTCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Qy      1741 CAGCAATTTCTGACACTAGAAATGAAAGATACAGATGAGAGCAAAATGATGATGATGATGATG 1800
Db      1741 CAGCAATTTCTGACACTAGAAATGAAAGATACAGATGAGAGCAAAATGATGATGATGATGATG 1800
Qy      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATTCATGAA 1860
Db      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATTCATGAA 1860
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Db      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATTCATGAA 1860
Qy      1861 GAAAAAGCATATGAAAGTGTGAAAAATGAAATTTGAGCTTTCTTTAGTTGTGAAGAA 1920
Db      1861 GAAAAAGCATATGAAAGTGTGAAAAATGAAATTTGAGCTTTCTTTAGTTGTGAAGAA 1920
Qy      1921 GAAAAAGCATATGAAAGTGTGAAAAATGAAATTTGAGCTTTCTTTAGTTGTGAAGAA 1980
Db      1921 GAAAAAGCATATGAAAGTGTGAAAAATGAAATTTGAGCTTTCTTTAGTTGTGAAGAA 1980
Qy      1981 GAGCTAGACACAAATGAAATCATGAGCCAGCTTAAAAATGAGCTTAAAAATGAGCTTAAAA 2040
Db      1981 GAGCTAGACACAAATGAAATCATGAGCCAGCTTAAAAATGAGCTTAAAAATGAGCTTAAAA 2040

RESULT 12
US-09-657-279-375
/ Sequence 375, Application US/09657279
/ Patent No. 6894146
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jianshun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqun
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedrick, Thomas S.
/ APPLICANT: Carter, Darlick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C19
/ CURRENT APPLICATION NUMBER: US/09/657.279
/ CURRENT FILING DATE: 2000-09-06
/ NUMBER OF SEQ ID NOS: 877
/ SOFTWARE: PasteSeq for Windows Version 3.0
/ SEQ ID NO: 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-09-657-279-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGTCGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTCGAAAGCATTTGATGCTC 60
Db      1 ATGTCGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTCGAAAGCATTTGATGCTC 60
Qy      61 AAGAGCAAGATGAGCAAGTGTGCTGCGTTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Db      61 AAGAGCAAGATGAGCAAGTGTGCTGCGTTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Qy      121 AGCAACGTGGGCACTTCTGAGAGACAGACGACTCTGCTATGAAAGCACTCAGAGCAAG 180
Db      121 AGCAACGTGGGCACTTCTGAGAGACAGACGACTCTGCTATGAAAGCACTCAGAGCAAG 180
Qy      181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGCG 240
Db      181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGCG 240
Qy      241 GCGGCTTCTGAGACACAGACGACTCTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
Db      241 GCGGCTTCTGAGACACAGACGACTCTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
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QY 301 TGGGCTGACCACTGCTTCCCTGCTGACGGGGGAGGGCAAGAGCAGTGGGGCTTGG 360
| | | | |
Db 301 TGGTGTGCGCACTGCTTCCCTGCTGACGGGGGAGGGCAAGAGCAGTGGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTTCATGAGCCCGAGTACCACTGCTGGAGAGATCTG 420
| | | | |
Db 361 GGAGACTACGATGACAGTGGCTTTCATGAGCCCGAGTACCACTGCTGGAGAGATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTTCATGTCATG 480
| | | | |
Db 421 GACAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTTCATGTCATG 480
QY 481 CTGAGGGGACCTGACGCGGACCAAGAGAGCAAGAAAGAGAGCTGCTTCACATCTGGCC 540
| | | | |
Db 481 CTGAGGGGACCTGACGCGGACCAAGAGAGCAAGAAAGAGAGCTGCTTCACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGACAGACGATGCACTTAAT 600
| | | | |
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGACAGACGATGCACTTAAT 600
QY 601 GTCTTTGACAAACAAAAGAGAGCAGCTCTGATAAAGCCGTCACATGCGAAGAGATGAA 660
| | | | |
Db 601 GTCTTTGACAAACAAAAGAGAGCAGCTCTGATAAAGCCGTCACATGCGAAGAGATGAA 660
QY 661 TGTGCGCTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGGAAT 720
| | | | |
Db 661 TGTGCGCTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATTAATGAGATTAATTAATGCGCAAGACGCTCTTA 780
| | | | |
Db 721 ACCACTCTGCACTACGCTATCTATTAATGAGATTAATTAATGCGCAAGACGCTCTTA 780
QY 781 TATGTGCTGATATCGAATCAAAAACAAGCATGCGCTCAACCACTGTTACTTGGTGA 840
| | | | |
Db 781 TATGTGCTGATATCGAATCAAAAACAAGCATGCGCTCAACCACTGTTACTTGGTGA 840
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Db 841 CATGAGAGAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAGGAAATTTAAATGCA 900
QY 901 CTGAGATGATGAGAGAGCTGCTCTCATCTTCTGATGTTGTTGAGTACAGCAAGTATA 960
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Db 901 CTGAGATGATGAGAGAGCTGCTCTCATCTTCTGATGTTGTTGAGTACAGCAAGTATA 960
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Db 961 GTGAGCCTTCTACTTGAACAAAATATGATGATCTTCTCAAGATCTATCTGACAGCG 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1081 AAAGAAAAACAGATGCTAAATCTCTCTGAAAACAGCAATCAGAAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAAGGTTCAAAAGGCGAGTAAATAGCCAGCAGAGAAA 1200
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Db 1141 CTGACATCAGAGAGAGTCACAAAGGTTCAAAAGGCGAGTAAATAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAGAACCCAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATAGAG 1260
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Db 1201 ATGTCTCAGAACCCAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATAGAG 1260
QY 1261 AAGCATGAAGTAAATATGTTGGGTTACTAGAAAACCTGACTAATGGTGCACCTGGGC 1320
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Db 1261 AAGCATGAAGTAAATATGTTGGGTTACTAGAAAACCTGACTAATGGTGCACCTGGGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAGAACCTGTAATAATGCAATTT 1380
| | | | |
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAGAACCTGTAATAATGCAATTT 1380

QY 1381 CTTGACAGCAAGATGAGAGTATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
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Db 1381 CTTGACAGCAAGATGAGAGTATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCAAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGATTAAGCTGACA 1500
| | | | |
Db 1441 AAAAGATGCAAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGATTAAGCTGACA 1500
QY 1501 TCAGAGAGAGATCACAAAGGCTTTGAGGCGAGTGAATGCGCAGCCAGAGAAAGATCT 1560
| | | | |
Db 1501 TCAGAGAGAGATCACAAAGGCTTTGAGGCGAGTGAATGCGCAGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
| | | | |
Db 1561 CAAGAACCGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GAAATGAGAGAGCAGGAAAGTACTGATGCGAATTCCTCAAGAAAGAGCAGAAACCTGAAAGC 1740
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Db 1621 GAAATGAGAGAGCAGGAAAGTACTGATGCGAATTCCTCAAGAAAGAGCAGAAACCTGAAAGC 1740
QY 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
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Db 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
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| | | | |
Db 1741 CAGCAATTTCTGCACTGAGATGAAATGAAAGTATCAAGATGATGATGATGATGATGAT 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGAAATTAATCAAGATGATGATGATGATGATGAT 1860
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QY 1861 GAAAAGCAGATGAGAGTGGTGAAGAAATGAAATTCGAGCTTCTCTTACTGTAAGAA 1920
| | | | |
Db 1861 GAAAAGCAGATGAGAGTGGTGAAGAAATGAAATTCGAGCTTCTCTTACTGTAAGAA 1920
QY 1921 GAAAAGCAGATGAGAGTGGTGAAGAAATGAAATTCGAGCTTCTCTTACTGTAAGAA 1980
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Db 1921 GAAAAGCAGATGAGAGTGGTGAAGAAATGAAATTCGAGCTTCTCTTACTGTAAGAA 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAATTAATTAATTAATTAATTAATTA 2040
| | | | |
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAATTAATTAATTAATTAATTAATTA 2040

RESULT 13
US-10-012-896-375
; Sequence 375, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocke, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Kaios, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Fey, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro

```
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: PaSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGTGGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAGAGCAATTTGGTCTC
DB      1 ATGGTGGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAGAGCAATTTGGTCTC
QY      61 AGGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG
DB      61 AGGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG
QY      121 AGCAACGTGGGCACTTCTGAGAGCAGAGCACTGCTATGAGACACTCAGAGCAAG
DB      121 AGCAACGTGGGCACTTCTGAGAGCAGAGCACTGCTATGAGACACTCAGAGCAAG
QY      181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGAGGGGAGTGTGCAAGCACTG
DB      181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGAGGGGAGTGTGCAAGCACTG
QY      241 GGGCGCTTCTGAGAGCAGAGCACTGCTATGAGACACTCAGAGCAAGTGTGCAAG
DB      241 GGGCGCTTCTGAGAGCAGAGCACTGCTATGAGACACTCAGAGCAAGTGTGCAAG
QY      301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGGAGTGGGCGCTTGG
DB      301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGGAGTGGGCGCTTGG
QY      361 GGAAGACTAGATGACAGTGTGCTTCTGAGAGCCAGGTACACGTCCTGTGAGAGTCTG
DB      361 GGAAGACTAGATGACAGTGTGCTTCTGAGAGCCAGGTACACGTCCTGTGAGAGTCTG
QY      421 GACAACTCAGACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCTAG
DB      421 GACAACTCAGACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCTAG
QY      481 CTGAGGACACTGACGTGAGCAAGAGCAAGCAAGAGGAGCTGCTACATCTGGCC
DB      481 CTGAGGACACTGACGTGAGCAAGAGCAAGCAAGAGGAGCTGCTACATCTGGCC
QY      541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGAGAGCAGATGTCACTTAAT
DB      541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGAGAGCAGATGTCACTTAAT
QY      601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGGCGGTACATGCAAGAGATGAA
DB      601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGGCGGTACATGCAAGAGATGAA
QY      661 TGTGCGTATGTGTGTGAGCACTGACCTGAATTCGAATATTCAGATGAGTAAAT
DB      661 TGTGCGTATGTGTGTGAGCACTGACCTGAATTCGAATATTCAGATGAGTAAAT
QY      721 ACCACTCTGCACTACGCTATCTATAATGAAGATTAATGAGCCAAAGCACTGCTTA
DB      721 ACCACTCTGCACTACGCTATCTATAATGAAGATTAATGAGCCAAAGCACTGCTTA
QY      781 TATGTGTGATATGCAATCAAAAACAAAGATGCTTCAACCACTGTTACTTGTGTGA
DB      781 TATGTGTGATATGCAATCAAAAACAAAGATGCTTCAACCACTGTTACTTGTGTGA
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901 CTGATAGATAGAGAGAGTGTCTCATCTGTGTGTATGTTGTGATCAGCAAGTATA
961 GTGACCTTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAG
961 GTGACCTTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAG
1021 GCCAGAGATAGTGTGTTCTGATCATCATGTAATTTGCGAGTTACTTCTGACTAC
1021 GCCAGAGATAGTGTGTTCTGATCATCATGTAATTTGCGAGTTACTTCTGACTAC
1081 AAGAAAAACAGATCTAAAAATCTTCTGAAAAACGAATCCAGAACAAAGCTTAAG
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1141 CTGACATCAGAGAGAGAGTCAAAAGCTTCAAAAGGCACTGAAATATGCCAGAGAAA
1141 CTGACATCAGAGAGAGAGTCAAAAGCTTCAAAAGGCACTGAAATATGCCAGAGAAA
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1201 ATGCTCAAGAACAGAAATTAATAGAGTGTGATAGAGGTTGAAGAAATGAG
1261 AAGCATGAAGATTAATAGTGGATTACTAGAAAACTGACTAATGTGTCTCTGCTG
1261 AAGCATGAAGATTAATAGTGGATTACTAGAAAACTGACTAATGTGTCTCTGCTG
1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATATGCAATTT
1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATATGCAATTT
1381 CTGACAGAGAGAGAGATGATCAGAAATTTGCAATTTGTTTCTGACTACAAAGAA
1381 CTGACAGAGAGAGAGATGATCAGAAATTTGCAATTTGTTTCTGACTACAAAGAA
1441 AAGCATGATGCAAAATCTTCTGAAAAACAGCAACCAAGAACAAAGCTTAAGCTGACA
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1501 TCAAGAGAGAGATCAAAAGGCTTGAAGGAGTGAATAATGGCAGCCAGAGAAAGATCT
1501 TCAAGAGAGAGATCAAAAGGCTTGAAGGAGTGAATAATGGCAGCCAGAGAAAGATCT
1561 CAAGAACAGAAATTAATAGAGTGTGATAGAGCTAGAAATTTTATGTGCTATCGAA
1561 CAAGAACAGAAATTAATAGAGTGTGATAGAGCTAGAAATTTTATGTGCTATCGAA
1621 GAATGAAGAGAGAGAGTACTGATGTGAGATTCAGAAAACTGACTAATGTGTGCTC
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1681 GAAATGAAGAGAGAGAGTACTGATGTGAGATTCAGAAAACTGACTAATGTGTGCTC
1681 GAAATGAAGAGAGAGAGTACTGATGTGAGATTCAGAAAACTGACTAATGTGTGCTC
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1801 CAGCAATTTCTGACACTGAGAGATTAAGAGATTAACAGTGAAGAGAGAGAGAGAGAG
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1861 AAGCAATTTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
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1920 GAAAAAGAGATGAAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTGTGAAGAA
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RESULT 15
US-09-352-616A-374
; Sequence 374, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuxi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FaSTSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-374

Query Match      76.0%; Score 1551; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGTTGATTCATGCGGCTGCTTTCTGTGAAAGCCATTGTGTC 60
DB 1 ATGTGTGTTGAGTTGATTCATGCGGCTGCTTTCTGTGAAAGCCATTGTGTC 60
QY 61 AGGAGCAAGTGGGCAAGTGTGCTGCCGTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGTGGGCAAGTGTGCTGCCGTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGTGGCACTTCTGAGACCAAGCACTCTGTAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGTGGCACTTCTGAGACCAAGCACTCTGTAAGACACTCAGAGCAAG 180
QY 122 AGCAAGTGTGGCACTTCTGAGACCAAGCACTCTGTAAGACACTCAGAGCAAG 180
DB 122 AGCAAGTGTGGCACTTCTGAGACCAAGCACTCTGTAAGACACTCAGAGCAAG 180
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DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAG 240
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAG 240
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DB 421 GACAAGTGTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGTGGCAAG 480
QY 481 CTCAGAGCACTGACGTGACCAAGAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAGAGCACTGACGTGACCAAGAGCAAGCAAGCAAGCAAGCAAGCAAG 540
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DB 541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGTCGACAGATGCACTTAAT 600
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DB 601 GTTCCTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 660
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DB 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCAAAATATTCAGATGATGGAAT 720
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DB 721 ACCACTCTGCACTAGCTATCTATATAGAAATTAATAGCCAAAGCACTGCTTA 780
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QY 841 CATGACAAAAACAAAGTGTGAAATTTTATCAAGAAAAACGAATTTAATGCA 900
DB 841 CATGACAAAAACAAAGTGTGAAATTTTATCAAGAAAAACGAATTTAATGCA 900
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DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
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DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACGAATCCAGAACAGCTTAAG 1140
QY 1141 CTGATATGAGAAAGATCAAAAGTTCAAGGCAAGTAATAGCAGCAGAGAA 1200
DB 1141 CTGATATGAGAAAGATCAAAAGTTCAAGGCAAGTAATAGCAGCAGAGAA 1200
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DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAAG 1260
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Job time : 365.535 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 21:07:27 : Search time 1660.28 Seconds

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Title: US-09-924-400-303

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Gapop 60.0, Gapext 60.0

Searched: 9793542 seqs, 413468905 residues

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Total number of hits satisfying chosen parameters: 19563930

Minimum DB seq length: 10
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Post-processing: Listing first 45 summaries

Database : Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2040	100.0	2040	3	US-09-759-143-375 Sequence 375, App
3	2040	100.0	2040	3	US-09-780-669-375 Sequence 375, App
4	2040	100.0	2040	3	US-09-810-936-303 Sequence 303, App
5	2040	100.0	2040	3	US-09-822-827-375 Sequence 375, App
6	2040	100.0	2040	3	US-09-429-755-303 Sequence 303, App
7	2040	100.0	2040	3	US-09-924-400-303 Sequence 303, App
8	2040	100.0	2040	3	US-09-895-793-375 Sequence 375, App
9	2040	100.0	2040	3	US-09-895-814-375 Sequence 375, App
10	2040	100.0	2040	5	US-10-012-896-375 Sequence 375, App
11	2040	100.0	2040	5	US-10-010-940-375 Sequence 375, App
12	2040	100.0	2040	6	US-10-212-679-303 Sequence 303, App
13	2040	100.0	2040	6	US-10-144-678A-375 Sequence 375, App
14	2040	100.0	2040	6	US-10-033-527-7 Sequence 7, Appl1
15	2040	100.0	2040	7	US-10-294-025-375 Sequence 375, App
16	2040	100.0	2040	6	US-10-079-137B-303 Sequence 303, App
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37	1128	55.3	1155	3	US-09-822-827-373 Sequence 373, App
38	1128	55.3	1155	3	US-09-429-755-301 Sequence 301, App
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ALIGNMENTS

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RESULT 1
US-09-825-301-7
: Sequence 7, Application US/09825301
: Patent No. US2002009738A1
: GENERAL INFORMATION:
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Dillon, David C.
: APPLICANT: Molese, David A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Zehentner, Barbara
: APPLICANT: Persing, David H.
: TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
: FILE REFERENCE: 210121.513
: CURRENT APPLICATION NUMBER: US/09/825,301
: CURRENT FILING DATE: 2001-04-02
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-825-301-7

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-759-143-375
Sequence 375, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaeli A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-780-669-375
Sequence 375, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelley, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGTGTTGAGGTGATTCATGCGGGTCTCTTCTGTGAAGAAGCATTTGGTCTC 60

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QY 241 GGGCGTTCTGAGACACAGAGACTCTGTCTATGAAGACACTCAGAGCAAGATGGCAAG 300
DB 241 GGGCGTTCTGAGACACAGAGACTCTGTCTATGAAGACACTCAGAGCAAGATGGCAAG 300

QY 301 TGGTGCTGCCACTGCTTCCCTGCTGAGGGGGAGGCGCAAGAGTGGCGCTTGG 360
DB 301 TGGTGCTGCCACTGCTTCCCTGCTGAGGGGGAGGCGCAAGAGTGGCGCTTGG 360

QY 361 GGAAGATTAAGTACAGTGGCTTCAATGAGAGCCAGGTAACGCTCCGTGAGAAAGTCTG 420
DB 361 GGAAGATTAAGTACAGTGGCTTCAATGAGAGCCAGGTAACGCTCCGTGAGAAAGTCTG 420

QY 421 GACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTACGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTACGTCATG 480

QY 481 CTCAGGGACACTGACGTGAACAAGAGACAAAGAGAGACTGCTTACATCTTGCC 540
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QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACCTCGCTGAGACAGAGATGCACTTAAT 600
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QY 601 GTCTTGAACACAAAGAGAGACAGCTCTGATTAAGCCGTACAAATGCCAGAGATGA 660
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QY 661 TGTGGTTATGTGTCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
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QY 721 ACCACTGCACTAGGCTATCTAATGAAGATTAATTAATGGCCAAAGCACTGCTTGA 780
DB 721 ACCACTGCACTAGGCTATCTAATGAAGATTAATTAATGGCCAAAGCACTGCTTGA 780

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DB 841 CATGAGCAAAAAACAGAAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900

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QY 1021 GCCAAGAGTATGCTGTTTCTATGATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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QY 1081 AAAAGAAAAACAGATCTAAATCTCTTCTGAAAAACAGAAATCCAGAACCAAGCTTAAAG 1140
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Db 1501 TCAGAGAGAGATGCAAAAGGCTTGAGGGAGTGAATATGCGCCAGAGAAAAGATCT 1560
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Db 1621 GAAATGAAGACGCGAATACTCATGTGCGATTCCAGAAAACCTGACTAATGTGTCC 1680
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Db 1741 CAGCAATTTCTGTGACATGAGATGAAGAGATATCACAGTACGAAACAAAATGATCTCAG 1800
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Db 1801 AAGCAATTTGTGTAAGACGAAACCTGGAATTTACAGATGAGATTCTGATTCAATGAA 1860
Qy 1861 GAAAGAGAGATAGAGGTGTGAAAAAATGAATTCGAGCTTCTCTAGTTGTAAGAA 1920
Db 1861 GAAAGAGAGATAGAGGTGTGAAAAAATGAATTCGAGCTTCTCTAGTTGTAAGAA 1920
Qy 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGAGAAATTTGCCATGTCTAAGCTG 1980
Db 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGAGAAATTTGCCATGTCTAAGCTG 1980
Qy 1981 GAGCTGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 4
US-09-810-936-303
; Sequence 303, Application US/09810936
; Patient No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasar A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-810-936-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGTGTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAACATTTGTCTC 60
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Db 61 AGAGCAAGATGGGCAAGTGTGTGTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
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Db 121 AGCAAGTGGGCACTTCTGAGAGCAAGACGACTCTGTATGAAAGACCTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGTGCGGCACTGTCTTCCCTGTGTGAGGGAGTGGCAAGACAGT 240
Db 181 ATGGGCAAGTGTGTGCGGCACTGTCTTCCCTGTGTGAGGGAGTGGCAAGACAGT 240
Qy 241 GGGCTTCTGAGAGACGACGACTGTGATGAAAGACCTGAGAAACAAGATGGGCAAG 300
Db 241 GGGCTTCTGAGAGACGACGACTGTGATGAAAGACCTGAGAAACAAGATGGGCAAG 300
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Db 301 TGGTGTGCACTGCTTCCCTGTGTGAGGGAGGCGGCAAGAGTGGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGTGTCTTATGAGAGCCAGGTACCACTCCGTGAGAGAGATCTG 420
Db 361 GGAAGCTACGATGACAGTGTCTTATGAGAGCCAGGTACCACTCCGTGAGAGAGATCTG 420
Qy 421 GACAAAGCTCAGAGAGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGCTAG 480
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Qy 481 CTCAGGAGACATGACCTGTGAACAAGAGCAAGACAAAGAGAGCTCTCTACATCTGGCC 540
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Qy 601 GTCCCTGACAAAGAAAGAGACAGCTGTGATTAAGCCGTAAAGCCAGGAAAGATGAA 660
Db 601 GTCCCTGACAAAGAAAGAGACAGCTGTGATTAAGCCGTAAAGCCAGGAAAGATGAA 660
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Db 661 TGTGCTTAATGTGTGTGGAACATGAGCACTGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACTGTGCACTACGCTATCTAATAAGATTAATTAATGAGCAAGCACTGCTTTA 780
Db 721 ACCACTGTGCACTACGCTATCTAATAAGATTAATTAATGAGCAAGCACTGCTTTA 780
Qy 781 TATGTGTGATATGCAATCAAAAACAAGCANTGGCTCACACACTGTACTTGTGTGA 840
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Qy 841 CATGACAAAAACAGAAAGTGTGAATTTTATCAAGAAAAACGAATTTAATGCA 900
Db 841 CATGACAAAAACAGAAAGTGTGAATTTTATCAAGAAAAACGAATTTAATGCA 900
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Qy 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGANTATCTGAGCAGAGC 1020
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Qy 1021 GCCAGAGATATGCTTTCTAGTCAATCATATGATTTGCAAGTTACTTCTGACTAC 1080
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Qy 1141 CTGACATCAGAGGAAGTCAAAAGTCAAAAGCAAGTGAATTTGCGAGCCAGAGAA 1200

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Db      1141 CTGACATCAGAGGAGAGTCACAAAAGTTCAAAAGCGATGAAATATGACCGACAGAGAAA 1200
QY      1201 ATGTCTCAAGAACCCAGAAATTAATAGATGTGATAGAGGTTGTAAGAAGAAATGAAG 1260
Db      1201 ATGTCTCAAGAACCCAGAAATTAATAGATGTGATAGAGGTTGTAAGAAGAAATGAAG 1260
QY      1261 AAGCATGAAAGATATATATGTGGATTACAGAAAACCTGACTATATGTGTCTACTGTGCG 1320
Db      1261 AAGCATGAAAGATATATATGTGGATTACAGAAAACCTGACTATATGTGTCTACTGTGCG 1320
QY      1321 AATGTGATATATGTGATTAATCTCTCAAGAGAGAGAGAACACCTGAAAATCAGCAATTT 1380
Db      1321 AATGTGATATATGTGATTAATCTCTCAAGAGAGAGAGAACACCTGAAAATCAGCAATTT 1380
QY      1381 CCTGACACGAAAGTGAAGATATCAGAAATTTGGAAATTTAGTTTCTGACTACAAAGAA 1440
Db      1381 CCTGACACGAAAGTGAAGATATCAGAAATTTGGAAATTTAGTTTCTGACTACAAAGAA 1440
QY      1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY      1501 TCAGAGAGAAAGTCACAAAAGCTTGAAGGCGATGTAATAATGGCCAGCCAGAGAAAGATT 1560
Db      1501 TCAGAGAGAAAGTCACAAAAGCTTGAAGGCGATGTAATAATGGCCAGCCAGAGAAAGATT 1560
QY      1561 CAGAAACAGAAATTAATAAGATGTGTGATAGAGACTAGAAATTTTATGTGCTATCGAA 1620
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QY      1621 GAAATGAGAGAGACGGAAGTACTCATGTGCGAATTCACAGAAAACCTGACTATGTGTGC 1680
Db      1621 GAAATGAGAGAGACGGAAGTACTCATGTGCGAATTCACAGAAAACCTGACTATGTGTGC 1680
QY      1681 ACTGCTGGCAATGTGTATATATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
Db      1681 ACTGCTGGCAATGTGTATATATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
QY      1741 CAGCAATTTCTGACACTGAGATGAAAGATATCAGATGACGAAACAAATGATCTGAC 1800
Db      1741 CAGCAATTTCTGACACTGAGATGAAAGATATCAGATGACGAAACAAATGATCTGAC 1800
QY      1801 AAGCAATTTTGTGAAGACAGAAACACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
Db      1801 AAGCAATTTTGTGAAGACAGAAACACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
QY      1861 GAAAGCAATATGAAATGTGTGAAAAAATGAATTTCTGAGCTTTCTTGTGTGTAAGAA 1920
Db      1861 GAAAGCAATATGAAATGTGTGAAAAAATGAATTTCTGAGCTTTCTTGTGTGTAAGAA 1920
QY      1921 GAAAAAGACATCTGATGATGAAAAATAGTACGTTGCGGGAAGAAATTGCCATGTAAGACTG 1980
Db      1921 GAAAAAGACATCTGATGATGAAAAATAGTACGTTGCGGGAAGAAATTGCCATGTAAGACTG 1980
QY      1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
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RESULT 5
US-09-822-827-375
; Sequence 375, Application US/09822827
; Patent No. US2002081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375

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; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGACAGGAGACGGCAAG 120
QY      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTGTGCTATGAAAGCACTCAGAGCAAG 180
Db      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTGTGCTATGAAAGCACTCAGAGCAAG 180
QY      181 ATGGCAAGTGTGCTGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
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QY      301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGGCGCTTGG 360
Db      301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGGCGCTTGG 360
QY      361 GGAAGCTACAGATGACAGTGTCTTCAATGAGCCAGATACAGTGTGCTGTGAGAAATCTG 420
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QY      481 CTCAGGAGCACTGACGTGAAACAGAGAGCAAGCAAAAGAGAGCTCTTCAATCTGCGC 540
Db      481 CTCAGGAGCACTGACGTGAAACAGAGAGCAAGCAAAAGAGAGCTCTTCAATCTGCGC 540
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Db      541 TTGTGCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGCATGTCTTAAT 600
QY      601 GTCTTGAACAACAAAAGAGGACAGCTCTGATTAAGGCGGTCAATGACAGAGATGAA 660
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Db      661 TGTGCTTAATGTGCTGGAACATGCACTGTAATGAGCCAAATATTCAGATGATGAAAT 720
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QY      901 CTGATATGATATGAGAGAGCTGCTCATCTTGTGATGATGTTGTGATCAGCAAGTATA 960
Db      901 CTGATATGATATGAGAGAGCTGCTCATCTTGTGATGATGTTGTGATCAGCAAGTATA 960

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Db 1501 TGAAGGAAAGATGCTCAAGGCTGAGGCGAGTGAAGAAATGGCCAGCAGAGAAAGATCT 1560
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Db 1561 CAAGAACCGAAGATTAATAGATGCTGATAGAGAGTGAAGAAATTTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGACGAGAGTACTCTGCGAATTTCCAGAAAACTGATGCTATGCTGCTC 1680
Db 1621 GAAATGAAGACGAGAGTACTCTGCGAATTTCCAGAAAACTGATGCTATGCTGCTC 1680
Qy 1681 AATGCTGCAATGCTGATATGATTAATTTCTCCAGAGAAAGCAAGCACTGAAAGC 1740
Db 1681 AATGCTGCAATGCTGATATGATTAATTTCTCCAGAGAAAGCAAGCACTGAAAGC 1740
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Db 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAAATTTCTGATTAAGAA 1860
Qy 1861 GAAAGACAGATTAAGATGCTGGAAGAAATGAAATTTCTGAGCTTTCTTTAGTTGAAGAA 1920
Db 1861 GAAAGACAGATTAAGATGCTGGAAGAAATGAAATTTCTGAGCTTTCTTTAGTTGAAGAA 1920
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Db 1921 GAAAAAGATCTTGCATGAAATATGTAAGTTCGGGAGAGAAATTCATGCTTAAGACTG 1980
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RESULT 7
US-09-924-400-303
; Sequence 303, Application US/09924400
; Patent No. US20020165371A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C12
; CURRENT APPLICATION NUMBER: US/09/924,400
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-924-400-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTAAGAAAGCAATTTGCTTC 60
Db 1 ATGCTGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTAAGAAAGCAATTTGCTTC 60
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Db 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGAGCAAGCTG 240
Qy 241 GCGGCTTCTGAGACACAGACGACTCTGCTATGAAGACATCAGAGAAACAAGATGGCAAG 300
Db 241 GCGGCTTCTGAGACACAGACGACTCTGCTATGAAGACATCAGAGAAACAAGATGGCAAG 300

Oy	301	TGTTCTCTCACTGCTTTCCCTCTGCAAGGGGAGCCGCAAGCAAGAGTGGCGCTTGG	360
Oy	301	TGTTCTCTCACTGCTTTCCCTCTGCAAGGGGAGCCGCAAGCAAGAGTGGCGCTTGG	360
Oy	301	TGTTCTCTCACTGCTTTCCCTCTGCAAGGGGAGCCGCAAGCAAGAGTGGCGCTTGG	360
Oy	361	GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACCACTCCCTGAGAAAGATCTG	420
Oy	361	GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACCACTCCCTGAGAAAGATCTG	420
Oy	361	GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACCACTCCCTGAGAAAGATCTG	420
Oy	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
Oy	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
Oy	481	CTCAGGGGACATGAGGTGACAAAGAGCAAGCAAAAGAGGACGTCTCTCATCTGGCC	540
Oy	481	CTCAGGGGACATGAGGTGACAAAGAGCAAGCAAAAGAGGACGTCTCTCATCTGGCC	540
Oy	541	TCCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGCAAGAGATGTCACCTTAAAT	600
Oy	541	TCCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGCAAGAGATGTCACCTTAAAT	600
Oy	601	GTCCTTGACAAACAAAAGAGCAGCTCTGATTAAGCCGTCAATGCCAGAGAGTAA	660
Oy	601	GTCCTTGACAAACAAAAGAGCAGCTCTGATTAAGCCGTCAATGCCAGAGAGTAA	660
Oy	661	TGTGGCTTAATGTTGCTGGAACATGGCCCTGATCCAAATATTCAGATGAGATGGAAT	720
Oy	661	TGTGGCTTAATGTTGCTGGAACATGGCCCTGATCCAAATATTCAGATGAGATGGAAT	720
Oy	721	ACCACTCTGCACATAGCTATCTATATAGATAATTAATAGCCAAAGCACTGCTCTTA	780
Oy	721	ACCACTCTGCACATAGCTATCTATATAGATAATTAATAGCCAAAGCACTGCTCTTA	780
Oy	781	TATGGTCTGATATCGAATCAAAAAACAAGCATGGCTTCAACCACTGTTACTTGGTGA	840
Oy	781	TATGGTCTGATATCGAATCAAAAAACAAGCATGGCTTCAACCACTGTTACTTGGTGA	840
Oy	841	CATAGACAAAAACAGCAAGTCTGTAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
Oy	841	CATAGACAAAAACAGCAAGTCTGTAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
Oy	901	CTGGATAGATATGGAAGAGCTGCTCATACCTGTGATGTTGGATGACGCAAGTATA	960
Oy	901	CTGGATAGATATGGAAGAGCTGCTCATACCTGTGATGTTGGATGACGCAAGTATA	960
Oy	961	GTCAGCCCTTCACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTTGACAGACG	1020
Oy	961	GTCAGCCCTTCACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTTGACAGACG	1020
Oy	1021	GCCAGAGGTATGCTGTTCTTCTAGTATCATCATGTTAAATTTTGCAAGTCTTCTGACATAC	1080
Oy	1021	GCCAGAGGTATGCTGTTCTTCTAGTATCATCATGTTAAATTTTGCAAGTCTTCTGACATAC	1080
Oy	1081	AAAGAAAAACAGATCTTAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTTAAG	1140
Oy	1081	AAAGAAAAACAGATCTTAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTTAAG	1140
Oy	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCACTGAAAATATGCAAGCAGAGAAA	1200
Oy	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCACTGAAAATATGCAAGCAGAGAAA	1200
Oy	1201	ATGTTCTCAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG	1260
Oy	1201	ATGTTCTCAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG	1260
Oy	1261	AAGCATGAAAGTAATATGTTGGGATTAATCAAGAAAACCTGAATATGAGTCACTGCTGC	1320
Oy	1261	AAGCATGAAAGTAATATGTTGGGATTAATCAAGAAAACCTGAATATGAGTCACTGCTGC	1320
Oy	1321	AATGTGTAAATGATTAATTTCTTCAAGAAAGACAGAACCTGAATAATCAGCAATTT	1380
Oy	1321	AATGTGTAAATGATTAATTTCTTCAAGAAAGACAGAACCTGAATAATCAGCAATTT	1380
Oy	1381	CCTGACAAACGAAAGTAAAGATATCAACGAATTTTCCGAATTATGTTTCTGACTACAAAGA	1440

Db	1381	CTGACACACGAAAGTGAAGAGTATCACAGAAATTTGGCAATTTAGTTTGTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATACTCTTTCTGAAACAGCAACCAGAACAGACCTTAAAGCTGACA	1500
Db	1441	AAAACAGATGCCAAATACTCTTTCTGAAACAGCAACCAGAACAGACCTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGAGTCACAAAGCTTGAGAGGCGAGTGAATAATGGCCAGCCAGAGAAAAGTCT	1550
Db	1501	TCAGAGGAAGAGTCACAAAGCTTGAGAGGCGAGTGAATAATGGCCAGCCAGAGAAAAGTCT	1550
Qy	1561	CAAGAACACAGAAATTAATTAAGATGATGATAGAGAGCTAGAGAAATTTTATGGCTATGAA	1620
Db	1561	CAAGAACACAGAAATTAATTAAGATGATGATAGAGAGCTAGAGAAATTTTATGGCTATGAA	1620
Qy	1621	GAATGGAAGAACACGGAAGTACTCATGTGCGAATTTCCAGAAAACTGACTAATGATGCC	1680
Db	1621	GAATGGAAGAACACGGAAGTACTCATGTGCGAATTTCCAGAAAACTGACTAATGATGCC	1680
Qy	1681	ACTGCTGGCAATGGTGTATGATGATTAATTCCTCCAGAAAGACAGACACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTATGATGATTAATTCCTCCAGAAAGACAGACACCTGAAAGC	1740
Qy	1741	CAGCAATTTCTCGTACACTGAGAAATGAAGAGATATCACAGTACGAAACAAATATGATCTAG	1800
Db	1741	CAGCAATTTCTCGTACACTGAGAAATGAAGAGATATCACAGTACGAAACAAATATGATCTAG	1800
Qy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTCGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTCGATTCATGAA	1860
Qy	1861	GAAGAACAGATAGAGTGGTTGAAAAAATGAATTCGAGCTTCTCTTAGTTGTAGAAA	1920
Db	1861	GAAGAACAGATAGAGTGGTTGAAAAAATGAATTCGAGCTTCTCTTAGTTGTAGAAA	1920
Qy	1921	GAAGAACACATCTTGCATGAAATATGATCGTGGGGAAGAAATTGGCATGCTAAGACTG	1980
Db	1921	GAAGAACACATCTTGCATGAAATATGATCGTGGGGAAGAAATTGGCATGCTAAGACTG	1980
Qy	1981	GAGCTTAGACACAATGAAACATCAGAGCCAGACTAATAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTTAGACACAATGAAACATCAGAGCCAGACTAATAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 8
US-09-895-793-375
Sequence 375, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghlon, Raymond L.
APPLICANT: Vinals de Basbols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTCTTCTGTGTAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTCTTCTGTGTAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGCAGGAGACGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGCAGGAGACGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAACGACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAAGCAACGACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCCGCACTGCTCCCTGCTGAGGGGAGAGTGGCAAGCAACTG 240
DB 181 ATGGGCAATGGTGGCCGCACTGCTCCCTGCTGAGGGGAGAGTGGCAAGCAACTG 240
QY 241 GCGCGCTTCTGAGAGCAGCAGCACTCTGATGAAGACATCAGAAATGGGCAAG 300
DB 241 GCGCGCTTCTGAGAGCAGCAGCACTCTGATGAAGACATCAGAAATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTGTGAAATCTG 420
DB 361 GGAAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTGTGAAATCTG 420
QY 421 GACAAGCTCCAGAGAGCTGCTGTGGGTAAAGTCCCGAAGAGATCTCATCTGCATG 480
DB 421 GACAAGCTCCAGAGAGCTGCTGTGGGTAAAGTCCCGAAGAGATCTCATCTGCATG 480
QY 481 CTCAGGGACACTGACCTGAACAAAGAGCAAGCAAAAGAGACTGCTCATCTGCGC 540
DB 481 CTCAGGGACACTGACCTGAACAAAGAGCAAGCAAAAGAGACTGCTCATCTGCGC 540
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QY 601 GTCTCTGACAAACAAAAGAGAGCAGCTGTATTAAGCCGTACAATGCCAGAAATGA 660
DB 601 GTCTCTGACAAACAAAAGAGAGCAGCTGTATTAAGCCGTACAATGCCAGAAATGA 660
QY 661 TGTGCGTTAATGTTGCTGANAATGGCACTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGANAATGGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACCTGCACTACGCTATCTATATATGAAGATTAATTAAGGCCAAACATGCTCTTA 780
DB 721 ACCACCTGCACTACGCTATCTATATATGAAGATTAATTAAGGCCAAACATGCTCTTA 780
QY 781 TATGTGCTGATATCGAATCAAAAACAAAGATGGCTCAGACCATCTTTAATTGGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAACAAAGATGGCTCAGACCATCTTTAATTGGTGA 840
QY 841 CATGACAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
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DB 841 CATGACAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGAATAGATAGGAAGACCTGCTCATPACTTGTGATATGTTGGATACACAAGTAA 960
DB 901 CTGGAATAGATAGGAAGACCTGCTCATPACTTGTGATATGTTGGATACACAAGTAA 960
QY 961 GTACACCTTCTTACCTGAGCAAAAATATGATGATCTTCAAGATCTATCTGACAGACG 1020
DB 961 GTACACCTTCTTACCTGAGCAAAAATATGATGATCTTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGATAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGATAC 1080
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DB 1081 AAGAAAAACAGATCTTAAATCTCTGTAAGAACAGAAATCCAGAACAAACTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGAGTCAACAAAGTTCAAAAGCAGTGAATAATGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGGAAGAGTCAACAAAGTTCAAAAGCAGTGAATAATGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGCTTGAGAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGCTTGAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCTCTGTGC 1320
DB 1261 AAGCATGAAGTAATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCTCTGTGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAAAGAGACAGAACACTGAAATACGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAAAGAGACAGAACACTGAAATACGCAATTT 1380
QY 1381 CCTGACCAAGAAAGTGAAGAGTATCAACGAATTTGCGAATTATGTTCTGATCAAGAA 1440
DB 1381 CCTGACCAAGAAAGTGAAGAGTATCAACGAATTTGCGAATTATGTTCTGATCAAGAA 1440
QY 1441 AAACAGATGCCAAATPACTCTTCTGAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATPACTCTTCTGAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCAAGTGAATAATGGCAGAGAAAAGTCT 1560
DB 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCAAGTGAATAATGGCAGAGAAAAGTCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGACTAGAAAATTTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGACTAGAAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAGCAGGAAGTACTATGTCCGATTCCAGAAAACCTGACTAAATGCTGCC 1680
DB 1621 GAAATGAAGAGCAGGAAGTACTATGTCCGATTCCAGAAAACCTGACTAAATGCTGCC 1680
QY 1681 ACTGTGCAATGTGATGATGATTAATCTCTCCAGAGAGAGAGCAACCTGAAAAGC 1740
DB 1681 ACTGTGCAATGTGATGATGATTAATCTCTCCAGAGAGAGAGCAACCTGAAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCAAGTACGAAACAAAATATATCTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCAAGTACGAAACAAAATATATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGACAGAACCTGGAATTAATACAGATGAATCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGACAGAACCTGGAATTAATACAGATGAATCTGATTCATGAA 1860
QY 1861 GAAAAGCAGATGAAGTGGTGAATAATGAATCTGAGCTTCTCTTATGTTGAAGAA 1920
DB 1861 GAAAAGCAGATGAAGTGGTGAATAATGAATCTGAGCTTCTCTTATGTTGAAGAA 1920
QY 1921 GAAAAGCAGATCTTGAATGAATAATGATAGTGTGCGGAGAAATTTGCCATGCTTAAGCTG 1980
DB 1921 GAAAAGCAGATCTTGAATGAATAATGATAGTGTGCGGAGAAATTTGCCATGCTTAAGCTG 1980
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QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 9
US-09-895-814-375
Sequence 375, Application US/09895814
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedavick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yaseir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basols, Carloca
APPLICANT: Roy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895.814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GGAGACTACATGACATGCTTTCATGAGCCCAAGTACCAAGTCCGTGGAGAAAGATCTG 420
DB 361 GGAGACTACATGACATGCTTTCATGAGCCCAAGTACCAAGTCCGTGGAGAAAGATCTG 420

QY 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATCTGTCATG 480
DB 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATCTGTCATG 480

QY 481 CTCAGGGACATGACCTGAAACAAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGGACATGACCTGAAACAAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540

QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGACAGAGATCTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGACAGAGATCTCACTTAAT 600

QY 601 GTCTTGAACAACAAAAGAGAGACAGCTGTATTAAGCCGTACAAATGCGAGAAAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGACAGCTGTATTAAGCCGTACAAATGCGAGAAAGATGAA 660

QY 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720

QY 721 ACCACTCTGACTACCTATCTATTAATGAAGATTAATGCGCAAGACATGCTCTTA 780
DB 721 ACCACTCTGACTACCTATCTATTAATGAAGATTAATGCGCAAGACATGCTCTTA 780

QY 781 TATGTCGTATATGATGCAATCAAAAACAAAGCATGCGTCAACACTGTTACTTGATGA 840
DB 781 TATGTCGTATATGATGCAATCAAAAACAAAGCATGCGTCAACACTGTTACTTGATGA 840

QY 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGAATTTAAATGCA 900

QY 901 CTGATATGATGGAAGAGCTGCTCATATCTGCTATGTTGTCATGACAGATATA 960
DB 901 CTGATATGATGGAAGAGCTGCTCATATCTGCTATGTTGTCATGACAGATATA 960

QY 961 GTGAGCTTCTACTGAGCAAAATATGATGTTCTTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGTTCTTCAAGATCTATCTGACAGAG 1020

QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATATGTAATTTGCGATTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATATGTAATTTGCGATTACTTCTGACTAC 1080

QY 1081 AAAAGAAAACAGATGCTAAATCTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAAAGAAAACAGATGCTAAATCTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140

QY 1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGCAAGTAAATGCGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGCAAGTAAATGCGCAGAGAAA 1200

QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGAGAGGTTAAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGAGAGGTTAAAGAAATGAAG 1260

QY 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320

QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAACTCTGAAATTAATGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAACTCTGAAATTAATGCAATTT 1380

QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440

QY 541 TCTGCCAATGGGAATTCAAGATAGTAAACTCTGCTGGACAGACGATGCAACTTAAT 600
 DB 541 TCTGCCAATGGGAATTCAAGATAGTAAACTCTGCTGGACAGACGATGCAACTTAAT 600
 QY 601 GTCTCTGACACAAAAAGAGACAGCTGATTAAGCCGTACATGCCAGGAAGATGA 660
 DB 601 GTCTCTGACACAAAAAGAGACAGCTGATTAAGCCGTACATGCCAGGAAGATGA 660
 QY 661 TGTGGCTATGTGTGTGGACATGGACATGATCCAAATATCCAGATAGATGAAT 720
 DB 661 TGTGGCTATGTGTGTGGACATGGACATGATCCAAATATCCAGATAGATGAAT 720
 QY 721 ACCACTCTGCACTACCTATCTAATATGAAGATTAATATGAGCCAAAGCATGCTCTTA 780
 DB 721 ACCACTCTGCACTACCTATCTAATATGAAGATTAATATGAGCCAAAGCATGCTCTTA 780
 QY 781 TATGTGTGATATGCAATCAAAAAAGACATGGCTGACACCACTGTTACTTGTGTGA 840
 DB 781 TATGTGTGATATGCAATCAAAAAAGACATGGCTGACACCACTGTTACTTGTGTGA 840
 QY 841 CATGAGCAAAAAACAGAACTCGTGAAATTTTATCAAGAAAAAGCAATTTAAATGA 900
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 QY 901 CTGATATGATGAAAGACAGCTGCTCATACTTGTGTATGTTGTGGATCAGCAAGTATA 960
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 QY 961 GTGACGCTTCTAATTGAGCAAAAAATATGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
 DB 961 GTGACGCTTCTAATTGAGCAAAAAATATGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
 QY 1021 GCCAAGAGATATGCTCTTCTAGTCAATCATATGTAATTTGGCAGTTACTTCTGACTAC 1080
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 QY 1081 AAGAGAAAAACAGATGCTAAATAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
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 QY 1141 CTGACATCAGAGAAAGTCAACAAGGTTCAAAAGGAGTGAATAATGACCCAGAGAAA 1200
 DB 1141 CTGACATCAGAGAAAGTCAACAAGGTTCAAAAGGAGTGAATAATGACCCAGAGAAA 1200
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 DB 1201 ATGTCTCAAGAACCGAATAATTAAGATGTGATAGAGAGGTTGAATAAGAAATGAAG 1260
 QY 1261 AAGCATGAAGATATATGTGGGATTTACTAGAAAACTGACTATATGTGTCACTGCTGAC 1320
 DB 1261 AAGCATGAAGATATATGTGGGATTTACTAGAAAACTGACTATATGTGTCACTGCTGAC 1320
 QY 1321 AATGTGATATGATTAATTTCTTCAAGAGAAAGAGACAACTTGAATAATGACAAATTT 1380
 DB 1321 AATGTGATATGATTAATTTCTTCAAGAGAAAGAGACAACTTGAATAATGACAAATTT 1380
 QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAATTAATTTCTGACTACAAAGAA 1440
 DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAATTAATTTCTGACTACAAAGAA 1440
 QY 1441 AAAACAGATGCAAAATACTCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
 DB 1441 AAAACAGATGCAAAATACTCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
 QY 1501 TCAGAGAAAGAGTCACAAAGGCTTGAAGGCAAGTGAATGAGCCAGCAGAGAAAGATCT 1560
 DB 1501 TCAGAGAAAGAGTCACAAAGGCTTGAAGGCAAGTGAATGAGCCAGCAGAGAAAGATCT 1560
 QY 1561 CAAGAACCGAATAATTAAGATGTGTATAGAGACTGAAAAATTTTATGTGCTATCGAA 1620
 DB 1561 CAAGAACCGAATAATTAAGATGTGTATAGAGACTGAAAAATTTTATGTGCTATCGAA 1620

QY 1621 GAATGAAGAAAGCAGGAAGTACTCATGTCCGATTTCCAGAAAACTGACTAATGTGCC 1680
 DB 1621 GAATGAAGAAAGCAGGAAGTACTCATGTCCGATTTCCAGAAAACTGACTAATGTGCC 1680
 QY 1681 ACTGTGCAATGTGTATGATGATTAATTTCTTCAAGAGAAAGACACCTGAAAGC 1740
 DB 1681 ACTGTGCAATGTGTATGATGATTAATTTCTTCAAGAGAAAGACACCTGAAAGC 1740
 QY 1741 CAGCAATTTCCGACATCGAAGATGAAGATATCAAGTGAAGAAACAAATGATCTGAG 1800
 DB 1741 CAGCAATTTCCGACATCGAAGATGAAGATATCAAGTGAAGAAACAAATGATCTGAG 1800
 QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAGATTTCTGATTCATGA 1860
 DB 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAGATTTCTGATTCATGA 1860
 QY 1861 GAAAAGCAGATGAGAGTGTGAAAAATGAATTTCTGAGCTTCTTGTGTGAAGAA 1920
 DB 1861 GAAAAGCAGATGAGAGTGTGAAAAATGAATTTCTGAGCTTCTTGTGTGAAGAA 1920
 QY 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGGCGGAAAGAAATGCCATGCTAAGACTG 1980
 DB 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGGCGGAAAGAAATGCCATGCTAAGACTG 1980
 QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
 DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 12
 US-10-212-679-303
 ; Sequence 303, Application US/10212679
 ; Publication No. US20030125536A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Hirst, Shannon Kathleen
 ; APPLICANT: Dillon, David
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Houghton, Ray
 ; APPLICANT: Persing, David
 ; APPLICANT: Kalos, Michael
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.419C14
 ; CURRENT APPLICATION NUMBER: US/10/212,679
 ; NUMBER OF SEQ ID NOS: 428
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 303
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-212-679-303

Query Match 100.0%; Score 2040; DB 6; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTTC 60
 DB 1 ATGTGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
 DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
 QY 121 AGCAACGTGGGCACTTCTGGAAGACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
 DB 121 AGCAACGTGGGCACTTCTGGAAGACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAACGTG 240
 DB 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAACGTG 240

QY 241 GGCGCTTGTGAGACCAAGCACTGCTATGAAGCACTGAGAAAGATGGGCAAG 300
 DB 241 GGCGCTTGTGAGACCAAGCACTGCTATGAAGCACTGAGAAAGATGGGCAAG 300
 QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGTGGCGCTGG 360
 DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGTGGCGCTGG 360
 QY 361 GGAAGATTAGATGACAGTGTCTTCAATGAGCCAGGATCCAGCTCCGTGGAAGATCTG 420
 DB 361 GGAAGATTAGATGACAGTGTCTTCAATGAGCCAGGATCCAGCTCCGTGGAAGATCTG 420
 QY 421 GACCACTCCAGAGCTGCTGGTGGGGATGAAGTCCCAAGAAAGATCTCATGCTGAG 480
 DB 421 GACCACTCCAGAGCTGCTGGTGGGGATGAAGTCCCAAGAAAGATCTCATGCTGAG 480
 QY 481 CTCAGGAGACATGACCTGAGCAAGAAAGCAAGCAAAAGAGAGCTGCTCTACATCTGGCC 540
 DB 481 CTCAGGAGACATGACCTGAGCAAGAAAGCAAGCAAAAGAGAGCTGCTCTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAGATGATGAATCTCTGCTGAGCAGAGATGCTCACTTAAT 600
 DB 541 TCTGCCAATGGGAATTCAGAGATGATGAATCTCTGCTGAGCAGAGATGCTCACTTAAT 600
 QY 601 GTCTCTGAGCAAAAGAGAGAGAGCTGATGAAGAGGCTGAAGGCTGAGCAAGATGGA 660
 DB 601 GTCTCTGAGCAAAAGAGAGAGAGCTGATGAAGAGGCTGAAGGCTGAGCAAGATGGA 660
 QY 661 TGTGCTTATGTTGTGAGCAAGTGGCACTGATCCAAATATTCAGATGATGAGAAAT 720
 DB 661 TGTGCTTATGTTGTGAGCAAGTGGCACTGATCCAAATATTCAGATGATGAGAAAT 720
 QY 721 ACCACTCTGCACTAGCTATCTATTAATGAAGATTAATGAGCCAAAGCACTGCTTA 780
 DB 721 ACCACTCTGCACTAGCTATCTATTAATGAAGATTAATGAGCCAAAGCACTGCTTA 780
 QY 781 TATGTGCTGATATCCAAATCAAAAGCAAGATGAGCTGCAACACTGTTACTGGTGA 840
 DB 781 TATGTGCTGATATCCAAATCAAAAGCAAGATGAGCTGCAACACTGTTACTGGTGA 840
 QY 841 CATGAGCAAAAGAGAGAGCTGGAATTTTATCAAGAAAGAGCAATTTAATGCA 900
 DB 841 CATGAGCAAAAGAGAGAGCTGGAATTTTATCAAGAAAGAGCAATTTAATGCA 900
 QY 901 CTGAGATGATGAGAGAGCTGCTCATATCTTGTGATGTTGTGATCAAGCAATATA 960
 DB 901 CTGAGATGATGAGAGAGCTGCTCATATCTTGTGATGTTGTGATCAAGCAATATA 960
 QY 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGC 1020
 DB 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGC 1020
 QY 1021 GCGAGAGATATGCTGTTCTAGTCAATCATATGATTTGTCAGTACTTCTGCTGAC 1080
 DB 1021 GCGAGAGATATGCTGTTCTAGTCAATCATATGATTTGTCAGTACTTCTGCTGAC 1080
 QY 1081 AAAAGAAAAAGATGCTAAATATCTTCTGAAACAGCAATCCAGAACAGCTTAAG 1140
 DB 1081 AAAAGAAAAAGATGCTAAATATCTTCTGAAACAGCAATCCAGAACAGCTTAAG 1140
 QY 1141 CTGACATGAGAGAGAGCTCAAGAGTTCAAGGCAAGTGAATATGCCAGCCAGAGAA 1200
 DB 1141 CTGACATGAGAGAGAGCTCAAGAGTTCAAGGCAAGTGAATATGCCAGCCAGAGAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAAGATGAAG 1260
 DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAAGATGAAG 1260
 QY 1261 AAGCATGAAGATTAATATGATGATTAAGAAAGCTGATTAATGATGCTGCTGAGC 1320
 DB 1261 AAGCATGAAGATTAATATGATGATTAAGAAAGCTGATTAATGATGCTGCTGAGC 1320

QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAACCTGAAATGACAATTT 1380
 DB 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAACCTGAAATGACAATTT 1380
 QY 1381 CCTGACAGAGAAAGTGAAGATATCAAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 DB 1381 CCTGACAGAGAAAGTGAAGATATCAAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 QY 1441 AAAAGATGCCAAATATCTTCTGTAAGAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
 DB 1441 AAAAGATGCCAAATATCTTCTGTAAGAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
 QY 1501 TCAGAGAGAGATGACAAAGGCTTGGAGGAGGAGAAATGGCAGCAGAGAAAGATCT 1560
 DB 1501 TCAGAGAGAGATGACAAAGGCTTGGAGGAGGAGAAATGGCAGCAGAGAAAGATCT 1560
 QY 1561 CAAGAACAGAAATTAATAGATGATGATGAGAGCTGAGAAATTTATGCTATCGAA 1620
 DB 1561 CAAGAACAGAAATTAATAGATGATGATGAGAGCTGAGAAATTTATGCTATCGAA 1620
 QY 1621 GAAATGAGAGAGAGAGAGTACTCATGTCGATTCAGAAACCTGACTAATGCTGCC 1680
 DB 1621 GAAATGAGAGAGAGAGAGTACTCATGTCGATTCAGAAACCTGACTAATGCTGCC 1680
 QY 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCAAGAGAGAGCAACCTGAAAGC 1740
 DB 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCAAGAGAGAGCAACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTGACACTGAGATGAGAGATGATCAAGTGAAGCAAAATGATCTGAG 1800
 DB 1741 CAGCAATTTCTGACACTGAGATGAGAGATGATCAAGTGAAGCAAAATGATCTGAG 1800
 QY 1801 AAGCAATTTTGTGAAGAGAGAGCACTGGAATATTAACAGATGATGATTCATGAA 1860
 DB 1801 AAGCAATTTTGTGAAGAGAGAGCACTGGAATATTAACAGATGATGATTCATGAA 1860
 QY 1861 GAAAGAGAGATGAGAGTGTGTAAGAAATGAAATTCGAGCTTCTTGTGTTAGAA 1920
 DB 1861 GAAAGAGAGATGAGAGTGTGTAAGAAATGAAATTCGAGCTTCTTGTGTTAGAA 1920
 QY 1921 GAAAGAGAGATGAGAGTGTGTAAGAAATGAAATTCGAGCTTCTTGTGTTAGAA 1980
 DB 1921 GAAAGAGAGATGAGAGTGTGTAAGAAATGAAATTCGAGCTTCTTGTGTTAGAA 1980
 QY 1981 GAGCTGAGACAGATGAGAAATCATGAGCCAGCTTAAGAAATGAGAAATGAGAA 2040
 DB 1981 GAGCTGAGACAGATGAGAAATCATGAGCCAGCTTAAGAAATGAGAAATGAGAA 2040

RESULT 13
 US-10-144-678A-375
 ; Sequence 375, Application US/10144678A
 ; Publication No. US20030157089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yudi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedick, Thomas S.
 ; APPLICANT: Carter, Darriek
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yaelir A. W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.

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/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals Y de Baesols, Carlota
/ APPLICANT: Foy, Teresa M.
/ APPLICANT: Matanabe, Yoshihiro
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C28
/ CURRENT APPLICATION NUMBER: US/10/144,678A
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-144-678A-375

Query Match      100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGATGAGTTGATTCATGCCGCTCTTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGTGATGAGTTGATTCATGCCGCTCTTCTGTGAAGAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGTGCGAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGTGCGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGCGTG 240
DB 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGCGTG 240
QY 241 GGGGCTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGTGCTGCAAGGAGAGCGGCAAGAGAGTGGGCGCTTG 360
DB 301 TGGTGTGCACTGCTTCCCTGTGCTGCAAGGAGAGCGGCAAGAGAGTGGGCGCTTG 360
QY 361 GGAAGCTAGAGTGAAGTGTGCTTCAATGAGGCCAGGTAACACGCTCGTGAAGAGATCTG 420
DB 361 GGAAGCTAGAGTGAAGTGTGCTTCAATGAGGCCAGGTAACACGCTCGTGAAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACATGACGCTGACCAAGAGACCAAGCAAAAGAGAGCTCTACATCTGGCC 540
DB 481 CTCAGGAGACATGACGCTGACCAAGAGACCAAGCAAAAGAGAGCTCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGACAGAGATGCTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGACAGAGATGCTCAACTTAAT 600
QY 601 GTCCTTGAACAACAAAGAGAGAGCTGATTAAGGCGGTAAAGCCAGAGAGATGTA 660
DB 601 GTCCTTGAACAACAAAGAGAGAGCTGATTAAGGCGGTAAAGCCAGAGAGATGTA 660
QY 661 TGTGCTTAATGTTGTGTAACATGACATGATCAAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGTGTAACATGACATGATCAAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTAATTAAGAGATTAATTAAGCCAAAGCACTGCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTAATTAAGAGATTAATTAAGCCAAAGCACTGCTTA 780
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QY 781 TATGTGCTGATATGGAATCAAAAAAAGAGATGGCTCAGACCACTGTTACTGGTGA 840
DB 781 TATGTGCTGATATGGAATCAAAAAAAGAGATGGCTCAGACCACTGTTACTGGTGA 840
QY 841 CATGACAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGACAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATGAGAGAGCTGCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATGAGAGAGCTGCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGACCTTCTACTGAGCAAAATATTAATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGACCTTCTACTGAGCAAAATATTAATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAATCTCTGAAAAACAGCAATCCAGAACAACTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAATCTCTGAAAAACAGCAATCCAGAACAACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGAAATATGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGAAATATGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATAGTGGATTTACTAGAAAACTGCACTAAATGATGCTGCTGAC 1320
DB 1261 AAGCATGAAAGTAAATAGTGGATTTACTAGAAAACTGCACTAAATGATGCTGCTGAC 1320
QY 1321 AATGGTATTAATGATTAATCTCAAAAGAGAGAGAGACAGCTGAATCAGCAATTT 1380
DB 1321 AATGGTATTAATGATTAATCTCAAAAGAGAGAGAGACAGCTGAATCAGCAATTT 1380
QY 1381 CCTGACAGAGAAAGTGAAGAGATATCAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAGAGAAAGTGAAGAGATATCAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACTTAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGATGCAAAAGGCTTGAGGAGTGAATGAGCAAGAGAGAGAGAGAGTCT 1560
DB 1501 TCAGAGAAAGATGCAAAAGGCTTGAGGAGTGAATGAGCAAGAGAGAGAGAGAGTCT 1560
QY 1561 CAAAGAACAGAAATTAATAGATGATGATAGAGCTAGAGAAATTTATAGCTATCGAA 1620
DB 1561 CAAAGAACAGAAATTAATAGATGATGATAGAGCTAGAGAAATTTATAGCTATCGAA 1620
QY 1621 GAAATGAGAGAGAGAGAGTCTCATGTCGATTTCCAGAAAACTGATCTAATGCTGAC 1680
DB 1621 GAAATGAGAGAGAGAGAGTCTCATGTCGATTTCCAGAAAACTGATCTAATGCTGAC 1680
QY 1681 ACTGCTGGCAATGATGATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGTCT 1740
DB 1681 ACTGCTGGCAATGATGATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGTCT 1740
QY 1741 CAGCAATTTCTGACATGAGATGAGAGATGACAGTGAAGCAAAATGATCTCAG 1800
DB 1741 CAGCAATTTCTGACATGAGATGAGAGATGACAGTGAAGCAAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACTGGAATATTTACAGATGAGATTTGATTCATGAA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACTGGAATATTTACAGATGAGATTTGATTCATGAA 1860
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Db 1561 CAAGAACCGAATAATAAGATGATGATAGAGACCTAGAAAATTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAAGACGGAAGTCTCATGTGCGATTTCCCGAAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAAGACGGAAGTCTCATGTGCGATTTCCCGAAGAAACCTGACTAATGCTGCC 1680
Qy 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAGGAAGACGAGAACCTGTAAGC 1740
Db 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAGGAAGACGAGAACCTGTAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTACGAGCAAAATGATTAATCTGAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTACGAGCAAAATGATTAATCTGAG 1800
Qy 1801 AAGCAATTTTGTGAAGAAGAACACTGGAATTTTCAAGATGAGATTTGATTTCTATGA 1860
Db 1801 AAGCAATTTTGTGAAGAAGAACACTGGAATTTTCAAGATGAGATTTGATTTCTATGA 1860
Qy 1861 GAAAGACAGATAGAAATGCTGTAAGAAATGAATTTCTGAGCTTTCTCTAGTTGTAGAA 1920
Db 1861 GAAAGACAGATAGAAATGCTGTAAGAAATGAATTTCTGAGCTTTCTCTAGTTGTAGAA 1920
Qy 1921 GAAAAAGACATCTTGCAATGAAAAATAGTACGTTGCGGAAAGAAATTCGATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCAATGAAAAATAGTACGTTGCGGAAAGAAATTCGATGCTAAGACTG 1980
Qy 1981 GAGCTGACACATGAATAACATCGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040
Db 1981 GAGCTGACACATGAATAACATCGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040

RESULT 15
US-10-294-025-375

/ Sequence 375, Application US/10294025
/ Publication No. US20030185830A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Stolk, John A.
/ APPLICANT: Kalos, Michael D.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C29
/ CURRENT APPLICATION NUMBER: US/10/294,025
/ CURRENT FILING DATE: 2002-11-12
/ NUMBER OF SEQ ID NOS: 1038
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-294-025-375

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTTGAGGTGATTTCCATGCGGCTGCTCTTCTGTGAAGAACCAATTTGCTTC 60
Db 1 ATGTGTGTTGAGGTGATTTCCATGCGGCTGCTCTTCTGTGAAGAACCAATTTGCTTC 60
Qy 61 AGGAGCAAGTGGGCAAGTGTGCTGCGGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGTGGGCAAGTGTGCTGCGGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGTATGAAGCACTCAAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGTATGAAGCACTCAAGAGCAAG 180
Qy 181 ATGGGCAATGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAATGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240

Qy 241 GCGCTCTGAGAGACCAAGACGACTCTGTATGAAGACACTCAGGAAACAGATGGGCAAG 300
Db 241 GCGCTCTGAGAGACCAAGACGACTCTGTATGAAGACACTCAGGAAACAGATGGGCAAG 300
Qy 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
Qy 361 GGAAGCTAGATGACAGTGCCTTCATGAGAGCCAGGTACCAAGTCGATGAGAAATCG 420
Db 361 GGAAGCTAGATGACAGTGCCTTCATGAGAGCCAGGTACCAAGTCGATGAGAAATCG 420
Qy 421 GACAACTCCACAGAGCTGCTGTGGGTAAGTCCCAAGAAAGATCTCATCTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGTGGGTAAGTCCCAAGAAAGATCTCATCTCATG 480
Qy 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTCAATCTGGCC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTCAATCTGGCC 540
Qy 541 TCTGCAATGGGAATTTCAAGAGTACTTAAATCTCTGCTGACAGACATGCTAAT 600
Db 541 TCTGCAATGGGAATTTCAAGAGTACTTAAATCTCTGCTGACAGACATGCTAAT 600
Qy 601 GTCTTGAACAACAAGAGAGACAGCTCTGATTAAGGCGGTACAATGCCAGGAATGA 660
Db 601 GTCTTGAACAACAAGAGAGACAGCTCTGATTAAGGCGGTACAATGCCAGGAATGA 660
Qy 661 TGTGCTTAATGTGCTGGAACATGCACTGATCCAAATTTCCAGATGATGAAAT 720
Db 661 TGTGCTTAATGTGCTGGAACATGCACTGATCCAAATTTCCAGATGATGAAAT 720
Qy 721 ACCACTGCACTAGGCTATCTATATGAAGTAATTAATGGCCAAAGCACTGCTT 780
Db 721 ACCACTGCACTAGGCTATCTATATGAAGTAATTAATGGCCAAAGCACTGCTT 780
Qy 781 TATGTGCTGATATGCAATCAAAAAACAAGCTGCTCAACAAGCTGTTACTTGTGTA 840
Db 781 TATGTGCTGATATGCAATCAAAAAACAAGCTGCTCAACAAGCTGTTACTTGTGTA 840
Qy 841 CATGAGCAAAAAACAGAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
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Db 901 CTGATATATATGAGAAAGACGCTCTCATCTGCTGTATGTTGTGATCAGCAAGTATA 960
Qy 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATGTAATTTGCAAGATCTATCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATGTAATTTGCAAGATCTATCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATCTTAAAAATCTCTGTAAGAACAGCAATCCAGAACAACTTAAAG 1140
Db 1081 AAAAGAAAAACAGATCTTAAAAATCTCTGTAAGAACAGCAATCCAGAACAACTTAAAG 1140
Qy 1141 CTGACATCAGAGGAAGTCAAAAGGTTCAAAAGGAGTAAGAAATAGCCAGCAGAGAA 1200
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Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGTATGAGAGGTTGAAGAAATGAG 1260
Qy 1261 AAGCATGAAGTAATTAATGTGGATTAATCAAGAAACCTGACTTAATGTGTCTGCTG 1320
Db 1261 AAGCATGAAGTAATTAATGTGGATTAATCAAGAAACCTGACTTAATGTGTCTGCTG 1320
Qy 1321 AATGTGATTAATGATTAATCTCAAGGAAGACAGAACACTGAAATTAATGCAATTT 1380

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Db 1321 AATGGATATGATTAATTCCTCAAGAGAGACGACACCTGAAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAGATGAGATATCACAGAAATTTGGAAATTAAGTTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAGATGAGATATCACAGAAATTTGGAAATTAAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACGATGCGCAAAATATCTCTCTGAAAACAGAACCCGAAACCAAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCGCAAAATATCTCTCTGAAAACAGAACCCGAAACCAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGATGACAAAGGCTTTGAGGCGAGTGAATGGCCAGCCAGAGAAAAGATCT 1560
Db 1501 TCAGAGAGAGATGACAAAGGCTTTGAGGCGAGTGAATGGCCAGCCAGAGAAAAGATCT 1560
QY 1561 CAAGAACCGAATAATTAAGATGGTATAGAGAGCTAGAAAATTTATGGCTATCGAA 1620
Db 1561 CAAGAACCGAATAATTAAGATGGTATAGAGAGCTAGAAAATTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAAGCAGGAGTACTCATGTCGGAATTCCTCCAAAGAGAGCAGAACCTGAAAGC 1680
Db 1621 GAAATGAAGAAGCAGGAGTACTCATGTCGGAATTCCTCCAAAGAGAGCAGAACCTGAAAGC 1680
QY 1681 ACTGCTGCAATGATGATGATTAATTTCTCCAAAGAGAGCAGAACCTGAAAGC 1740
Db 1681 ACTGCTGCAATGATGATGATTAATTTCTCCAAAGAGAGCAGAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAGAGATATCAAGTACGAAACAAATGATATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAGAGATATCAAGTACGAAACAAATGATATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATTTTACAGATGAGATTCGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATTTTACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAAGCAGATAGAGTGGTGAATAATGAATTCGAGCTTCTCTTAGTTGTAGAAA 1920
Db 1861 GAAAAGCAGATAGAGTGGTGAATAATGAATTCGAGCTTCTCTTAGTTGTAGAAA 1920
QY 1921 GAAAAGACATCTTGATGAAAAATAGTAGTTGCCGGAAGAAATGCCATGCTAAGACTG 1980
Db 1921 GAAAAGACATCTTGATGAAAAATAGTAGTTGCCGGAAGAAATGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCGCTTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACACATGAAACATCAGAGCCGCTTAAAAAATGAAAAAATGAAAAA 2040
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Search completed: December 19, 2005, 09:03:20
Job time : 1666.28 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 01:38:47 ; Search time 248.436 Seconds
(Without alignments)
4025.047 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgctgctgctgagctgcttc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4161431 seqs, 245089505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8322154

Minimum DB seq length: 10
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA.New:*
1: /cgn2_6/prodata/1/pubpna/us09_NEW_PUB.seq:*
2: /cgn2_6/prodata/1/pubpna/us06_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/us07_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/us08_NEW_PUB.seq:*
5: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/us10_NEW_PUB.seq:*
7: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq:*
8: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq2:*
9: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq3:*
10: /cgn2_6/prodata/1/pubpna/us60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	1.6	201	6	US-10-995-561-30293
2	32	1.6	201	6	US-10-995-561-30293
3	32	1.6	201	6	US-10-995-561-30411
4	32	1.6	201	6	US-10-995-561-30414
5	32	1.6	148220	7	US-11-121-086-90
6	32	1.6	187986	6	US-10-995-561-13252
7	31	1.5	201	6	US-10-995-561-82843
8	31	1.5	66131	6	US-10-995-561-13501
9	31	1.5	167891	7	US-11-121-086-14
10	31	1.5	179892	7	US-11-112-908-39
11	30	1.5	201	6	US-10-995-561-26191
12	30	1.5	201	6	US-10-995-561-46434
13	30	1.5	201	6	US-10-995-561-50343
14	30	1.5	201	6	US-10-995-561-50425
15	30	1.5	201	6	US-10-995-561-51237
16	30	1.5	201	6	US-10-995-561-68585
17	30	1.5	201	6	US-10-995-561-68607
18	30	1.5	201	6	US-10-995-561-68609
19	30	1.5	356	6	US-10-508-424-8
20	30	1.5	600	7	US-11-123-896-256
21	30	1.5	722	6	US-10-689-742-79
22	30	1.5	779	7	US-11-051-568-22
23	30	1.5	1279	7	US-11-179-411-31

24	30	1.5	1279	7	US-11-175-766-31	Sequence 31, Appl
25	30	1.5	1478	6	US-10-909-125-1744	Sequence 1744, Ap
26	30	1.5	1968	6	US-10-131-826A-163	Sequence 163, App
27	30	1.5	2036	6	US-10-996-217A-8	Sequence 8, Appl
28	30	1.5	2120	7	US-11-167-856-29	Sequence 29, Appl
29	30	1.5	2408	7	US-11-090-439-55	Sequence 55, Appl
30	30	1.5	3001	7	US-11-145-703-153	Sequence 153, Appl
31	30	1.5	3001	7	US-11-145-703-153	Sequence 153, Appl
32	30	1.5	14082	6	US-10-995-561-13445	Sequence 13445, A
33	30	1.5	48763	6	US-10-663-794-3	Sequence 3, Appl
34	30	1.5	56054	6	US-10-995-561-13402	Sequence 13402, A
35	30	1.5	86950	6	US-10-857-780-5	Sequence 5, Appl
36	30	1.5	87672	6	US-10-995-561-13237	Sequence 13237, A
37	30	1.5	119160	7	US-11-121-086-12	Sequence 12, Appl
38	30	1.5	120096	7	US-11-121-086-24	Sequence 24, Appl
39	30	1.5	127340	7	US-11-112-908-35	Sequence 35, Appl
40	30	1.5	146656	7	US-11-121-086-68	Sequence 68, Appl
41	30	1.5	146656	7	US-11-121-086-68	Sequence 68, Appl
42	30	1.5	149419	7	US-11-112-908-49	Sequence 49, Appl
43	30	1.5	153376	7	US-11-121-086-5	Sequence 5, Appl
44	30	1.5	155515	7	US-11-112-908-42	Sequence 42, Appl
45	30	1.5	159497	7	US-11-112-908-61	Sequence 61, Appl

ALIGNMENTS

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RESULT 1
US-10-995-561-30293/C
; Sequence 30293, Application US/10995561
; Publication No. US20050272054A1
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30293
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-30293

Query Match      1.6%; Score 32; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db      145 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 114

RESULT 2
US-10-995-561-30411/C
; Sequence 30411, Application US/10995561
; Publication No. US20050272054A1
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30411
; LENGTH: 201
; TYPE: DNA
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ORGANISM: Homo sapiens
US-10-995-561-30411

Query Match 1.6%; Score 32; DB 6; Length 201;
Best Local Similarity 100.0%; Pred.No. 0.0011;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 148 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 117

RESULT 3
US-10-995-561-30414/C
Sequence 30414, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30414

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-10-995-561-30414

Query Match 1.6%; Score 32; DB 6; Length 201;
Best Local Similarity 100.0%; Pred.No. 0.0011;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 98 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 67

RESULT 4
US-11-121-086-90
Sequence 90, Application US/11121086
Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3

SEQ ID NO 90

LENGTH: 148220

TYPE: DNA

ORGANISM: Homo sapiens

US-11-121-086-90

Query Match 1.6%; Score 32; DB 7; Length 148220;
Best Local Similarity 100.0%; Pred.No. 0.00047;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 144334 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 144365

RESULT 5
US-10-995-561-13252/C

Sequence 13252, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13252

LENGTH: 187986

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc.feature

LOCATION: (1)...(187986)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13252

Query Match 1.6%; Score 32; DB 6; Length 187986;
Best Local Similarity 100.0%; Pred.No. 0.00046;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 139832 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 139801

RESULT 6
US-10-995-561-82843/C
Sequence 82843, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 82843

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-10-995-561-82843

Query Match 1.5%; Score 31; DB 6; Length 201;
Best Local Similarity 100.0%; Pred.No. 0.0028;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2010 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 152 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 122

RESULT 7
US-10-995-561-13501/C
Sequence 13501, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702


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; Sequence 50343, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50343
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-50343

Query Match      1.5%; Score 30; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB      132 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 103

RESULT 13
US-10-995-561-50425/c
; Sequence 50425, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50425
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-50425

Query Match      1.5%; Score 30; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB      94 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 65

RESULT 14
US-10-995-561-51237/c
; Sequence 51237, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51237
; LENGTH: 201
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-995-561-51237

Query Match      1.5%; Score 30; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB      131 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 102

RESULT 15
US-10-995-561-68585
; Sequence 68585, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68585
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-68585

Query Match      1.5%; Score 30; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB      141 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 170

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Search completed: December 19, 2005, 09:12:38
Job time : 251.436 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:08:19 ; Search time 8222.61 Seconds

(without alignments)
11607.702 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040
Sequence: 1 atgctgtgtgaggtgatcc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82154912

Minimum DB seq length: 10

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_est8:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492	24.1	729	5	BU930826
2	184	9.0	521	9	AQ204617 HS_3229_B
3	141	6.9	865	2	BF676987 602084215
4	140	6.9	451	1	AI804733 t42203.x
5	137	6.7	289	1	AAS33501
6	129	6.3	531	9	AQ615477 HS_5144_B
7	117	5.7	621	3	BM763942 K-EST0045
8	117	5.7	633	3	BM763453 K-EST0044
9	117	5.7	817	5	BQ441373
10	90	4.4	263	10	AG192933
11	89	4.4	400	9	AQ124119 HS_3122_A
12	87	4.3	339	9	AQ030111 RPI11-39
13	87	4.3	544	1	AL703938 DKF2P868
14	79	3.9	279	3	B1461255 603206584
15	76	3.7	6098	4	HSMB09270
16	74	3.6	505	5	EX492731 DKF2P781C
17	73	3.6	385	5	AQ063365 CIT-HSP-2
18	65	3.2	232	5	BU584009 2275475H1
19	64	3.1	381	7	CR747857 CR747857
20	59	2.9	707	10	AG045796 Pan trogl
21	57	2.8	607	9	B48260 RPI11-6K4
22	52	2.5	380	2	BF329652 RCG-BN027

23	50	2.5	592	9	AQ372700
24	49	2.4	493	10	AG193231
25	49	2.4	495	9	AQ469831
26	49	2.4	557	9	AQ469663
27	49	2.4	667	10	AG156382
28	49	2.4	697	9	AQ030113
29	47	2.3	187	2	BE069869
30	47	2.3	476	2	AQ392059
31	46	2.3	351	7	CV383025
32	46	2.3	400	9	AQ057106
33	45	2.2	218	5	BU584404
34	45	2.2	259	5	BU584020
35	45	2.2	338	5	BU584405
36	45	2.2	423	5	BU584403
37	45	2.2	874	6	CD358418
38	45	2.2	894	6	BF675049
39	45	2.2	5483	4	BC063888
40	44	2.2	460	9	AQ360298
41	41	2.0	710	10	AG165908
42	40	2.0	503	9	B55862
43	40	2.0	632	7	CV341500
44	39	1.9	1011	9	AQ090910
45	38	1.9	458	9	AQ247090

ALIGNMENTS

RESULT 1	BU930826	729 bp	RNA	linear	EST 18-OCT-2002
LOCUS	AGENCOURT_10425351 NIH_MGC_83	Homo sapiens	cDNA clone	IMAGE:6668956	
DEFINITION	5', mRNA sequence.				
ACCESSION	BU930826				
VERSION	BU930826.1	GI:24119645			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 729)				
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L10M2943 row: 0 column: 04 High quality sequence stop: 555. Location/Qualifiers 1. 729 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6668956" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH MGC 83" /note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site1: SfiI (ggccatcgcc); Site2: SfiI (ggccatcgcc); 5' and 3' adaptor were used in cloning as follows: 5' adaptor sequence: 5'-ATTCGTAGAGCGAGCGCCGACATGATG-3' and 3' adaptor sequence: 5'-CACGGCCATTATGACC-3' 5'-ATTCGTAGAGCGAGCGCCGACATG-3' (30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 clones contained inserts by PCR. This library was enriched for full-length clones				

ORIGIN and was constructed by Clontech Laboratories (Palo Alto, CA)."

Query Match 24.1%; Score 492; DB 5; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.3e-230;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 AGGCGCTACAAATCCGAGAAAGATGATGCGTTAATGTCGTAACATGGCAGTATC 694
DB 89 AGGCGCTACAAATCCGAGAAAGATGATGCGTTAATGTCGTAACATGGCAGTATC 148
QY 695 CAAATATCCAGATGATGATGAAATACCACTCTGCATACGCTATCTAATGAGATAT 754
DB 149 CAAATATCCAGATGATGATGAAATACCACTCTGCATACGCTATCTAATGAGATAT 208
QY 755 AATTATGGCCAAAGACATGCTCTTATATGTCCTATATCGAATCAAAAAACAGCATG 814
DB 209 AATTATGGCCAAAGACATGCTCTTATATGTCCTATATCGAATCAAAAAACAGCATG 268
QY 815 GCCTCACACCACTGTTACTTGTGTATGATGACAAAGCAAGTCGTGAATTTTAA 874
DB 269 GCCTCACACCACTGTTACTTGTGTATGATGACAAAGCAAGTCGTGAATTTTAA 328
QY 875 TCAGAAAAAAGCAATTTAATGACCTGATGATGAAAGCACTGCTCATATCTG 934
DB 329 TCAGAAAAAAGCAATTTAATGACCTGATGATGAAAGCACTGCTCATATCTG 388
QY 935 CTGTATGTTGTGATGATGACAAATGATGATGATGATGATGATGATGATGATGAT 994
DB 389 CTGTATGTTGTGATGATGACAAATGATGATGATGATGATGATGATGATGATGAT 448
QY 995 CTCTCAAGATCTATCTGACAGACGCGCAGAGATGATGATGATGATGATGATGAT 1054
DB 449 CTCTCAAGATCTATCTGACAGACGCGCAGAGATGATGATGATGATGATGATGAT 508
QY 1055 TAATTTGCCAGTTACTTTCTGACTACAAAGAAAAACAGATGCTAAATCTCTTGAAA 1114
DB 509 TAATTTGCCAGTTACTTTCTGACTACAAAGAAAAACAGATGCTAAATCTCTTGAAA 568
QY 1115 ACAGCAATCCAG 1126
DB 569 ACAGCAATCCAG 580

RESULT 2
LOCUS AQ04617 521 bp DNA linear GSS 17-SEP-1998
DEFINITION HS_3229_B1.G12.T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=23 Row=N, genomic survey sequence.

ACCESSION AQ04617
VERSION AQ04617.1 GI:3615187
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,D., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

FEATURES
source
1..521
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3229 Col=23 Row=N"
/sex="male"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBel0BAC11; BAC clones in E-Coli DH10B"

ORIGIN
Query Match 9.0%; Score 184; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 8.6e-79;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGCTGAAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTATGTCGAT 1654
DB 231 AGCTGAAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTATGTCGAT 290
QY 1655 TCCGAGAAACCTGACTAATGATGTCGACATGTCGCAATGATGATGATTAATTCCTC 1714
DB 291 TCCGAGAAACCTGACTAATGATGTCGACATGTCGCAATGATGATGATTAATTCCTC 350
QY 1715 CAAGGAAGACGAAACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGATATC 1774
DB 351 CAAGGAAGACGAAACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGATATC 410
QY 1775 ACAG 1778
DB 411 ACAG 414

RESULT 3
LOCUS BF676987 865 bp mRNA linear EST 21-DEC-2000
DEFINITION 602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5', mRNA sequence.

ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L10C1067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers
1..865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/lab_host="DH10B (TI phage-resistant)"

ORIGIN

/clone.lib="NIH_MGC_83"
/note="Organ: prostate; Vector: PDNR-LIB (Clontech);
Site_1: SfiI (ggcgccggcc); Site_2: SfiI
(ggccatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTAGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGCGCCGACATG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

Query Match 6.9%; Score 141; DB 2; Length 865;
Best Local Similarity 100.0%; Pred. No. 1.4e-57;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 ACTGCTCATCTCTGATGTTGATGATGAGCAAGTATGATGACCTTCTACTTGA 978
DB 353 ACTGCTCATCTCTGATGTTGATGATGAGCAAGTATGATGACCTTCTACTTGA 412
QY 979 CAAATATGATGATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGTT 1038
DB 413 CAAATATGATGATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGTT 472
QY 1039 TCTAGTCATCATCATGTAATT 1059
DB 473 TCTAGTCATCATCATGTAATT 493

RESULT 4
AI804733 451 bp mRNA linear EST 07-MAR-2000
LOCUS tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253677 3',
DEFINITION mRNA sequence.
ACCESSION AI804733
VERSION AI804733.1 GI:5370205
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
www.bio.lnlnl.gov/bbrp/image/image.html
Insert Length: 543 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source

1..451
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2253677"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="NCI CGAP Pr28"
/note="Organ: prostate; Vector: PT773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the

ORIGIN

normalized library NCI CGAP Pr22 was prepared, and as
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

Query Match 6.9%; Score 140; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 4.2e-57;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 AGGACTGCTCATCTCTGATGTTGATGATGAGCAAGTATGATGACCTTCTACTT 975
DB 47 AGGACTGCTCATCTCTGATGTTGATGATGAGCAAGTATGATGACCTTCTACTT 106
QY 976 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCT 1035
DB 107 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCT 166
QY 1036 GTTCTAGTCATCATCATGTT 1055
DB 167 GTTCTAGTCATCATCATGTT 186

RESULT 5
AA533501 289 bp mRNA linear EST 21-AUG-1997
LOCUS nj96a04.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000302,
DEFINITION mRNA sequence.
ACCESSION AA533501
VERSION AA533501.1 GI:2277597
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chasqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
www.bio.lnlnl.gov/bbrp/image/image.html
Insert Length: 217 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham.

FEATURES
source

1..289
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1000302"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/clone.lib="NCI CGAP Pr11"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells, cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."

ORIGIN

Query Match 6.7%; Score 137; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1788 AATGATCTCAGAACCAATTTTGTGAAGAACCAACTGTGAAATTTACAGATGAGT 1847
 DB 9 AATGATCTCAGAACCAATTTTGTGAAGAACCAACTGTGAAATTTACAGATGAGT 68
 QY 1848 TCTGATTCATGAAGAAAGACATAGAGTGTGTAAGAAAATGAAATTCGAGCTTCTCT 1907
 DB 69 TCTGATTCATGAAGAAAGACATAGAGTGTGTAAGAAAATGAAATTCGAGCTTCTCT 128
 QY 1908 TAGTTGTGAAGAAAGAAA 1924
 DB 129 TAGTTGTGAAGAAAGAAA 145

RESULT 6
 LOCUS A0615477 531 bp DNA linear GSS 15-JUN-1999
 DEFINITION HS 5144.B1.G01.T7A.RPCT-11 Human Male BAC Library Homo sapiens
 ACCESSION A0615477
 VERSION A0615477.1 GI:5076753
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;
 MAMMALIA; BUTHERIA; EUARCHONTOGLIRES; PRIMATES; CATARRHINI;
 HOMINIDAE; Homo.
 1 (bases 1 to 531)
 Mahitras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 CONTACT: Mahitras GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCT-11. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.bufileo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering/bac.htm>)
 or from Research Genetics (<http://www.resgen.com>). BAC end Web Server:
<http://www.htec.washington.edu>
 Plate: 720 row: N column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 531.
 Location/Qualifiers
 1..531
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=720 Col=1 Row=N"
 /sex="male"
 /clone_lib="RPCT-11 Human Male BAC Library"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"

ORIGIN
 Query Match 6.3%; Score 129; DB 9; Length 531;
 Best Local Similarity 100.0%; Pred. No. 1.1e-51;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CATGGACGTGATCCAAATATTCCAGATGATGTGAATATACCACTTGCACTACGCTATC 741
 DB 117 CATGGACGTGATCCAAATATTCCAGATGATGTGAATATACCACTTGCACTACGCTATC 176
 QY 742 TATATGAAGATTAATTAATGGCCAAAGCACTGCTTATATATGATGCTGATATCA 801
 DB 177 TATATGAAGATTAATTAATGGCCAAAGCACTGCTTATATATGATGCTGATATCA 236
 QY 802 AAAACCAAG 810
 DB 237 AAAACCAAG 245

RESULT 7
 LOCUS BM763942 621 bp mRNA linear EST 04-MAR-2002
 DEFINITION K-EST0045367 S13KM55 Homo sapiens CDNA clone S13KM55-25-A11 5',
 mRNA sequence.
 ACCESSION BM763942
 VERSION BM763942.1 GI:19093557
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;
 MAMMALIA; BUTHERIA; EUARCHONTOGLIRES; PRIMATES; CATARRHINI;
 HOMINIDAE; Homo.
 1 (bases 1 to 621)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 25 row: A column: 11
 High quality sequence stop: 621.
 Location/Qualifiers
 1..621
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KM55-25-A11"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10P"
 /clone_lib="S13KM55"
 /note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
 (A)+ RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tobacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was
 ligated with DNA-RNA linker including EcoRI site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dt-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10P by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

ORIGIN
 Query Match 5.7%; Score 117; DB 3; Length 621;
 Best Local Similarity 99.1%; Pred. No. 9.3e-46;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 510 CAAGCAAAAGAGACGCTCTTACATCTGGCTCTGCCAATGGCAATTCAGAGTAGTAAA 569
Db 1 CAAGCAAAAGAGACGCTCTTACATCTGGCTCTGCCAATGGCAATTCAGAGTAGTAAA 60
QY 570 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGACAAACAAAAGAGACAGCTCT 629
Db 61 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGACAAACAAAAGAGACAGCTCT 120
QY 630 GATTAAGGCCGTACCAATGCCAGGAAGATGATGTCCTTAATGTCTTGACAAATGGCAC 689
Db 121 GACAAAGGCCGTACCAATGCCAGGAAGATGATGTCCTTAATGTCTTGACAAATGGCAC 180
QY 690 TGATCCAAATATTCAGATGATGTAATGGAATACCACTCT 728
Db 181 TGATCCAAATATTCAGATGATGTAATGGAATACCACTCT 219

RESULT 8
LOCUS BM763453 633 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5',
mRNA sequence.
ACCESSION BM763453
VERSION BM763453.1 GI:19093068
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 633)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
JOURNAL 21C Frontier Korean EST Project 2001
COMMENT Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 11
high quality sequence stop: 633.
Location/Qualifiers
1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-16-A11"
/issue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10"
/clone_1b="S13KMS5"
/note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then deapped with tobacco acid
pyrophosphatase (TAP). The deapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10" by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

ORIGIN

ORIGIN

Query Match 5.7%; Score 117; DB 3; Length 633;
Best Local Similarity 99.1%; Pred. No. 9, 3e-46;
Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 510 CAAGCAAAAGAGACGCTCTTACATCTGGCTCTGCCAATGGCAATTCAGAGTAGTAAA 569
Db 1 CAAGCAAAAGAGACGCTCTTACATCTGGCTCTGCCAATGGCAATTCAGAGTAGTAAA 60
QY 570 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGACAAACAAAAGAGACAGCTCT 629
Db 61 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGACAAACAAAAGAGACAGCTCT 120
QY 630 GATTAAGGCCGTACCAATGCCAGGAAGATGATGTCCTTAATGTCTTGACAAATGGCAC 689
Db 121 GACAAAGGCCGTACCAATGCCAGGAAGATGATGTCCTTAATGTCTTGACAAATGGCAC 180
QY 690 TGATCCAAATATTCAGATGATGTAATGGAATACCACTCT 728
Db 181 TGATCCAAATATTCAGATGATGTAATGGAATACCACTCT 219

RESULT 9
LOCUS BQ441373 817 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
5', mRNA sequence.
ACCESSION BQ441373
VERSION BQ441373.1 GI:21180449
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2340 row: m column: 08
high quality sequence stop: 516.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6103855"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1b="NIH MGC 82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccgtcgcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGAGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN

Query Match 5.7%; Score 117; DB 5; Length 817;
Best Local Similarity 100.0%; Pred. No. 9, 4e-46;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1408 AGAATTGGGAATTAGTTCTGACTACAAAGAAAACAGATGCCAAATTAATTCTTGTGA 1467
DB      319 AGAATTTGGGAATTAGTTCTGACTACAAAGAAAACAGATGCCAAATTAATTCTTGTGA 378
QY      1468 AACAGACACCCAGAACAGACTTAAAGTCATCATCAGAGAAAGTTCACAAAGGCTT 1524
DB      379 AACAGACACCCAGAACAGACTTAAAGTCATCATCAGAGAAAGTTCACAAAGGCTT 435

RESULT 10
LOCUS   AG192933/c
DEFINITION Pan troglodytes DNA, clone: RP43-069123.TU, genomic survey
ACCESSION AG192933
VERSION   AG192933.1 GI:45225109
KEYWORDS  GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes

REFERENCE
AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
           Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
           BAC end sequences of library RP-43
           Unpublished
           2 (bases 1 to 263)
           Direct Submission
           Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
           Bioscience and Biotechnology (KIRIB), Genome Research Center (GRC);
           52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
           (E-mail:redstone@mail.kirib.re.kr, URL:http://phs.grc.kirib.re.kr/,
           Tel:82-42-866-7181, Fax:82-42-860-4409)
           Clones are derived from the chimpanzee BAC library RP-43 This BAC
           end was generated during the Rad process and may have higher chance
           of clone tracking errors.
           PRIMERS
           Sequencing: TU
           LIBRARY
           Vector      : pBACe3.6
           R Site 1    : EcoRI
           R Site 2    : EcoRI.
           Location/Qualifiers
             1. 263
               /organism="Pan troglodytes"
               /mol_type="genomic DNA"
               /db_xref="taxon:9598"
               /clone="RP43-069123.TU"
               /sex="male"
               /cell_type="lymphocytes"
               /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match      4.4%; Score 90; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1784 AACCAATGATCTACTGAGACGATTTTGGAGACAGACACTGGAATTTTACAGATG 1843
DB      90 AACCAATGATCTACTGAGACGATTTTGGAGACAGACACTGGAATTTTACAGATG 31
QY      1844 AGATTCTGATTCATGAAGAAAGACAGATAG 1873
DB      30 AGATTCTGATTCATGAAGAAAGACAGATAG 1

RESULT 11
LOCUS   AQ124119
LOCUS   400 bp DNA linear GSS 22-SEP-1998

```

```

DEFINITION HS_3122_A1_C07_MR_C17 Approved Human Genomic Sperm Library D Homo
           sapiens genomic clone Plate=3122 Col=13 Row=E, genomic survey
           sequence.
ACCESSION AQ124119
VERSION   AQ124119.1 GI:3501285
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Mahairas GG, Wallace JC, Hood L
           1 (bases 1 to 400)
           Sequence-tagged connectors: A sequence approach to mapping and
           scanning the human genome
           Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
           Hood L.
           Sequence-tagged connectors: A sequence approach to mapping and
           scanning the human genome
           Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
           Contact: Mahairas GG, Wallace JC, Hood L
           High Throughput Sequencing Center
           University of Washington
           401 Queen Anne Avenue North, Seattle, WA 98109, USA
           Tel: (206) 616-3618
           Fax: (206) 616-3887
           Email: jwallace@u.washington.edu
           Sequence Tagged Connector
           Plate: 3122 Row: E Column: 13
           Class: BAC ends
           High quality sequence stop: 400.
           Location/Qualifiers
             1. 400
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /clone="Plate=3122 Col=13 Row=E"
               /sex="male"
               /clone_lib="C17 Approved Human Genomic Sperm Library D"
               /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
               E-Coli DH10B"

ORIGIN
Query Match      4.4%; Score 89; DB 9; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.7e-32;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      635 AGCGCGTACATGCCAGAAAGATGATGCGTTATGTTGCTGGAACATGCGACTGATC 694
DB      237 AGCGCGTACATGCCAGAAAGATGATGCGTTATGTTGCTGGAACATGCGACTGATC 296
QY      695 CAAATTTTCCAGATGATGGAATATAC 723
DB      297 CAAATTTTCCAGATGATGGAATATAC 325

RESULT 12
LOCUS   AQ030111/c
DEFINITION RPEC11-39K18.TP RPEC11 Homo sapiens genomic clone RPEC11-39K18,
           genomic survey sequence.
ACCESSION AQ030111
VERSION   AQ030111.1 GI:3274075
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
           Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
           Venter,J.C.
           Use of BAC End Sequences for Sequence-Ready Map Building (1998)

```

JOURNAL COMMENT

Unpublished (1998)
 Other GSSs: RPCI11-39K18.TV
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadm@icigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers

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 /mol_type="genomic DNA"
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 /db_xref="taxon:9606"
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 /sex="Male"
 /cell_type="lymphocytes"
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 RPCI11 Human Male BAC library"

ORIGIN

Query Match 4.3%; Score 87; DB 9; Length 399;
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 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1777 AGTACGACAAACAATATCTCTGAGAGCAATTTTGTGAGAGACAGAACTGTGAATATTA 1836
 |||||
 DB 102 AGTACGACAAACAATATCTCTGAGAGCAATTTTGTGAGAGACAGAACTGTGAATATTA 43
 |||||
 QY 1837 CACGATGAGATTCTGATTTCATGAGAA 1863
 |||||
 DB 42 CACGATGAGATTCTGATTTCATGAGAA 16
 |||||

RESULT 13
 AL703938 544 bp mRNA linear EST 04-SEP-2003
 LOCUS DKFP686E1728_r1.686 (synonym: hlc3) Homo sapiens cDNA clone
 DEFINITION DKFP686E1728_5', mRNA sequence.
 ACCESSION AL703938
 VERSION AL703938.1 GI:19687293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 544)
 Otsenweider, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
 Wiemann, S.
 EST (Otsenweider, B., Obermaier, B., Mewes, H.W., Weil, B. and
 Wiemann, S.)
 Unpublished (2001)
 CONTACT: MIPS
 JOURNAL
 COMMENT

MIPS
 Ingstedter landstr. 1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert.
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by Medigenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No 31 sequence
 available.
 This clone (DKFP686E1728) is available at the RZPD in Berlin.

FEATURES

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers

1..544
 /organism="Homo sapiens"
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 /dev_stage="adult"
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 /note="Vector: pTribEx2; Site_1: SfiI; Site_2: SfiIb;
 cDNA-collection"

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 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 AAGAGAAAACAGATGCTAAATCTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
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 DB 432 AAGAGAAAACAGATGCTAAATCTCTGAAAACAGCAATCCAGAACAGCTTAAG 491
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 QY 1141 CTGACATCAGAGAGAGTCACAAAG 1167
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 DB 492 CTGACATCAGAGAGAGTCACAAAG 518
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RESULT 14

BI461255/ 279 bp mRNA linear EST 21-AUG-2001
 LOCUS 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
 DEFINITION mRNA sequence.
 ACCESSION BI461255
 VERSION BI461255.1 GI:15251911

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 279)
 NIH-MGC http://mgc.mci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@rs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshinuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUM)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLUM at:
 http://image.llnl.gov
 Plate: ILLUM1687 row: 9 column: 21
 High quality sequence stop: 236.
 Location/Qualifiers

FEATURES

source

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 /clone="IMAGE:5272364"
 /lab_host="DH10B"
 /clone_11b="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptPR (modified
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 (gtcag); Oligo-dr primed using primer
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 insert size 2.2 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein

(NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

ORIGIN

Query Match 3.9%; Score 79; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 4.7e-27;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGTTCATTCATCCGCGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
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DB 84 ATGGTGTTGAGTTCATTCATCCGCGCTCTTCTGTGAAGAAGCATTTGGTCTC 25
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QY 61 AGGAGCAAGATGGGCAAGT 79
|||||
DB 24 AGGAGCAAGATGGGCAAGT 6
|||||

RESULT 15

HSMB09270

LOCUS 6098 bp mRNA linear HTC 20-JAN-2005

DEFINITION Homo sapiens mRNA; cDNA DKFZp686J0529 (from clone DKFZp686J0529).

ACCESSION BX649118

VERSION BX649118.1 GI:34368290

KEYWORDS HTC.

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 6098)

Bahr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Oeanger, A.,

Fodor, G., Han, M., and Wiemann, S.

The German cDNA Consortium

Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764

Neuberberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;

consortium of the German Genome Project.

This clone (DKFZp686J0529) is available at the RZPD Deutsches

Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp686J0529

Further information about the clone and the sequencing project is

available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

1..6098

/organism="Homo sapiens"

/mol_type="mRNA"

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/db_xref="taxon:9606"

/clone="DKFZp686J0529"

/issue_type="testis"

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DH10B; sites SfiIA + SfiIB"

/dev_stage="adult"

/note="putative transcript"

ORIGIN

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Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1426 TTGATGATCTTCTCAAGATCTATCTGACAGACGCGCAGAGATGCTGTTCTAGTC 1485
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QY 1046 ATCATCATGTAATTTG 1061
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DB 1486 ATCATCATGTAATTTG 1501
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Search completed: December 19, 2005, 20:05:02
Job time : 8223.61 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:28:25 : Search time 10314.6 Seconds
(without alignments)
11242.353 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atcggtgctgaggtgcttc.....aaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: GenEmb1:*
2: gb_ba:*
3: gb_in:*
4: gb_env:*
5: gb_cm:*
6: gb_ov:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	6	BD242273
2	2040	100.0	2040	6	AR278480 Sequence
3	2040	100.0	2040	6	AR350944 Sequence
4	2040	100.0	2040	6	AR367176 Sequence
5	2040	100.0	2040	6	AR371072 Sequence
6	2040	100.0	2040	6	AR400212 Sequence
7	2040	100.0	2040	6	AR405479 Sequence
8	2040	100.0	2040	6	AR433320 Sequence
9	2040	100.0	2040	6	AR563859 Sequence
10	2040	100.0	2040	6	AR588845 Sequence
11	2040	100.0	2040	6	AR605665 Sequence
12	2040	100.0	2040	6	AR642106 Sequence
13	2040	100.0	2040	6	AR657004 Sequence
14	2040	100.0	2040	6	AR657004 Sequence
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16	2040	100.0	2040	6	AX140885 Sequence
17	2040	100.0	2040	6	AX200745 Sequence
18	2040	100.0	2040	6	AX267401 Sequence

19	2040	100.0	2040	6	AX282958 Sequence
20	2040	100.0	2040	6	AX316966 Sequence
21	1999.8	98.0	2188	8	AY462871 Homo sapi
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23	1940	95.1	2000	6	AR278479 Sequence
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25	1940	95.1	2000	6	AR367175 Sequence
26	1940	95.1	2000	6	AR371071 Sequence
27	1940	95.1	2000	6	AR400211 Sequence
28	1940	95.1	2000	6	AR405478 Sequence
29	1940	95.1	2000	6	AR433319 Sequence
30	1940	95.1	2000	6	AR563858 Sequence
31	1940	95.1	2000	6	AR588844 Sequence
32	1940	95.1	2000	6	AR605664 Sequence
33	1940	95.1	2000	6	AR615063 Sequence
34	1940	95.1	2000	6	AR642105 Sequence
35	1940	95.1	2000	6	AR657003 Sequence
36	1940	95.1	2000	6	AX106593 Sequence
37	1940	95.1	2000	6	AX140884 Sequence
38	1940	95.1	2000	6	AX200744 Sequence
39	1940	95.1	2000	6	AX267400 Sequence
40	1940	95.1	2000	6	AX282957 Sequence
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43	1759.4	86.2	2072	8	AY462873 Homo sapi
44	1641.2	80.5	2027	8	AY462868 Homo sapi
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ALIGNMENTS

RESULT 1	BD242273	LOCUS	BD242273	DEFINITION	2040 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD242273.1	GI:33052043		Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.				
VERSION	BD242273.1	GI:33052043						
KEYWORDS	JP 2002520054-A/360.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	1 (bases 1 to 2040)							
AUTHORS	Dillon,D.C., Harlocker,S.L., Yugu,J., Xu,J. and Mitcham,J.L.							
TITLE	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use							
JOURNAL	Patent: JP 2002520054-A 360 09-JUL-2002;							
COMMENT	CORIXA CORP							
OS	Homo sapiens (human)							
PN	JP 2002520054-A/360							
PD	09-JUL-2002							
PF	14-JUL-1999 JP 2000560247							
PR	14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR							
23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR								
15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR								
09-APR-1999 US 09/288946								
PI	DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YIQIU, PI							
JIANGCHUN XU,								
PI	JENNIFER LYNN MITCHAM							
PC	C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,							
PC	C12N5/10,							
PC	C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,							
PC	A61K37/02,							
PC	C12N5/00							
CC	Compounds for immunotherapy and diagnosis of prostate cancer							
CC	and methods							
CC	for their use							
FT	Key							
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FT	1. 2040							
FT	Location/Qualifiers							
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FEATURES
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ORIGIN

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTTGAAGTTGATTCATCCGCGTCCCTCTTCTGTGAAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAAGTTGATTCATCCGCGTCCCTCTTCTGTGAAAGCCATTGGTCTC 60
QY 61 AGGAGCAATATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCCGCAAG 120
DB 61 AGGAGCAATATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGAGCAGAGCACTCTGTATGAAAGACCTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGAGCAGAGCACTCTGTATGAAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
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DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGATGGGCGCTTGG 360
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DB 601 GTCTCTGACAAACAAAAGAGAGACAGTCTGATTAAGCCGTACATATGCCAGAAAGATGAA 660
QY 661 TGTGCGTTATGTTGCTGGAACATGGCACTGATCCAAATATTCACAATGAGTAGTAAAT 720
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QY 1381 CCTGACAAAGAAAGGAGAGATATCAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
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DB 1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
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DB 1501 TCGAGGAAAGATCACAAGGCTTTGAGGCACTGAAAAATGGCAGCCAGAGAAAAAGATCT 1560
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DB 1561 CAAGAACCAAGAAATTAATGAAGATGATAGAGAGCTAGAAATTTTATGCTATCGAA 1620
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DB 1621 GAAATGAAGAAACAGAAAGTACTCATGTGCGAATTCAGAAAAACCTGACTAATGTGTGC 1680
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QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAAAATGATACTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGCAAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAAATTTACAGAGTAGAGTTCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAAATTTACAGAGTAGAGTTCTGATTCATGAA 1860
QY 1861 GAAAAAGCATGTGATGAAAGTGTGAAAAATGAATTCGAGCTTTCTTATGTTGAAGAA 1920
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QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040
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RESULT 2
AR278480 2040 bp DNA linear PAT 10-Apr-2003
LOCUS AR278480
DEFINITION Sequence 375 from patent US 6512094.
ACCESSION AR278480
VERSION AR278480.1 GI:29712726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Recter,M.W., Stolk,J.A., Day,C.H.,
Vedvyck,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 375 28-JAN-2003;
Cortixa Corporation; Seattle, WA
FEATURES
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/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
AR350944
LOCUS AR350944 2040 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 303 from patent US 6586570.
ACCESSION AR350944
VERSION AR350944.1 GI:33752584
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Fridakis,T.N., Reed,S.G., Smith,J.M. and Misher,L.
TITLE Compositions and methods for the treatment and diagnosis of breast
JOURNAL Patent: US 6586570-A 303 01-JUN-2003;
FEATURES
source location/Qualifiers
1..2040
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
AR367176 2040 bp DNA linear PAT 12-SEP-2003
LOCUS AR367176 Sequence 375 from patent US 6329505.
DEFINITION AR367176
ACCESSION AR367176
VERSION AR367176.1 GI:34600151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yugi,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6329505-A 375 11-DEC-2001;
FEATURES
source Corixa Corporation; Seattle, WA
1..2040
Location/Qualifiers
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCTGAGTTCATTCATTCGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
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RESULT 5
AR371072
LOCUS AR371072
DEFINITION Sequence 375 from patent US 6395278.
ACCESSION AR371072
VERSION AR371072.1 GI:34607965
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 2040)
AUTHORS Ku,J., Dillon,P.C., Mitcham,J.L., Harlocker,S.L. and Yugiu,J.
TITLES Prostate specific fusion protein compositions
JOURNAL Patent: US 6395278-A 375 28-MAY-2002;
Corixa Corporation; Seattle, WA

FEATURES
source Location/Qualifiers
1..2040
/organism="unknown"
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Query Match 100.0%; Score 2040; DB 6; Length 2040;
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Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION AR405479
 VERSION AR405479.1 GI:40154316
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 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 2040)

REFERENCE
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kadosh,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H., Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepfler,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: US 6630305-A 375 07-OCT-2003;
 Corixa Corporation; Seattle, WA;
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 ACCESSION AR433320
 VERSION AR433320.1 GI:40196102
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 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2040)
 AUTHORS Renter, M.W. and Dillon, D.C.
 TITLE Compositions and methods for the treatment and diagnosis of breast cancer
 JOURNAL Patent: US 6656480-A 303 02-DEC-2003;
 Corixa Corporation; Seattle, WA
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AUTHORS	Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Veevik, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W.,				

Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: US 6759515-A 375 06-JUL-2004;
Corixa Corporation; Seattle, WA

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LOCUS Sequence 375 from patent US 6818751.
DEFINITION AR605665
ACCESSION AR605665
VERSION AR605665.1 GI:56657329
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stoik,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6818751-A 375 16-NOV-2004;
Corixa Corporation; Seattle, WA
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source 1. 2040
/organism="unknown"
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Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION	Sequence 303 from patent US 6828431.				
ACCESSION	AR615064				
VERSION	AR615064.1		GI:56671468		
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2040)				
	Fridakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,				
	Rettler,M.W., Wang,A., Skelky,Y.A.W. and Harlocker,S.L.				
TITLE	Compositions and methods for the therapy and diagnosis of breast cancer				
JOURNAL	Patent: US 6828431-A 303 07-DEC-2004;				
FEATURES	Corixa Corporation; Seattle, WA				
SOURCE	Location/Qualifiers				
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ORIGIN					

Query Match	100.0%	Score 2040;	DB 6;	Length 2040;
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RESULT 13
AR642106
LOCUS AR642106 2040 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 303 from patent US 6861506.
ACCESSION AR642106
VERSION AR642106.1 GI:62778254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 2040)
AUTHORS Frudakis,T.N., Smith,J.M., Reed,S.G., Misher,L.E., Retter,M.W. and
Dillon,D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast
cancer
JOURNAL Patent: US 6861506-A 303 01-MAR-2005;
Corixa Corporation; Seattle, WA
FEATURES
Location/Qualifiers
1..2040
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Query Match 100.0%; Score 2040; DB 6; Length 2040;
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 TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
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 Corixa Corporation; Seattle, WA
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 Homidae; Homo.

REFERENCE
 AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
 TITLE Compositions and methods for therapy and diagnosis of prostate cancer
 JOURNAL Patent: WO 0125272-A 375 12-APR-2001;
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CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
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QY 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAAGCCAAAGCATGCTCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAAGCCAAAGCATGCTCTTA 780
QY 781 TATGTGCTGATATCGATCAAAAACAAAGCATGGCTCAACCATGTTACTTGGTGA 840
DB 781 TATGTGCTGATATCGATCAAAAACAAAGCATGGCTCAACCATGTTACTTGGTGA 840
QY 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
```

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DB 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATGAAAGAGCTGCTCAATCTGCTGATGTGTGGATACAGCAATATA 960
DB 901 CTGATATGATGAAAGAGCTGCTCAATCTGCTGATGTGTGGATACAGCAATATA 960
QY 961 GTCACTCTTCACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
DB 961 GTCACTCTTCACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAAGAGTATGCTGTTTCTATGATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
DB 1021 GCCAAGAGTATGCTGTTTCTATGATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATCTAAATCTCTCTGAAAACAGCAATCCAGAACTTAATAG 1140
DB 1081 AAAAGAAAACAGATCTAAATCTCTCTGAAAACAGCAATCCAGAACTTAATAG 1140
QY 1141 CTGACATCAGAGAAAGAGTCACAAAAGTTCAAAGGCAAGTAAATAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAAAGAGTCACAAAAGTTCAAAGGCAAGTAAATAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATAGAGCTTGAGAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATAGAGCTTGAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGTTGGGATTTACTAGAAAACCTGACTAATGGTGTCACTGTGGC 1320
DB 1261 AAGCATGAAGATTAATGTTGGGATTTACTAGAAAACCTGACTAATGGTGTCACTGTGGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGCAGAACCACTGAATACAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGCAGAACCACTGAATACAGCAATTT 1380
QY 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
DB 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGGCCAAAATPACTCTTCTGAAAACAGCAACCCAGAACTTAATAGCTGACA 1500
DB 1441 AAAAGATGGCCAAAATPACTCTTCTGAAAACAGCAACCCAGAACTTAATAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCACAAAAGCTTGAAGGCACTGAAAATGGCCAGCAGAGAAAAGTCT 1560
DB 1501 TCAGAGGAAGAGTCACAAAAGCTTGAAGGCACTGAAAATGGCCAGCAGAGAAAAGTCT 1560
QY 1561 CAAGAACCAAGAAATTAATGAAGATGATAGAGCTAGAAAATTTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATGAAGATGATAGAGCTAGAAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGACAGGAAGTACTCATGTCCGATTCCTCAAGAAAACCTGACTAATGGTGGC 1680
DB 1621 GAAATGAAGACAGGAAGTACTCATGTCCGATTCCTCAAGAAAACCTGACTAATGGTGGC 1680
QY 1681 ACTGTGCAATGTGATGATGATTAATTTCTTCAAGAGAAAGCAGAACACTGAAAAGC 1740
DB 1681 ACTGTGCAATGTGATGATGATTAATTTCTTCAAGAGAAAGCAGAACACTGAAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGAACAAATATATCTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGAACAAATATATCTCAG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATACAGAGAAATCTGATTAAGAA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATACAGAGAAATCTGATTAAGAA 1860
QY 1861 GAAAAGCAGATGAAGTGTGTAAGAAAATGAATTTGAGCTTTCTTATGTTGAAGAA 1920
DB 1861 GAAAAGCAGATGAAGTGTGTAAGAAAATGAATTTGAGCTTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGCATTTTGATGATGAAAAATAGTACGTTGCGGAGAAAGAAATGGCATGCTAAGACTG 1980
DB 1921 GAAAAAGCATTTTGATGATGAAAAATAGTACGTTGCGGAGAAAGAAATGGCATGCTAAGACTG 1980
```

QY 1981 GAGCTAGACATGAATGAACCTCAGAGCCACTAATAAAAAAAAAAAAAAAAAAAAA 2040
DB 1981 GAGCTAGACATGAATGAACCTCAGAGCCACTAATAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 2

ID AAH93716 standard; cDNA; 2040 BP.

AAH93716;

04-OCT-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #10.

Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.

OS Homo sapiens.

PN M0200151633-A2.

PD 19-JUL-2001.

PF 16-JAN-2001; 2001MO-US001574.

PR 14-JAN-2000; 2000US-00483672.

(CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YW,
Wang A, Mesgher MJ;

PI Wang A, Mesgher MJ;

DR WPI; 2001-425873/45.

PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
monitoring and treating prostate cancer in a patient and for use in
vaccines.

PT vaccines.

PS Claim 1; Page 348; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX prepared using (I) or (II) are used treat cancer in a patient. (I) and
XX the antibodies are also used in the detection of cancer in a patient. The
XX cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX and (II) can be used in vaccines. The antibodies or (I) can be used for
XX monitoring the progression of cancer in a patient. (I) and (II) can also
XX be used to improve diagnostic and therapeutic methods for prostate
XX cancer. They can indicate the level of metastasis as well as the prostate
XX volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
XX polynucleotide and amino acid sequences used in the exemplification of
XX the present invention

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 4; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGCTC 60

DB 1 ATGGTGGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120

DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120

QY 121 AGCAAGCTGGGCACTTGTGAGACGACGACGACTGTGTAAGACATCAGAGCAAG 180

DB 121 AGCAAGCTGGGCACTTGTGAGACGACGACGACTGTGTAAGACATCAGAGCAAG 180

QY 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 240

DB 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 240

QY 241 GGGCTTCTGAGACCAAGCAAGCTTCTGTAAGACATCAGAAACAAGATGGCAAG 300

DB 241 GGGCTTCTGAGACCAAGCAAGCTTCTGTAAGACATCAGAAACAAGATGGCAAG 300

QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGACGGCAAG 360

DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGACGGCAAG 360

QY 361 GGAGACTAGATGACATGCTTCAATGAGCCAGGATACCATCCGTGGAAGATCTG 420

DB 361 GGAGACTAGATGACATGCTTCAATGAGCCAGGATACCATCCGTGGAAGATCTG 420

QY 421 GACAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

DB 421 GACAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 481 CTCAGGGAGACTGAGCTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540

DB 481 CTCAGGGAGACTGAGCTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540

QY 541 TCTGCCAATGGGAATCAGAAATGTAATAAATCTCTGCTGCAAGAGATGCAATTAAT 600

DB 541 TCTGCCAATGGGAATCAGAAATGTAATAAATCTCTGCTGCAAGAGATGCAATTAAT 600

QY 601 GTCTTGAACAACAAAAGAGACAGCTGTATTAAGCCGTACATGCAAGAAATGAA 660

DB 601 GTCTTGAACAACAAAAGAGACAGCTGTATTAAGCCGTACATGCAAGAAATGAA 660

QY 661 TGTGGCTTAATGTTGTGTAAGCAAGGCACTGATCCAAATTAATTCAGATGTAATGA 720

DB 661 TGTGGCTTAATGTTGTGTAAGCAAGGCACTGATCCAAATTAATTCAGATGTAATGA 720

QY 721 ACCACTGCTCACTACGCTATCTTAATGAAGTAATAATGAGCAAGCAAGCAAGCA 780

DB 721 ACCACTGCTCACTACGCTATCTTAATGAAGTAATAATGAGCAAGCAAGCAAGCA 780

QY 781 TATGTGCTGATATGCAATCAAAAAACAAGATGCTGCAACACTGTTACTTGTGTA 840

DB 781 TATGTGCTGATATGCAATCAAAAAACAAGATGCTGCAACACTGTTACTTGTGTA 840

QY 841 CATGACCAAAAACAGAAATGCTGAAATTTTAAATCAAGAAAAAACCAATTTAAATGCA 900

DB 841 CATGACCAAAAACAGAAATGCTGAAATTTTAAATCAAGAAAAAACCAATTTAAATGCA 900

QY 901 CTGATATGATATGGAAGAGCTGCTCATATCTGCTGTAATGTTGTGATCAGCAATATA 960

DB 901 CTGATATGATATGGAAGAGCTGCTCATATCTGCTGTAATGTTGTGATCAGCAATATA 960

QY 961 GTCAAGCTTCTAATTGAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAG 1020

DB 961 GTCAAGCTTCTAATTGAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAG 1020

QY 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCAAGATCTATCTGAGACAG 1080

DB 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCAAGATCTATCTGAGACAG 1080

QY 1081 AAAAGAAAAACAGATGCTAATAATCTTCTGAAAAACAGCAATCAGAAACAAGATTAAAG 1140

DB 1081 AAAAGAAAAACAGATGCTAATAATCTTCTGAAAAACAGCAATCAGAAACAAGATTAAAG 1140

QY 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAAGCAATGAAATTAAGCAAGCAAGAA 1200

DB 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAAGCAATGAAATTAAGCAAGCAAGAA 1200

QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTTAAAGAAAGAG 1260

DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTTAAAGAAAGAG 1260

Db 1201 ATGTCTCAAGAACCCAGAAATAAATGAAGATGTGATAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGCGGATTAATCTAGAAAACCTGATAGTGTGCTGCTGGC 1320
Db 1261 AAGCATGAAGATTAATATGCGGATTAATCTAGAAAACCTGATAGTGTGCTGCTGGC 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGACACCTGAAAATGACAAATT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGACACCTGAAAATGACAAATT 1380
Qy 1381 CCTGACACGAAAGTGAAGAGATTCACAGAAATTTGCGAATTAATTTCTGACAAAGAA 1440
Db 1381 CCTGACACGAAAGTGAAGAGATTCACAGAAATTTGCGAATTAATTTCTGACAAAGAA 1440
Qy 1441 AAACAGATGCGAAATTAATCTCTGAAAAACAGACCCAGAAACCTTAAGCTGACA 1500
Db 1441 AAACAGATGCGAAATTAATCTCTGAAAAACAGACCCAGAAACCTTAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCACAAAAGCTTGAAGGCGATGAAATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGAGTCACAAAAGCTTGAAGGCGATGAAATGGCCAGCAGAGAAAGATCT 1560
Qy 1561 CAAGAACCCAGAAATAAATGAAGATGTGATAGAGCTAGAGAAATTTTATGCTATGAA 1620
Db 1561 CAAGAACCCAGAAATAAATGAAGATGTGATAGAGCTAGAGAAATTTTATGCTATGAA 1620
Qy 1621 GAAATGAAGAGACCGAAGTACTCATGTCGGATTCGCCAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAGACCGAAGTACTCATGTCGGATTCGCCAGAAACCTGACTAATGCTGCC 1680
Qy 1681 ACTGTGCGCAATGTGATGATGATTAATCTCTCAAGAGAGAGAGACACCTGAAAGC 1740
Db 1681 ACTGTGCGCAATGTGATGATGATTAATCTCTCAAGAGAGAGAGACACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACAGACAAATAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACAGACAAATAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGAAGAGACAGACACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
Db 1801 AAGCAATTTTGAAGAGACAGACACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
Qy 1861 GAAAGCAGATAGAGTGTGTTGAAAAATGAAATTTCTGAGCTTCTCTAGTTGTAAGAA 1920
Db 1861 GAAAGCAGATAGAGTGTGTTGAAAAATGAAATTTCTGAGCTTCTCTAGTTGTAAGAA 1920
Qy 1921 GAAAAAGACATCTTTCATGAAAAATAGTACGTTGCGGAGAGAAATTTGCCATGTAAGCTG 1980
Db 1921 GAAAAAGACATCTTTCATGAAAAATAGTACGTTGCGGAGAGAAATTTGCCATGTAAGCTG 1980
Qy 1981 GAGCTAGACACATGAAGACATGACGAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040
Db 1981 GAGCTAGACACATGAAGACATGACGAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040

RESULT 3
AAI67213
ID AAI67213 standard, cDNA; 2040 BP.
XX AAI67213;
AC AAI67213;
XX
DT 11-FEB-2002 (first entry)
XX
DE B305D isoform C splice variant 3 encoding cDNA.
XX
KM Genetic subraction; DNA microarray analysis; polymerase chain reaction;
XX cancer; B305D; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..2016
CDS
FT /*tag= a

FT /product= "B305D isoform C splice variant"
XX
PN MO200175171-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US010631.
XX
PR 03-APR-2000; 2000US-0194241P.
PR 20-JUL-2000; 2000US-0219862P.
PR 27-JUL-2000; 2000US-0221300P.
PR 18-DEC-2000; 2000US-0256592P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RI, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
DR
DX MPI; 2001-626449/72.
XX
DR P-PSDB; AAG65978.
XX
PT Identifying tissue (tumor)-specific polynucleotides overexpressed in
PT tissue of interest as compared to control tissue, for detecting cancer
PT cells in patient, comprises DNA microarray analysis or quantitative
PT polymerase chain reaction.
XX
PS Claim 4; Page 94-95; 127pp; English.
XX
CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (SPI) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on SPI to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGTGTTGAGGTTGATTCATGCGCGGTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
Db 1 ATGTGTGTTGAGGTTGATTCATGCGCGGTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
Qy 61 AGGAGCAGATGGGCAAGTGTGTCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGGAGCAGATGGGCAAGTGTGTCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTTTGGAGACCAAGCAAGCTCTGCTATGAAGACATTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTTTGGAGACCAAGCAAGCTCTGCTATGAAGACATTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTA 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTA 240
Qy 241 GCGGCTTTCGAGACCAAGCAAGCTCTGCTATGAAGACATTCAGAGCAAGTGGGCAAG 300
Db 241 GCGGCTTTCGAGACCAAGCAAGCTCTGCTATGAAGACATTCAGAGCAAGTGGGCAAG 300
Qy 301 TGTGTGCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGACAGTGGGCGTCTG 360
Db 301 TGTGTGCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGACAGTGGGCGTCTG 360
Qy 361 GGAAGACTAGATGAGAGTGTCTTCAATGAGAGCCAGGTACAGTCCGTGGAAGATCTG 420

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Db      361 GGAGACTAGATGACAGTCCCTTCATGAGCCAGGTACACGTCCTGCGAGAAAGATCTG 420
Qy      421 GACAACTCCACAGAGCTCCCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db      422 GACAACTCCACAGAGCTCCCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
Qy      481 CTCAGGACACTGACGTGAAACAAGAGAACAGCAAGAGAGAGCTGCTTACACTGGCC 540
Db      481 CTCAGGACACTGACGTGAAACAAGAGAACAGCAAGAGAGAGCTGCTTACACTGGCC 540
Qy      541 TCTGCCAATGGGAATTCAGAAAGTAATAATCTCTGCTGAGACAGAGATGCACTTAAT 600
Db      541 TCTGCCAATGGGAATTCAGAAAGTAATAATCTCTGCTGAGACAGAGATGCACTTAAT 600
Qy      601 GTCTTGACACAAACAAAGAGACAGCTTGATTAAGCCGTACATGCGAAGAGATGA 660
Db      601 GTCTTGACACAAACAAAGAGACAGCTTGATTAAGCCGTACATGCGAAGAGATGA 660
Qy      661 TGTGGCTTAATGTTGCTGGAACAATGACATGCAATATTCAGATGATGTAAT 720
Db      661 TGTGGCTTAATGTTGCTGGAACAATGACATGCAATATTCAGATGATGTAAT 720
Qy      721 ACCACTGCTACCTACGCTATCTAATGAAGTAATAATGAGCCAAAGCACTGCTTAA 780
Db      721 ACCACTGCTACCTACGCTATCTAATGAAGTAATAATGAGCCAAAGCACTGCTTAA 780
Qy      781 TATGCTGATATTCGAATCAAAAAACAAGATGGCTGACACACTGTTACTGGTGA 840
Db      781 TATGCTGATATTCGAATCAAAAAACAAGATGGCTGACACACTGTTACTGGTGA 840
Qy      841 CATGAGCAAAAAACAGAACTCGTGAATTTTATTAAGAAAAAAGCGAATTTAAATGA 900
Db      841 CATGAGCAAAAAACAGAACTCGTGAATTTTATTAAGAAAAAAGCGAATTTAAATGA 900
Qy      901 CTGATATGATGAGAAAGACTGCTCATACTGCTGATGTTGTTGATGAGCAAGTATA 960
Db      901 CTGATATGATGAGAAAGACTGCTCATACTGCTGATGTTGTTGATGAGCAAGTATA 960
Qy      961 GTGAGCTTCTAATGAGCAAAAAATATGATGTAATCTTCAAGATCTATCTGAGACAG 1020
Db      961 GTGAGCTTCTAATGAGCAAAAAATATGATGTAATCTTCAAGATCTATCTGAGACAG 1020
Qy      1021 GCCAAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db      1021 GCCAAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy      1081 AAAAGAAAAACAGATGCTAAATAATCTCTGCAAAAACAGCAATTCAGAAAGCTTAAAG 1140
Db      1081 AAAAGAAAAACAGATGCTAAATAATCTCTGCAAAAACAGCAATTCAGAAAGCTTAAAG 1140
Qy      1141 CTGACATCAGAGAAAGTCACAAAGTTCAAAAGGAGTGAATAATGAGCCAGCAGAGAAA 1200
Db      1141 CTGACATCAGAGAAAGTCACAAAGTTCAAAAGGAGTGAATAATGAGCCAGCAGAGAAA 1200
Qy      1201 ATGCTCAAGAAACAGAAATTAATTAAGATGATGAGAGGTTGAAGAAATGAAG 1260
Db      1201 ATGCTCAAGAAACAGAAATTAATTAAGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy      1261 AAGCAATGAAGTAATTAATGAGATTAATCTAGAAAACCTAATATGCTGCTGAGC 1320
Db      1261 AAGCAATGAAGTAATTAATGAGATTAATCTAGAAAACCTAATATGCTGCTGAGC 1320
Qy      1321 AATGCTATATGATTAATTTCTCAAGAGAAAGACAGCACTGAAATACGAATTT 1380
Db      1321 AATGCTATATGATTAATTTCTCAAGAGAAAGACAGCACTGAAATACGAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAAATGATTTCTGATCAAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAAATGATTTCTGATCAAAAGAA 1440
Qy      1441 AAACAGATGCCAAAATTAATCTTCTGAAAAACAGCAATCCGAACCAACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAAATTAATCTTCTGAAAAACAGCAATCCGAACCAACTTAAAGCTGACA 1500

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Db      1441 AAACAGATGCCAAAATTAATCTTCTGAAAAACAGCAATCCGAACCAACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGATCACAAAGGCTTTGAGGCACTGAAATGCGCAGCAGAGAAAGATCT 1560
Db      1501 TCAGAGAAAGATCACAAAGGCTTTGAGGCACTGAAATGCGCAGCAGAGAAAGATCT 1560
Qy      1561 CAAGAACCGAATTAATTAATGAGATGATGATGAGAGCTGAAATTTTATGCTATCGAA 1620
Db      1561 CAAGAACCGAATTAATTAATGAGATGATGATGAGAGCTGAAATTTTATGCTATCGAA 1620
Qy      1621 GAAATGAAGAACACAGAAAGTACATGTCGATTCAGAAAACTGACTAATGCTGAC 1680
Db      1621 GAAATGAAGAACACAGAAAGTACATGTCGATTCAGAAAACTGACTAATGCTGAC 1680
Qy      1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAAAGACAACTGAAAGC 1740
Db      1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAAAGACAACTGAAAGC 1740
Qy      1741 CAGCAATTTCTGACACTGAGAAATGAGATGATCAAGTGAAGAACAAATGATACTCAG 1800
Db      1741 CAGCAATTTCTGACACTGAGAAATGAGATGATCAAGTGAAGAACAAATGATACTCAG 1800
Qy      1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTTACAGATGAGATTTCTGATTCAGAA 1860
Db      1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTTACAGATGAGATTTCTGATTCAGAA 1860
Qy      1861 GAAAAACAGATAGAGTGTGAAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Db      1861 GAAAAACAGATAGAGTGTGAAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Qy      1921 GAAAAAGCATTTGTCATGAAAAATGATGATGTTGCGGAGAAATTTGCCATGCTAAGACG 1980
Db      1921 GAAAAAGCATTTGTCATGAAAAATGATGATGTTGCGGAGAAATTTGCCATGCTAAGACG 1980
Qy      1981 GAGCTAGACACAAATGAAACATGACAGCCAGCTTAAATTTTTTTTTTTTTTTTTT 2040
Db      1981 GAGCTAGACACAAATGAAACATGACAGCCAGCTTAAATTTTTTTTTTTTTTTTTT 2040

RESULT 4
AAS63809
ID AAS63809 standard; cDNA; 2040 BP.
XX
AC AAS63809;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #10.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX

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PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Renter MW, Stolk JA, Day CH, Vedrick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX MPI; 2001-639232/73.
XX P-PSDB; AAU69779.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Claim 1; Page 350; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polynucleotide of the invention
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGGTTGATTCATGCGCGTGCCTCTTCTGTGAGAGGCAATTTGGTCTC 60
DB 1 ATGGTGTTGAGGTTGATTCATGCGCGTGCCTCTTCTGTGAGAGGCAATTTGGTCTC 60
QY 61 AGAGCAAGATGAGGCAAGTGTGCTGCGCTTCTTCCCTGTGCGAGGAGACCGCAAG 120
DB 61 AGAGCAAGATGAGGCAAGTGTGCTGCGCTTCTTCCCTGTGCGAGGAGACCGCAAG 120
QY 121 ACCAAGTGGGCACTTCTGAGACCAACAGACTGTCTATGAGACACTCAGAGAGCAG 180
DB 121 ACCAAGTGGGCACTTCTGAGACCAACAGACTGTCTATGAGACACTCAGAGAGCAG 180
QY 121 ACCAAGTGGGCACTTCTGAGACCAACAGACTGTCTATGAGACACTCAGAGAGCAG 180
DB 121 ACCAAGTGGGCACTTCTGAGACCAACAGACTGTCTATGAGACACTCAGAGAGCAG 180
QY 181 ATGGGCAATGTGTGCGCCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGAGCAAGC 240
DB 181 ATGGGCAATGTGTGCGCCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGAGCAAGC 240
QY 241 GGCCTTTCTGAGACCAACAGACTGTCTATGAGACACTCAGAGAGCAATGGGCAAG 300
DB 241 GGCCTTTCTGAGACCAACAGACTGTCTATGAGACACTCAGAGAGCAATGGGCAAG 300
QY 301 TGGTGTCGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGAGCAATGGGCAAG 360
DB 301 TGGTGTCGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGAGCAATGGGCAAG 360
QY 361 GGAGACTTACGATGACAGTGTCTTCAATGAGCCAGGATACAGTCCGTGGAAGATCTG 420
DB 361 GGAGACTTACGATGACAGTGTCTTCAATGAGCCAGGATACAGTCCGTGGAAGATCTG 420
QY 421 GACCACTTCCAGAGCTGCTGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGTGAG 480
DB 421 GACCACTTCCAGAGCTGCTGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGTGAG 480
QY 481 CTCAGGAGACACTGACTGAAACAAGAGACAGCAAAAGAGACTGCTTCACTTGTGCC 540
DB 481 CTCAGGAGACACTGACTGAAACAAGAGAGCAAGCAAAAGAGACTGCTTCACTTGTGCC 540
QY 541 TCTGCAATGGGAAATTCAGAGATGTAAGATCTCTCTGAGACGAGATGTAAGTAAAT 600
DB 541 TCTGCAATGGGAAATTCAGAGATGTAAGATCTCTCTGAGACGAGATGTAAGTAAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCGGTACAAATGCCAGAGAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCGGTACAAATGCCAGAGAGATGAA 660

DB 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCGGTACAAATGCCAGAGAGATGAA 660
QY 661 TGTGGTTAAAGTGTGCTGGAACATGCACTGATCCAAATATCCAGATGAGATGAAAT 720
DB 661 TGTGGTTAAAGTGTGCTGGAACATGCACTGATCCAAATATCCAGATGAGATGAAAT 720
QY 721 ACCACTGTGCACTACGCTATCTATATGAGAAATTAATATGAGCCAAAGCACTGCTTA 780
DB 721 ACCACTGTGCACTACGCTATCTATATGAGAAATTAATATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTGCTGATATGATGATCAAAAAACAAGATGAGCTTCAACCACTGTTAGTGTGA 840
DB 781 TATGTGCTGATATGATGATCAAAAAACAAGATGAGCTTCAACCACTGTTAGTGTGA 840
QY 841 CATGAGCAAAAAACAGAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAAACAGAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATATGAGAGCACTGCTCATACTTGTGATGTTGTGATCAGACAGTATA 960
DB 901 CTGATATGATATGAGAGCACTGCTCATACTTGTGATGTTGTGATCAGACAGTATA 960
QY 961 GTGACCTTTCTATCTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
DB 961 GTGACCTTTCTATCTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAAGAGTATGCTGTTTCTGATCATCATGATATTTGGCAGTTACTTCTGATC 1080
DB 1021 GCCAAGAGTATGCTGTTTCTGATCATCATGATATTTGGCAGTTACTTCTGATC 1080
QY 1081 AAAGAAAAACAGATCTAAATAATCTCTGAAAAACAGCAATCCAGAACAAACTTAAAG 1140
DB 1081 AAAGAAAAACAGATCTAAATAATCTCTGAAAAACAGCAATCCAGAACAAACTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCAAGTAAATATGCCAGCAAGAAA 1200
DB 1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCAAGTAAATATGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTTGATGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTTGATGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAATATGTTGAGTTAATAGAAAACTGTACTATGTTGTCTGCTGAC 1320
DB 1261 AAGCATGAAAGTAATATGTTGAGTTAATAGAAAACTGTACTATGTTGTCTGCTGAC 1320
QY 1321 AATGTGATATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAATAGCAATTT 1380
DB 1321 AATGTGATATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAATAGCAATTT 1380
QY 1381 CCTGACCAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440
DB 1381 CCTGACCAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440
QY 1441 AAAAGATGCCAAATATCTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCCAAATATCTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
QY 1501 TCAAGAGAAAGTCACAAAAGCTTGAAGGCAAGTAAATGTCAGCAGAGAGAAAGATCT 1560
DB 1501 TCAAGAGAAAGTCACAAAAGCTTGAAGGCAAGTAAATGTCAGCAGAGAGAAAGATCT 1560
QY 1561 CAAGAAACCAAAATTAATAGATGTTGATTAAGAGCTTGAAGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAAACCAAAATTAATAGATGTTGATTAAGAGCTTGAAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAGAGACAGAAAGTACTATGCGATTTCCAGAAAACTGACTATGAGTGC 1680
DB 1621 GAAATGAGAGACAGAAAGTACTATGCGATTTCCAGAAAACTGACTATGAGTGC 1680
QY 1681 ACTGTGGCAATGTGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAGC 1740
DB 1681 ACTGTGGCAATGTGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAGC 1740


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Db 1021 GCCAGAGATAGCTGTTCTGATCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAAAATCTCTGAGAAAAGAGAAATCCAGAAAGCAATTAAG 1140
Db 1081 AAGAGAAAAAGATGCTAAAAATCTCTGAGAAAAGAGAAATCCAGAAAGCAATTAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGAGTGAATAATAGCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGAGTGAATAATAGCAGCAGAGAAA 1200
QY 1201 ATGCTCTCAAGAACCAAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAGATGAAG 1260
Db 1201 ATGCTCTCAAGAACCAAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAGATGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGGGATTACTAGAAAACCTGATATGCTGCTGCTGAC 1320
Db 1261 AAGCATGAAGATTAATGATGGGATTACTAGAAAACCTGATATGCTGCTGCTGAC 1320
QY 1321 AATGCTGATATGATTAATTTCTCTCAAGAGAGAGAGAGAACTGAAATCAGCAATTT 1380
Db 1321 AATGCTGATATGATTAATTTCTCTCAAGAGAGAGAGAGAACTGAAATCAGCAATTT 1380
QY 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGCGAAATTTGTTCTGATACAAAGAA 1440
Db 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGCGAAATTTGTTCTGATACAAAGAA 1440
QY 1441 AAAACAGATGCCAAAATACCTCTCTGAAAACAGCAACCCAGAACCAACTTAAGCTGACA 1500
Db 1441 AAAACAGATGCCAAAATACCTCTCTGAAAACAGCAACCCAGAACCAACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAAGGCTTGAAGGAGAGTGAATAATGCGCAGCAGAGAAAAGATCT 1560
Db 1501 TCAGAGAGAGAGTCAAAAAGGCTTGAAGGAGAGTGAATAATGCGCAGCAGAGAAAAGATCT 1560
QY 1561 CAAAGAACCAAAATTAATAGATGCTGATAGAGCTGAGAAATTTTAATGCTATCGAA 1620
Db 1561 CAAAGAACCAAAATTAATAGATGCTGATAGAGCTGAGAAATTTTAATGCTATCGAA 1620
QY 1621 GAAATGAAGAAGACGGAAGTACTCATGTCGGAATTCGCCAGAAAACCTGATTAATGCTGCC 1680
Db 1621 GAAATGAAGAAGACGGAAGTACTCATGTCGGAATTCGCCAGAAAACCTGATTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGCTGATGATGATTAATTTCTCTCAAGAGAGAGAGAGCACTGTAAGC 1740
Db 1681 ACTGCTGCAATGCTGATGATGATTAATTTCTCTCAAGAGAGAGAGAGCACTGTAAGC 1740
QY 1741 CAGCAATTTCTGCACTGAGAAATGAAGATATCAAGTGAAGCAAAATGATTAATCTCAG 1800
Db 1741 CAGCAATTTCTGCACTGAGAAATGAAGATATCAAGTGAAGCAAAATGATTAATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAAGAACTGGAATTTTCAAGATGAATTTGATTTCTATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAAGAACTGGAATTTTCAAGATGAATTTGATTTCTATGAA 1860
QY 1861 GAAAGACAGATGAAGTGTGTTGAAAAATGAATTTGAGCTTTCTCTTATGTTGAAGA 1920
Db 1861 GAAAGACAGATGAAGTGTGTTGAAAAATGAATTTGAGCTTTCTCTTATGTTGAAGA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTTGAACACATGAAACCTCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTTGAACACATGAAACCTCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040
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RESULT 6
AAH85030
ID AAH85030 standard; cDNA; 2040 BP.
XX
AC AAH85030;

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XX 25-SEP-2001 (first entry)
DT Human prostate-specific CDNA sequence B305D splice variant #10.
XX
DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000MO-US030904.
XX
PR 12-NOV-1999; 99US-00439313.
XX
PR 18-NOV-1999; 99US-00443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SJ, Jiang Y, Reed SG;
XX Kalos MD, Rector MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
XX prostate-specific protein, useful in the diagnosis and therapy of
XX prostate cancer.
XX
PS Claim 31; Page 248; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
XX at least an immunogenic portion of a prostate-specific protein, or its
XX variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
XX (N1) have cytostatic activity and can be used in vaccine production. The
XX polypeptides, nucleic acids and antibodies from the present invention are
XX useful in the diagnosis and therapy of prostate cancer. Prostate specific
XX genes P704P, P712B, P774P, P775P and B305D are located in a genomic
XX region on chromosome 22q11.2 known as the cat eye syndrome region.
XX CC Prostate specific antigen (PSA) P5015 was located on chromosome 1.
XX CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
XX CC and polypeptide sequences used in the exemplification of the present
XX CC invention.
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCTTGAAGTTCATGCGGCTGCTCTTCTGTAAGAGCCATTTGGTCTC 60
Db 1 ATGTGCTTGAAGTTCATGCGGCTGCTCTTCTGTAAGAGCCATTTGGTCTC 60
QY 61 AAGAGACAGATGAGAGAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCCGCAAG 120
Db 61 AAGAGACAGATGAGAGAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGCTATGAAGACATCTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGCTATGAAGACATCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGCTG 240
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGCTG 240
QY 241 GGGCGCTTCTGAGACACAGACGACTGCTATGAAGACATCTCAGAGCAAG 300
Db 241 GGGCGCTTCTGAGACACAGACGACTGCTATGAAGACATCTCAGAGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCCGCAAGAGCAAGTGGGCGCTGG 360
```

Db 301 TGGTGTGCGCAGCTGCTTCCCTGCTCTCAGGGGAGGCGGCAAGGCGAGGTGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGTGCCTTCATGAGCCCGAGTACCACTCCGTGGAGAAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGCCCGAGTACCACTCCGTGGAGAAAGATCTG 420
Qy 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
Qy 481 CTCAGGGACACTGACGTGAAACAAGAAAGCAAGCAAAAGAGAGCTGCTCATCATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAAACAAGAAAGCAAGCAAAAGAGAGCTGCTCATCATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGACAGAGATGCAACTTAAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGACAGAGATGCAACTTAAAT 600
Qy 601 GTCTTGAACAACAAAAGAGAGACGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGA 660
Db 601 GTCTTGAACAACAAAAGAGAGACGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAAGCCAAAGCATCTCTTA 780
Db 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAAGCCAAAGCATCTCTTA 780
Qy 781 TATGTGCTGATATCGAATCAAAAACAAGCATGCGCTCACACACTGTTACTTGTGTGA 840
Db 781 TATGTGCTGATATCGAATCAAAAACAAGCATGCGCTCACACACTGTTACTTGTGTGA 840
Qy 841 CATTGACAAAACAGCAAGCTGTAATTTTAAATGAAGAAAACCGAAATTTAAATGCA 900
Db 841 CATTGACAAAACAGCAAGCTGTAATTTTAAATGAAGAAAACCGAAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCATATCTGTATGTTGTGATCAGCAATGATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATATCTGTATGTTGTGATCAGCAATGATA 960
Qy 961 GTCAAGCTTCTAATTGAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGACG 1020
Db 961 GTCAAGCTTCTAATTGAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGACG 1020
Qy 1021 GGCAGAGATATGCTGTTCTGATCATCATCATGTAATTTGCGATTACTTTCTGATAC 1080
Db 1021 GGCAGAGATATGCTGTTCTGATCATCATCATGTAATTTGCGATTACTTTCTGATAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAATAATCTCTCTGAAAACAGCAATCAGAACAGATTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTCTGAAAACAGCAATCAGAACAGATTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGCTTCAAGGCAATGAAATTAAGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGCTTCAAGGCAATGAAATTAAGCCAGCCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGTAAATATGAGGATTAAGTAAAGAACTGACTAATGCTGCTGAGC 1320
Db 1261 AAGCATGAAGTAAATATGAGGATTAAGTAAAGAACTGACTAATGCTGCTGAGC 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGAAAAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGAAAAATCAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAAGATTCACAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAAGATTCACAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440

Db 1381 CCTGACAAAGAAAGTAAAGATTCACAAATTTGGCAATTTAGTTCTGACTACAAAGAA 1440
Qy 1441 AAACAGATCCAAAATACCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATCCAAAATACCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCACTGTAATAATGCTCAGCAAGAAAGATCT 1560
Db 1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCACTGTAATAATGCTCAGCAAGAAAGATCT 1560
Qy 1561 CAAGAACAGAAATTAATAGATGATGATAGAGCTAGAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATAGATGATGATAGAGCTAGAAATTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGACACGAAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGCTGAC 1680
Db 1621 GAAATGAAGACACGAAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGCTGAC 1680
Qy 1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAAAGCAACACTGAAAGC 1740
Db 1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAAAGCAACACTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTACGAAACAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTACGAAACAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGACAGAACACTGAAATATTAACAGATGAGATTTCTGATTCAGAA 1860
Db 1801 AAGCAATTTTGTGAAGACAGAACACTGAAATATTAACAGATGAGATTTCTGATTCAGAA 1860
Qy 1861 GAAAAGCAGATGAAGTGTGAAAAAATGAATTTCTGAGCTTTCTTTAGTTGAAGAA 1920
Db 1861 GAAAAGCAGATGAAGTGTGAAAAAATGAATTTCTGAGCTTTCTTTAGTTGAAGAA 1920
Qy 1921 GAAAAAGCATCTGATGATGAATATGATGCTGCGGGAAGAAATGCGATGTAAGACTG 1980
Db 1921 GAAAAAGCATCTGATGATGAATATGATGCTGCGGGAAGAAATGCGATGTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040

RESULT 7
ACAS9617
ID ACAS9617 standard; cDNA; 2040 BP.
XX
ACAS9617;
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #360.
XX
KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSM; Gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 99US-0157455F.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S. L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M. D.
 PA (FANG/) FANGER G. R.
 PA (RETT/) RETTER M. W.
 PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y. A. W.
 PA (HEPL/) HEPLER W. T.
 PA (HEND/) HENDERSON R. A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P. D.
 PA (HOUN/) HOUGHTON R. L.
 PA (DBAS/) Y. DE BASSOLS C. V.
 PA (FOYT/) FOY T. M.
 XX
 PI Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
 DR MPI; 2001-245062/25.
 XX P-PSDB; ABU71670.
 PT Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.
 PS Example 11; SEQ ID NO 375; 85bp; English.
 XX
 CC The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 3 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This sequence represents a prostate cancer
 CC therapy associated cDNA. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docid=US20020192763
 CC
 XX
 SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2040; DB 5; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGACAGGTGGCGCTTGG 360
 DB |||||
 QY 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGACAGGTGGCGCTTGG 360
 DB |||||
 QY 361 GGAGACTAGATGACAGTGCCTTTCATGAGGCCAGGTACAGTCCGTGAGAAATCTG 420
 DB |||||
 QY 361 GGAGACTAGATGACAGTGCCTTTCATGAGGCCAGGTACAGTCCGTGAGAAATCTG 420
 DB |||||
 QY 421 GACAACTTCAAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
 DB |||||
 QY 421 GACAACTTCAAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
 DB |||||
 QY 481 CTCAGGACACTGAGCTGACCAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
 DB |||||
 QY 481 CTCAGGACACTGAGCTGACCAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
 DB |||||
 QY 541 TCTGCCAATGGGAATTGAGAACTGTAATAAATCTCTGTGACAGACAGATGTCAACTTAAT 600
 DB |||||
 QY 541 TCTGCCAATGGGAATTGAGAACTGTAATAAATCTCTGTGACAGACAGATGTCAACTTAAT 600
 DB |||||
 QY 601 GTCTTTGACAAACAAAAGAGACAGCTGTGATTAAGCCGTACAAATGCCAGAAATGAA 660
 DB |||||
 QY 601 GTCTTTGACAAACAAAAGAGACAGCTGTGATTAAGCCGTACAAATGCCAGAAATGAA 660
 DB |||||
 QY 661 TGTGGCTTAATGTGCTGGAAATGAGCATGACCTGATCCAAATATTCAGATGATGGAAT 720
 DB |||||
 QY 661 TGTGGCTTAATGTGCTGGAAATGAGCATGACCTGATCCAAATATTCAGATGATGGAAT 720
 DB |||||
 QY 721 ACCACTGTGACATGCTATCTATATGAAATTAATGATTAATGAGCCAAAGACTGCTTTA 780
 DB |||||
 QY 721 ACCACTGTGACATGCTATCTATATGAAATTAATGATTAATGAGCCAAAGACTGCTTTA 780
 DB |||||
 QY 781 TATGTGTGCTGATATGGAATCAAAAACAAAGCATGAGCTTCAACCACTGTACTTGGTGA 840
 DB |||||
 QY 781 TATGTGTGCTGATATGGAATCAAAAACAAAGCATGAGCTTCAACCACTGTACTTGGTGA 840
 DB |||||
 QY 841 CATGACAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
 DB |||||
 QY 841 CATGACAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
 DB |||||
 QY 901 CTGATATGATATGAAAGACATGCTCTCATTACTTGTGATATGTTGTGATACAGCAATATA 960
 DB |||||
 QY 901 CTGATATGATATGAAAGACATGCTCTCATTACTTGTGATATGTTGTGATACAGCAATATA 960
 DB |||||
 QY 961 GTACAGCTTCTATCTGAGAAAATTAATGATATCTTCCAGATCTATCTGACAGAGAG 1020
 DB |||||
 QY 961 GTACAGCTTCTATCTGAGAAAATTAATGATATCTTCCAGATCTATCTGACAGAGAG 1020
 DB |||||
 QY 961 GTACAGCTTCTATCTGAGAAAATTAATGATATCTTCCAGATCTATCTGACAGAGAG 1020
 DB |||||
 QY 1021 GCCAGAGATATGCTGTTCTATGATCATCATGATATTTGCGAGTTACTTCTGACTAC 1080
 DB |||||
 QY 1021 GCCAGAGATATGCTGTTCTATGATCATCATGATATTTGCGAGTTACTTCTGACTAC 1080
 DB |||||
 QY 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTTAAG 1140
 DB |||||
 QY 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTTAAG 1140
 DB |||||
 QY 1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCATAGAAATTAAGCCAGCAAGAAA 1200
 DB |||||
 QY 1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCATAGAAATTAAGCCAGCAAGAAA 1200
 DB |||||
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATAATGAAG 1260
 DB |||||
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATAATGAAG 1260
 DB |||||
 QY 1261 AAGCATGAAAGTAATATGATGAGATTAATGAGAAACCTGACTAATGATGTCACTGTGAC 1320
 DB |||||
 QY 1261 AAGCATGAAAGTAATATGATGAGATTAATGAGAAACCTGACTAATGATGTCACTGTGAC 1320
 DB |||||
 QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAAAGAGCAAACTGAAATATCAGCAATTT 1380
 DB |||||
 QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAAAGAGCAAACTGAAATATCAGCAATTT 1380
 DB |||||
 QY 1381 CCTGACAAAGAAAGTAAGATATCAAGAAATTTGGGAATTTGATTTCTGACTTCAAAAGAA 1440

```

Db      1381  |||||CTGACACACGAAAGTAGAGTATCACAGAAATTGGAAATTAGTTCTGACTCAAAAGAA 1440
Qy      1441  |||||AAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Db      1441  |||||AAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Qy      1501  |||||TCAGAGGAAGTCACAAAAGCTTGAGGGAGTGAATAATGGCCAGCCAGAGAAAGTCT 1560
Db      1501  |||||TCAGAGGAAGTCACAAAAGCTTGAGGGAGTGAATAATGGCCAGCCAGAGAAAGTCT 1560
Qy      1561  |||||CAAGAACCCAGAAATAAATTAAGATGCTATAGAGAGCTAGAAAAATTTATGCTATGAA 1620
Db      1561  |||||CAAGAACCCAGAAATAAATTAAGATGCTATAGAGAGCTAGAAAAATTTATGCTATGAA 1620
Qy      1621  |||||GAAATGAAGACGACGGAATGCTCATGTGGAATTCACAGAAAACTGACTAATGCTGCC 1680
Db      1621  |||||GAAATGAAGACGACGGAATGCTCATGTGGAATTCACAGAAAACTGACTAATGCTGCC 1680
Qy      1681  |||||ACTGCTGGCAATGATGATGATTAATTCCTCCAAAGAGACGAGAACCTGAAGC 1740
Db      1681  |||||ACTGCTGGCAATGATGATGATTAATTCCTCCAAAGAGACGAGAACCTGAAGC 1740
Qy      1741  |||||CAGCAATTTCTCTGACACTGAGATGAAGATATCAAGTACGAAACAAATGATCTCAG 1800
Db      1741  |||||CAGCAATTTCTCTGACACTGAGATGAAGATATCAAGTACGAAACAAATGATCTCAG 1800
Qy      1801  |||||AAGCAATTTTGAAGACAGAAACACTGGAATTAACAGATGAGATTCGATTCATGAA 1860
Db      1801  |||||AAGCAATTTTGAAGACAGAAACACTGGAATTAACAGATGAGATTCGATTCATGAA 1860
Qy      1861  |||||GAAAGCAGATAGAGGCTGTAAGAAAAATTCGAGTTTCTCTAGTTGTAAGAA 1920
Db      1861  |||||GAAAGCAGATAGAGGCTGTAAGAAAAATTCGAGTTTCTCTAGTTGTAAGAA 1920
Qy      1921  |||||GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGCTG 1980
Db      1921  |||||GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGCTG 1980
Qy      1981  |||||GAGCTTGACACATGAATAACTCAGAGCCGCTTAATAAAAAAAAAAAAAAAAAAAAA 2040
Db      1981  |||||GAGCTTGACACATGAATAACTCAGAGCCGCTTAATAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 8
ABL95180 standard; cDNA; 2040 BP.
XX
AC ABL95180;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human B305D splice variant cDNA sequence SEQ ID NO 375.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; se.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-00759143.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.

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PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00439386.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.

XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
PI WPI; 2002-255649/30.

XX
DR New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer.
XX
PS Claim 1; SEQ ID NO 375; 87bp; English.
XX
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancer, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGTGAGATTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGCTTC 60
Db 1 ATGGTGTGAGATTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGCTTC 60
Qy 61 AGAGCAGATGAGGCAAGTGTGCTGCTTCCCTGCTGCGAGAGCGGCAG 120
Db 61 AGAGCAGATGAGGCAAGTGTGCTGCTTCCCTGCTGCGAGAGCGGCAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCGTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCGTG 240
Qy 241 GGCCTTCTGAGACCAAGCACTCTGCTATGAAGACACTCAGAAACAAGATGGCAAG 300

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Db 241 GGGGCTTCTGGAGACCAAGACGACTGCTATGAAACACTCAGAAACAAGATGGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGGAGGGAGCAAGGATGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGGAGGGAGCAAGGATGGGCGCTTGG 360
Qy 361 GGAAGCTAGATGACAGTGTCTTATGAGGCCAGGTACACGTCCTGGAGAGATCTG 420
Db 361 GGAAGCTAGATGACAGTGTCTTATGAGGCCAGGTACACGTCCTGGAGAGATCTG 420
Qy 421 GACAACTCCACAGACCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATGCTAG 480
Db 421 GACAACTCCACAGACCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATGCTAG 480
Qy 481 CTCAGGAGACCTGACGTTGAAACAAGAGCAAGCAAAAGAGAGCTGCTACATCGGCC 540
Db 481 CTCAGGAGACCTGACGTTGAAACAAGAGCAAGCAAAAGAGAGCTGCTACATCGGCC 540
Qy 541 TCTGCCAATGGGAATTCAAGAGTAGTAAATCTCTGCTGACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAAGAGTAGTAAATCTCTGCTGACAGAGATGCACTTAAT 600
Qy 601 GTCTCTGACACAACAAAAGAGACAGCTCTGATTAAGCCGTACATGCAAGAAATGA 660
Db 601 GTCTCTGACACAACAAAAGAGACAGCTCTGATTAAGCCGTACATGCAAGAAATGA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACAAGGACCTGATCCAAATTTCCAAATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACAAGGACCTGATCCAAATTTCCAAATGATGGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATAATTAATGGCCAAACACTGCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATAATTAATGGCCAAACACTGCTTA 780
Qy 781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGGTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAAGAGAGCTGGAATTTTAAATGAAGAAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAAAGAGAGCTGGAATTTTAAATGAAGAAAAAAGCAATTTAAATGA 900
Qy 901 CTGGATAGATATGGAAGAGCTGCTCATATCTGATGTTGTTGGATCAGCAATATA 960
Db 901 CTGGATAGATATGGAAGAGCTGCTCATATCTGATGTTGTTGGATCAGCAATATA 960
Qy 961 GTTCAGCTTCTACTTGAAGCAAAATATTGATGTAATCTTCAAGATCTATCTGACAG 1020
Db 961 GTTCAGCTTCTACTTGAAGCAAAATATTGATGTAATCTTCAAGATCTATCTGACAG 1020
Qy 1021 GCCAGAGATAGCTGCTTCTAGTCATCATATGTAATTTGCCAGTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATAGCTGCTTCTAGTCATCATATGTAATTTGCCAGTACTTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCAGAAACAAGCTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCAGAAACAAGCTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGACAGTGAATAATAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGACAGTGAATAATAGCCAGAGAAA 1200
Qy 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAAGAAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAAGAAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGAGATTACTAGAAAACCTGACTAATGGTCACTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATGAGATTACTAGAAAACCTGACTAATGGTCACTGCTGGC 1320
Qy 1321 AATGTGATATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
Db 1321 AATGTGATATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380

Db 1321 AATGTGATATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
Qy 1381 CCTGCAACGAAAGAGAGATGACAGAAATTTGCGAATTGATTGACTACAAAGAA 1440
Db 1381 CCTGCAACGAAAGAGAGATGACAGAAATTTGCGAATTGATTGACTACAAAGAA 1440
Qy 1441 AAACAGATGCCAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGAC 1500
Db 1441 AAACAGATGCCAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGAC 1500
Qy 1501 TCAGAGAAAGATGACAAAAGCTTTGAGGGCAGTGAATAATGGCAGCAGAGAAAAGTCT 1560
Db 1501 TCAGAGAAAGATGACAAAAGCTTTGAGGGCAGTGAATAATGGCAGCAGAGAAAAGTCT 1560
Qy 1561 CAAGAACCGAAATTAATTAAGATGTTGATAGAGGCTAGAAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACCGAAATTAATTAAGATGTTGATAGAGGCTAGAAAATTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAGACAGAAAGTACTCATGTCGATTCAGAAAACCTGACTAATGGTGC 1680
Db 1621 GAAATGAAGAGACAGAAAGTACTCATGTCGATTCAGAAAACCTGACTAATGGTGC 1680
Qy 1681 ACTGCTGCAATGTTGATGATGATTAATTTCTTCAAGAGAGACAAACCTGAAAGC 1740
Db 1681 ACTGCTGCAATGTTGATGATGATTAATTTCTTCAAGAGAGACAAACCTGAAAGC 1740
Qy 1741 CAGCAATTTCCGACACTGAGAAATGAAGATGATCAAGAGAGAAACAAATGATCTGAG 1800
Db 1741 CAGCAATTTCCGACACTGAGAAATGAAGATGATGATTAATTTCTTCAAGAGAGAA 1800
Qy 1801 AAGCAATTTTGAAGAACAGAAACCTGAAATATTACAGATGAGATTTCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGAAGAACAGAAACCTGAAATATTACAGATGAGATTTCTGATTCATGAA 1860
Qy 1861 GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 1861 GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Qy 1921 GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Qy 1981 GAGCTAGACACATGAAACATGAGAGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 GAGCTAGACACATGAAACATGAGAGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 9
AAS9859
ID AAS9859 strand; cdna; 2040 BP.
XX
AC AAS9859;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11g1 splice variant B11C-9,16.
XX
KW Human; breast cancer; PCR primer; ss; cyrostatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN MO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX

(CORI-) CORIXA CORP.

Frudakis TM, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
Wang A, Sheiky YAM, Harlocker SL, Day CH;

WPI; 2002-089919/12.

P-PSDB; AAU74379.

New breast tumor proteins and polynucleotides encoding them, useful for
treating and/or preventing cancer, particularly breast cancer, and for
eliciting humoral and/or cellular immune response.

Claim 1, Page 224-225; 245pp; English.

The invention relates to novel breast tumour polynucleotides and
polypeptides. The polypeptides and polynucleotides are useful in
pharmaceutical compositions for treating and/or preventing cancer,
particularly breast cancer, and for eliciting an immune response,
particularly humoral and/or cellular immune response. The polynucleotides
may be used as probes or primers for nucleic acid hybridisation, in the
design and preparation of ribozyme molecules for inhibiting expression of
tumour polypeptides and proteins, and in recombinant DNA molecules to
direct expression of a polypeptide in host cells. AAS9570-AAS9988
represent novel human breast cancer protein coding sequences and PCR
primers of the invention

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 6; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGTTGATTCATGCGGCTCTTCTGTGAGAGCCATTGGTCTC 60
DB 1 ATGGTGTTGAGTTGATTCATGCGGCTCTTCTGTGAGAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTGCTTCCCTGCGCAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTGCTTCCCTGCGCAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTGTATGAAACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTGTATGAAACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGTGG 240
DB 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGTGG 240
QY 241 GGGCGTCTGAGACCAAGCACTCTGTATGAAACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGCGTCTGAGACCAAGCACTCTGTATGAAACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 GGAAGCACTAGTACAGTGCCTTCTGAGAGCCCAAGTACCACTGCTGAGAGAGTCTG 420
DB 361 GGAAGCACTAGTACAGTGCCTTCTGAGAGCCCAAGTACCACTGCTGAGAGAGTCTG 420
QY 421 GACAAGTCTCAGAGCTGCGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAAG 480
DB 421 GACAAGTCTCAGAGCTGCGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAAG 480
QY 481 CTGAGGACACTGACGTGAAACAAGAGCAAGCAAAAGAGAGTCTTCAATCTGAGCC 540
DB 481 CTGAGGACACTGACGTGAAACAAGAGCAAGCAAAAGAGAGTCTTCAATCTGAGCC 540
QY 541 TCTGCCAATGGAATTCAGAGTAAACTCTGCTGAGACAGAGATGTCAATCTTAAT 600
DB 541 TCTGCCAATGGAATTCAGAGTAAACTCTGCTGAGACAGAGATGTCAATCTTAAT 600
QY 601 GTCTTGAACAAGAGAGAGAGTCTGATTAAGGCGGTACATGCAAGAGAGTGA 660

DB 601 GTCTTGAACAAGAGAGAGAGTCTGATTAAGGCGGTACATGCAAGAGTGA 660
QY 661 TGTGGCTTAATGTTGCTGAGACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGGCTTAATGTTGCTGAGACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGGCTATCTTAATGAAGTTAAATTAATGCCCAGACCTGCTTA 780
DB 721 ACCACTCTGCACTAGGCTATCTTAATGAAGTTAAATTAATGCCCAGACCTGCTTA 780
QY 781 TATGGTGTGATATGCAATCAAAAAACAGACAGTGGCTCACAACCTGTTACTGGTGA 840
DB 781 TATGGTGTGATATGCAATCAAAAAACAGACAGTGGCTCACAACCTGTTACTGGTGA 840
QY 841 CATGACAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGAATTTAAATGCA 900
DB 841 CATGACAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGAATTTAAATGCA 900
QY 901 CTGATATGATATGAAAGACTGCTCATCTTGTCTGTATGTTGTGATCAGCAAGTAT 960
DB 901 CTGATATGATATGAAAGACTGCTCATCTTGTCTGTATGTTGTGATCAGCAAGTAT 960
QY 961 GTGACGCTTCTACTTGAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
DB 961 GTGACGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTATCATCATATATTTGCACTTCTGCACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTATCATCATATATTTGCACTTCTGCACTAC 1080
QY 1081 AAAAGAAAAACAGATCTAAAAATCTCTTGTAAAAACAGCAATCCAGAAACCACTTAAG 1140
DB 1081 AAAAGAAAAACAGATCTAAAAATCTCTTGTAAAAACAGCAATCCAGAAACCACTTAAG 1140
QY 1141 CTGATCATGAGAGAGAGTCAAAAGGTTCAAAAGCAAGTAAATAGCAGCAGAGAA 1200
DB 1141 CTGATCATGAGAGAGAGTCAAAAGGTTCAAAAGCAAGTAAATAGCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATGTTGAGATTTACTAGAAAACTGCACTAATGATGTCCTGCTGC 1320
DB 1261 AAGCATGAAGTAAATGTTGAGATTTACTAGAAAACTGCACTAATGATGTCCTGCTGC 1320
QY 1321 AATGTTGATTAATGATTAATTCCTCAAGAGAGACAGAACTGAAATAGCAATTT 1380
DB 1321 AATGTTGATTAATGATTAATTCCTCAAGAGAGACAGAACTGAAATAGCAATTT 1380
QY 1381 CCTGCAACAGAAAGTGAAGAGATATCAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
DB 1381 CCTGCAACAGAAAGTGAAGAGATATCAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAGCTTAAGCTGACA 1500
DB 1441 AAAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCGAGTGAATATGGCAACAGAGAAAGATCT 1560
DB 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCGAGTGAATATGGCAACAGAGAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATGAAGATGATATGAGAGCTAGAAATTTTAATGCTATCGAA 1620
DB 1561 CAAGAACAGAAATTAATGAAGATGATATGAGAGCTAGAAATTTTAATGCTATCGAA 1620
QY 1621 GAAATGAAGAGAGAGAGAGTATCATATGCGATTTCCAGAAAACTGATCTAATGCTGCC 1680
DB 1621 GAAATGAAGAGAGAGAGAGTATCATATGCGATTTCCAGAAAACTGATCTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCAAGAGAGAGAGAACTGTAAGC 1740

Db 1681 ACTGCTGCATGATGATGATGATTAATTCCTCAAGGAAGACGAAACCTGAAAGC 1740
 QY 1741 CAGCAATTCCTGACACCTGAGATGAAGAGTATCAAGTACGAGCAAAATGATCTCG 1800
 Db 1741 CAGCAATTCCTGACACCTGAGATGAAGAGTATCAAGTACGAGCAAAATGATCTCG 1800
 QY 1801 AAGCAATTTTGTGAGAGAGAGAACTGGAATTTACAGATGAGATTCGATTCATGA 1860
 Db 1801 AAGCAATTTTGTGAGAGAGAGAACTGGAATTTACAGATGAGATTCGATTCATGA 1860
 QY 1861 GAAACACAGATGAGAGTGTGTTGAAAAATGAAATTCGAGCTTCTCTTATGTTGAAGA 1920
 Db 1861 GAAACACAGATGAGAGTGTGTTGAAAAATGAAATTCGAGCTTCTCTTATGTTGAAGA 1920
 QY 1921 GAAAAAGACATCTTGATGATGAAAAATAGTACGTTGCGGAGAGAAATTCCTCAAGCAG 1980
 Db 1921 GAAAAAGACATCTTGATGATGAAAAATAGTACGTTGCGGAGAGAAATTCCTCAAGCAG 1980
 QY 1981 GAGCTAGACATGAAATGAAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
 Db 1981 GAGCTAGACATGAAATGAAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
 RESULT 10
 ACC95344
 ID ACC95344 standard; cDNA; 2040 BP.
 AC ACC95344;
 AC ACC95344;
 DT 28-AUG-2003 (first entry)
 DE Prostate tumour specific cDNA sequence SEQ ID 375.
 XX
 KW Cytostatic; gene therapy; prostate-specific protein; psp; human;
 KW Immune response; prostate cancer; ss.
 OS Homo sapiens.
 XX
 PN MO200289747-A2.
 PD 14-NOV-2002.
 XX
 PP 09-MAY-2002; 2002MO-US014753.
 XX
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Panger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De Baesio SC, Foy TM, Watanabe Y;
 PI Deng T;
 XX
 DR MPI; 2003-167130/16.
 XX
 PT New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or creating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.
 XX
 PS Example 11; Page 416; 691pp; English.
 XX
 CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in a patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention
 CC
 SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 8; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
 Matches 2040; Conservative 0; Indels 0;

QY 1 ATGGTGTGATGATGATTCATGCGCGCTGCTCTTGTGAGAAAGCATTTGGTCTC 60
 Db 1 ATGGTGTGATGATGATTCATGCGCGCTGCTCTTGTGAGAAAGCATTTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTCTTCCCTGCTGCAAGGAGCGGCAAG 120
 Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTCTTCCCTGCTGCAAGGAGCGGCAAG 120
 QY 121 AGCAACGTGGGCACTTGTGAGACACAGCACTGCTGCTATGAGACACTGAGAGCAAG 180
 Db 121 AGCAACGTGGGCACTTGTGAGACACAGCACTGCTGCTATGAGACACTGAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAGT 240
 Db 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAGT 240
 QY 241 GCGGCTTCTGAGACCAAGCACTCTGCTATGAGACACTGAGAAACAAGTGGCAAG 300
 Db 241 GCGGCTTCTGAGACCAAGCACTCTGCTATGAGACACTGAGAAACAAGTGGCAAG 300
 QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
 Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
 QY 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACCACTGCTGAGAGATCTG 420
 Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACCACTGCTGAGAGATCTG 420
 QY 421 GACAACTTCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATTCATCGTCATG 480
 Db 421 GACAACTTCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATTCATCGTCATG 480
 QY 481 CTCAGGGACACTGAGAGTGAACAAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 Db 481 CTCAGGGACACTGAGAGTGAACAAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGAGACAGATGTCACCTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGAGACAGATGTCACCTTAAT 600
 QY 601 GTCTCTTGACAAACAAAAGAGACAGCTGTGATAAAGGCGGTACCAATGCGAGAAATGAA 660
 Db 601 GTCTCTTGACAAACAAAAGAGACAGCTGTGATAAAGGCGGTACCAATGCGAGAAATGAA 660
 QY 661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAAT 720
 Db 661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAAT 720
 QY 721 ACCACTCTGCACTAGGCTATCTATATGAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780
 Db 721 ACCACTCTGCACTAGGCTATCTATATGAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780
 QY 781 TATGTGCTGATATGATCAAAAAACAAGCATGGCTTCAACCACTGTTACTTGGTGTAA 840
 Db 781 TATGTGCTGATATGATCAAAAAACAAGCATGGCTTCAACCACTGTTACTTGGTGTAA 840
 QY 841 CATGAGCAAAAAACAGAAAGTGTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGGA 900
 Db 841 CATGAGCAAAAAACAGAAAGTGTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGGA 900
 QY 901 CTGATATGATGAGAGAGCTGCTCATACTTGTGATGTTGTGATGACCAAGTATA 960
 Db 901 CTGATATGATGAGAGAGCTGCTCATACTTGTGATGTTGTGATGACCAAGTATA 960
 QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGACAGACG 1020
 Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGACAGACG 1020

QY	1021	GCCAGAGAGTACTGCTGTTTCTAAGTCATCATCTGAATATTTGCCAGTTACTTTCTGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAAGTCATCATCTGAATATTTGCCAGTTACTTTCTGACTAC	1080
QY	1081	AAAGAAAAACGATGCTTAAAAATCTCTGTGAAAACACCATTCAGAACCAAGACTTAAAG	1140
Db	1081	AAAGAAAAACGATGCTTAAAAATCTCTGTGAAAACACCATTCAGAACCAAGACTTAAAG	1140
QY	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA	1200
QY	1201	ATGCTCTCAAGAACCCGAAATTAATAAGATGCTGTATAGAGCTTTGAAGAAATGAG	1260
Db	1201	ATGCTCTCAAGAACCCGAAATTAATAAGATGCTGTATAGAGCTTTGAAGAAATGAG	1260
QY	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACTGACTAATGCTGACTGCTGGC	1320
Db	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACTGACTAATGCTGACTGCTGGC	1320
QY	1321	AATGCTGATTAATGATTTAATTCCTCAAGGAAGACAGAACACTGAAATCAGCAATTT	1380
Db	1321	AATGCTGATTAATGATTTAATTCCTCAAGGAAGACAGAACACTGAAATCAGCAATTT	1380
QY	1381	CCTGACAAACGAAGAGGAGATATCACGAATTTGCCAATTAATGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAGAGGAGATATCACGAATTTGCCAATTAATGTTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAAAATACTCTTCTGTAACAACGAAACCCAGAACAAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAAATACTCTTCTGTAACAACGAAACCCAGAACAAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGTCACAAAAGCCTTGAGGGCAGTGAAAATGSCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGGAAGTCACAAAAGCCTTGAGGGCAGTGAAAATGSCCAGCCAGAGAAAAGATCT	1560
QY	1561	CAGAACAACAGAAATTAATTAAGAGTGGTGTATGAGAGCTGAGAAAATTTTATGCTATAGAA	1620
Db	1561	CAGAACAACAGAAATTAATTAAGAGTGGTGTATGAGAGCTGAGAAAATTTTATGCTATAGAA	1620
QY	1621	GAATGGAAGACACGGAAGTACTCATGTCCGATTTCCAGAAAACCTGACTAATGATGCTCC	1680
Db	1621	GAATGGAAGACACGGAAGTACTCATGTCCGATTTCCAGAAAACCTGACTAATGATGCTCC	1680
QY	1681	ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGGAAGAGCAGAACACTCTGAAGC	1740
Db	1681	ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGGAAGAGCAGAACACTCTGAAGC	1740
QY	1741	CAGCAATTTCTCTGACACTGAGAAATGAAGAGTATCACAGTGCAGAACAAAATGATATCTAG	1800
Db	1741	CAGCAATTTCTCTGACACTGAGAAATGAAGAGTATCACAGTGCAGAACAAAATGATATCTAG	1800
QY	1801	AAGCAATTTTGTGAAGAACAGAAACCTGGAATATTAACGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAAACCTGGAATATTAACGATGAGATTTCTGATTCATGAA	1860
QY	1861	GAAAGACGATGAGAGTGGTTGAAAAATGAATTCGTAGCTTTCTCTTAAGTTGTAAGAA	1920
Db	1861	GAAAGACGATGAGAGTGGTTGAAAAATGAATTCGTAGCTTTCTCTTAAGTTGTAAGAA	1920
QY	1921	GAAGAAAGCATCTTGCATGAATAATAGTACTGTCGGGGAAGAAATTCGCATGCTTAAGCTG	1980
Db	1921	GAAGAAAGCATCTTGCATGAATAATAGTACTGTCGGGGAAGAAATTCGCATGCTTAAGCTG	1980
QY	1981	GAGCTTACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTTACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040

RESULT 11
ADAl1382
ID ADAl1382 standard; cDNA; 2040 BP.
XX

AC ADA11382;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human breast cancer specific cDNA B11C-9,16.
XX
KW ss; gene; human; breast cancer; cytosstatic; tumour; gene therapy.
XX OS Homo sapiens.
PM US2002165371-A1.
XX
PD 07-NOV-2002.
PF 07-AUG-2001; 2001US-00924400.
PR 11-JAN-1996; 96US-00585392.
PR 10-JAN-1997; 97WO-US000485.
PR 09-APR-1997; 97US-00838762.
PR 11-DEC-1997; 97US-00991789.
PR 17-APR-1998; 98US-00662451.
PR 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX
PA (FRUD/) FRUDAKIS T N.
PA (REED/) REED S G.
PA (SMIT/) SMITH J M.
PA (MISH/) MISHER L E.
PA (DILL/) DILLON D C.
PA (RETT/) RETTER M W.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HARL/) HARLOCKER S L.
PA (DAYC/) DAY C H.
PA (LISX/) LI S X.
PA (DENG/) DENG T.
XX
PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
XX
DR P-PSDB; ADA11385.
XX
PT New breast tumor proteins nucleic acids encoding such proteins, useful in
PT diagnosing, preventing and/or treating diseases such as cancer,
PT particularly breast cancer, and as markers for detecting the presence of
PT a cancer.
XX
PS Claim 1; Page 141; 190pp; English.

The invention relates to a breast tumour polynucleotide selected from one of the 275 fully defined nucleotide sequences (a) given in the specification, including their complements, sequences consisting of at least 20 contiguous residues of a sequence in (a), sequences that hybridise to a sequence in (a) under moderately stringent conditions, or sequences having at least 75% or 90% identity to a sequence in (a), or degenerate variants of a sequence in (a). Also included are an isolated polypeptide (II) (comprising an amino acid sequence selected from sequences encoded by (a), sequences having at least 70% or 90% identity to a sequence encoded by (a), sequences of 30 fully defined amino acid sequences (c), and sequences having at least 70% or 90% identity to a sequence in (c)), expression vectors comprising (a), a host cell transformed or transfected with the expression vector, an isolated antibody or its antigen-binding fragment that specifically binds to (II), a method for detecting the presence of a cancer in a patient, a fusion protein comprising at least one polypeptide (II), an oligonucleotide that hybridises to (a), under moderately stringent conditions, a method for stimulating and/or expanding T cells specific for a tumour protein (bv

QY 1861 GAAAAGCAGATGAAAGTGGTGGAAAAAATGAATTCAGCTTCTCTAGTGTAGAAA 1920
DB 1861 GAAAAGCAGATGAAAGTGGTGGAAAAAATGAATTCAGCTTCTCTAGTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAAAGAAATTCCTAGTAAAGCTG 1980
DB 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAAAGAAATTCCTAGTAAAGCTG 1980
QY 1981 GAGCTAGACACAATGAAATGAAATGAGCCAGCTTAAAAAATTCCTAGTAAAGCTG 2040
DB 1981 GAGCTAGACACAATGAAATGAAATGAGCCAGCTTAAAAAATTCCTAGTAAAGCTG 2040

RESULT 12
ADCL5355
ID ADCL5355 standard; DNA; 2040 BP.
XX
XX ADCL5355;
XX
XX 18-DEC-2003 (first entry)
XX
XX DE Human breast tumour protein DNA, SEQ ID 303.
XX
XX KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
XX ds.
XX OS Homo sapiens.
XX
XX WO2003013431-A2.
XX
XX PD 20-FEB-2003.
XX
XX PF 05-AUG-2002; 2002WO-US024917.
XX
XX PR 07-AUG-2001; 2001US-00924400.
XX PR 20-FEB-2002; 2002US-00079137.
XX PR 02-AUG-2002; 2002US-00212679.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH,
XX PI Kalos MD;
XX
XX DR WPI; 2003-342398/32.
XX
XX PT New polynucleotide, useful for preparing a composition for diagnosing,
XX PT treating or preventing cancer.
XX
XX PS Example 1; SEQ ID NO 303; 308bp; English.
XX
XX CC The present invention relates to compositions and methods for the therapy
XX CC and diagnosis of cancer, particularly breast cancer. The method for
XX CC detecting the presence of a cancer in a patient comprises: obtaining a
XX CC biological sample from the patient; contacting the biological sample with
XX CC a binding agent that binds to the polypeptide; detecting in the sample an
XX CC amount of the polypeptide that binds to the binding agent; and comparing
XX CC the amount of the polypeptide to a predetermined cut-off value. Treating
XX CC breast cancer comprises administering a composition comprising breast
XX CC tumour proteins and nucleic acids, which stimulates and/or expands T cells
XX CC specific for the tumour protein. The present sequence was used to
XX CC illustrate the invention.
XX
XX SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGTTGAGGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCAATTTGCTTC 60
DB 1 ATGGGTGTTGAGGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCAATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGCAGGAGAGCGGCAG 120

DB 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGCAGGAGAGCGGCAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGCAAGTGGTGGCTGCTTCCCTGCTGCAGGAGAGCGGCAG 240
DB 181 ATGGCAAGTGGTGGCTGCTTCCCTGCTGCAGGAGAGCGGCAG 240
QY 241 GCGCTTCTGAGAGCAAGCACTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
DB 241 GCGCTTCTGAGAGCAAGCACTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTCTGCTGCACTGCTTCCCTGCTGCAGGAGAGCGGCAG 360
DB 301 TGGTCTGCTGCACTGCTTCCCTGCTGCAGGAGAGCGGCAG 360
QY 361 GGAAGCTAGATGACAGTGGCTTCAATGAGCCAGGTACCACTCGTGGAGAAATCTG 420
DB 361 GGAAGCTAGATGACAGTGGCTTCAATGAGCCAGGTACCACTCGTGGAGAAATCTG 420
QY 421 GACAAAGCTTCCAGAGCTGCTGAGGAGTAAAGTCCCGAAGAGATCTCATGCTG 480
DB 421 GACAAAGCTTCCAGAGCTGCTGAGGAGTAAAGTCCCGAAGAGATCTCATGCTG 480
QY 481 CTCAGGGAACCTGACGTGAAACAAGAGCAAGCAAGAGAGAGCTGCTTACATCTG 540
DB 481 CTCAGGGAACCTGACGTGAAACAAGAGCAAGCAAGAGAGAGCTGCTTACATCTG 540
QY 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGAGACAGAGATGCACTTA 600
DB 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGAGACAGAGATGCACTTA 600
QY 601 GTCTTGAACAACAAAG 660
DB 601 GTCTTGAACAACAAAG 660
QY 661 TGTGCTTGAACAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TGTGCTTGAACAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACCACTCTGCACTAGCTATCTATATGAAATTAATGAGCAAGCACTGCTCTTA 780
DB 721 ACCACTCTGCACTAGCTATCTATATGAAATTAATGAGCAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATGATGAAATCAAAAGCAAGTGGCTTCAACCACTGCTTCTGCTTA 840
DB 781 TATGCTGCTGATGATGAAATCAAAAGCAAGTGGCTTCAACCACTGCTTCTGCTTA 840
QY 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900
DB 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900
QY 901 CTGATATGATGAG 960
DB 901 CTGATATGATGAG 960
QY 961 GTGACCTTCTGATGAG 1020
DB 961 GTGACCTTCTGATGAG 1020
QY 1021 GCGAGAGATAGCTGTTCTAGTATCATCATGTAATTTGCAAGTCTTCTGAGTAC 1080
DB 1021 GCGAGAGATAGCTGTTCTAGTATCATCATGTAATTTGCAAGTCTTCTGAGTAC 1080
QY 1081 AAAGAAAAACAGATCTTAAATCTCTTGAAGAACCAATCCAGAACCAATTTAAG 1140
DB 1081 AAAGAAAAACAGATCTTAAATCTCTTGAAGAACCAATCCAGAACCAATTTAAG 1140
QY 1141 CTGATCATGAG 1200

Db	1141	CTGACATCAGAGGAAGTCTCAAAAGTTCCAAAGCACTGAAATATGCCACCGAGAAA	1200
OY	1201	ATGTCCTAAGAACCGAAAAATAATAGAGTGGTGAAGAGGTTGAAAGAAATGAG	1268
Db	1201	ATGTCCTAAGAACCGAAAAATAATAGAGTGGTGAAGAGGTTGAAAGAAATGAG	1268
OY	1261	AAGCATGAAAGTAATATGTGGGATTACTTAAAGAACTTGACTAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAAGTAATATGTGGGATTACTTAAAGAACTTGACTAATGTGTCACTGTGGC	1320
OY	1321	AATGTGATTAATGATTAATTCCTCAAGAGAGACAGAACCTCGAATAATCAGCAATTT	1380
Db	1321	AATGTGATTAATGATTAATTCCTCAAGAGAGACAGAACCTCGAATAATCAGCAATTT	1380
OY	1381	CCTGACAAAGAAAGTGAAGAGTATCACGAATTTGCGAATTTGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAAGAAAGTGAAGAGTATCACGAATTTGCGAATTTGTTCTGACTACAAAGAA	1440
OY	1441	AAACGATAGCCCAAATTAATCTTTCTGAAAAACAGCAACCCAGAACAAAGATTAAAGTGACA	1500
Db	1441	AAACGATAGCCCAAATTAATCTTTCTGAAAAACAGCAACCCAGAACAAAGATTAAAGTGACA	1500
OY	1501	TCAGAGAAAGAGTCACAAAAGCTTGAGGGCAGTGAATAATGGCAGCCGAGAGAAAAGTCT	1568
Db	1501	TCAGAGAAAGAGTCACAAAAGCTTGAGGGCAGTGAATAATGGCAGCCGAGAGAAAAGTCT	1568
OY	1561	CAGAACCCAGAAATTAATTAAGAGTGGTATAGAGAGCTTAAAGAAATTTTATGGCTATCGAA	1620
Db	1561	CAGAACCCAGAAATTAATTAAGAGTGGTATAGAGAGCTTAAAGAAATTTTATGGCTATCGAA	1620
OY	1621	GAAATGAAGAAAGCAGGAAGTCTCATGTCCGATTCCAGAAAACCTGACTTAATGTGGCC	1680
Db	1621	GAAATGAAGAAAGCAGGAAGTCTCATGTCCGATTCCAGAAAACCTGACTTAATGTGGCC	1680
OY	1681	ACTGCTGGCAATGENTGATGATGATTAATTCCTCCAGAAAGACAGAACACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGENTGATGATGATTAATTCCTCCAGAAAGACAGAACACCTGAAAGC	1740
OY	1741	CAGCAATTTCTGCACTGAGATGAAAGATGATCACTGATGACAGAACAAATGATACTCAG	1800
Db	1741	CAGCAATTTCTGCACTGAGATGAAAGATGATCACTGATGACAGAACAAATGATACTCAG	1800
OY	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACACGATGAGATTCTGATTCATGAA	1868
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACACGATGAGATTCTGATTCATGAA	1868
OY	1861	GAAAAAGCAGATGAAAGTGGTTGAAAAAATGAAATCTGAGCTTTCTTAAAGTGAAGAA	1920
Db	1861	GAAAAAGCAGATGAAAGTGGTTGAAAAAATGAAATCTGAGCTTTCTTAAAGTGAAGAA	1920
OY	1921	GAAAAAGCAGATCTTGATGATGAAATATGATAGCTTGCAGGAAGAAATTCATGCTAAAGCTG	1980
Db	1921	GAAAAAGCAGATCTTGATGATGAAATATGATAGCTTGCAGGAAGAAATTCATGCTAAAGCTG	1980
OY	1981	GAGCTTAGACACATATGAAACATCAGAGCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAAA	2040
Db	1981	GAGCTTAGACACATATGAAACATCAGAGCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAAA	2040
RESULT 13			
ADBI3825			
ID	ADBI3825	standard; cDNA; 2040 BP.	
XX	ADBI3825;		
AC	ADBI3825;		
XX	18-DEC-2003	(first entry)	
DE	Human prostate specific cDNA B305 splice variant #10.		
XX			
XX	Human; ss; prostate specific cDNA; cytosolic; immunostimulant;		
KM	gene therapy; cell therapy; vaccine; T-cell epitope;		
KM	class I major histocompatibility complex allele; MHC; prostate cancer;		
KM	tumour; antigen presenting cell.		

XX Homo sapiens.
OS
XX
PN US2003185830-A1.
XX
PD
XX 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 05-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012856.
PR 09-MAY-2002; 2002US-00144678.
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Kalos MD;
XX
DR WPI, 2003-756193/71.
DR P-PSDB; ADB13830.
XX
PT
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Example 11; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADB13563 comprising a sequence ADB1487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC CDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB13558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docId=20030185830.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 10; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACTCTGTATGAAGACATCAGAGACCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACTCTGTATGAAGACATCAGAGACCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 240
QY 241 GGGGCTTCTGAGACACAGACTCTGTATGAAGACATCAGAGACCAAGTGTG 300
DB 241 GGGGCTTCTGAGACACAGACTCTGTATGAAGACATCAGAGACCAAGTGTG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGGCAAGCAAGTGTGCGGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGGCAAGCAAGTGTGCGGCTTGG 360
QY 361 GGAAGACTAGATGACAGTGTCTTCAATGAGCCAGATACAGTCCGTGGAGAGATCTG 420
DB 361 GGAAGACTAGATGACAGTGTCTTCAATGAGCCAGATACAGTCCGTGGAGAGATCTG 420
QY 421 GACAACTTCAAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAACTTCAAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGGAACATGACCTGTGAACAAGAGACACAGCAAAAGAGACTGCTTCACTCTG 540
DB 481 CTCAGGGAACATGACCTGTGAACAAGAGACACAGCAAAAGAGACTGCTTCACTCTG 540
QY 541 TCTGCAATGGGAATTCAAGAGTAAACTCTGCTGGAACAGAGATGCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAAGAGTAAACTCTGCTGGAACAGAGATGCAACTTAAT 600
QY 601 GTCTTGGACAAACAAAAGAGAGACAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGA 660
DB 601 GTCTTGGACAAACAAAAGAGAGACAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGA 660
QY 661 TGTGCTTAAATGTTGTGTGGAACATGGCACTGATCCAAATTTTCAAGATGATATGA 720
DB 661 TGTGCTTAAATGTTGTGTGGAACATGGCACTGATCCAAATTTTCAAGATGATATGA 720
QY 721 ACCACTGTGCACTACGCTATCTATATGAAGATTAATTAAGSCAAAGACACTGCTCTTA 780
DB 721 ACCACTGTGCACTACGCTATCTATATGAAGATTAATTAAGSCAAAGACACTGCTCTTA 780
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QY 781 TATGTCGTGATATGATATCAACAAAACAGCATGCGCTCACACACTGTTACTTGGTGT 840
DB 781 TATGTCGTGATATGATATCAACAAAACAGCATGCGCTCACACACTGTTACTTGGTGT 840
QY 841 CATGACAAAACAGCAAGTCGGAATTTTAAATCAAGAAAACGAAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTCGGAATTTTAAATCAAGAAAACGAAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGACATGCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGACATGCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTTCAGCTTCTACTTGAACAAAATATGATATCTTCTCAAGATCTATCTGACAGCG 1020
DB 961 GTTCAGCTTCTACTTGAACAAAATATGATATCTTCTCAAGATCTATCTGACAGCG 1020
QY 1021 GCACAGATATGCTGTTCTAGTCATCATATGTAATTTGACAGTTACTTGTGACTAC 1080
DB 1021 GCACAGATATGCTGTTCTAGTCATCATATGTAATTTGACAGTTACTTGTGACTAC 1080
QY 1081 AAAAGAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
DB 1081 AAAAGAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGATCACAAAAGTTCAAAAGGCAATGAAATATGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGATCACAAAAGTTCAAAAGGCAATGAAATATGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCGAATAATTAAGATGTGTATGAGAGGTGAAGAAAGAAAGAG 1260
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QY 1261 AAGCATGAAGATTAATATGTGGATTTACAGAAAACCTGACTAATGTGTCACTGTGCG 1320
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QY 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGAGCAAAACCTGAAATATGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGAGCAAAACCTGAAATATGCAATTT 1380
QY 1381 CCTGCAAGAAAGGAAGATATCAAGAAATTTGGGATTTGTCTGACTACAAAGAA 1440
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QY 1441 AAAAGATGCCAAAATATCTCTTCTGAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
DB 1441 AAAAGATGCCAAAATATCTCTTCTGAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
QY 1501 TCAAGGAAGAGTCACAAAAGCTTGAAGGCAAGTGAATATGTTGTGATCAAAAGAA 1560
DB 1501 TCAAGGAAGAGTCACAAAAGCTTGAAGGCAAGTGAATATGTTGTGATCAAAAGAA 1560
QY 1561 CAAGAACCGAATAATTAAGATGTGTATGAAGCTGAGAAATTTATGTGCTATCGAA 1620
DB 1561 CAAGAACCGAATAATTAAGATGTGTATGAAGCTGAGAAATTTATGTGCTATCGAA 1620
QY 1621 GAAATGAAGAACACGGAAGTACTCATGTGCGAATTTCCAGAAAACCTGACTAATGCTGCC 1680
DB 1621 GAAATGAAGAACACGGAAGTACTCATGTGCGAATTTCCAGAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGTGGCAATGTGATGATGATTAATTCCTCAAGGAAGAGCAAGCACTGGAAGC 1740
DB 1681 ACTGTGGCAATGTGATGATGATTAATTCCTCAAGGAAGAGCAAGCACTGGAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGGTATCAAGTGAAGAACAAATATGATCTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGGTATCAAGTGAAGAACAAATATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTCTGATTCATGAA 1860
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QY 1861 GAAAGCAGATGAAAGTGGTGAAGAAATTCAGCTTCTTGTAGTGAAGAA 1920
DB 1861 GAAAGCAGATGAAAGTGGTGAAGAAATTCAGCTTCTTGTAGTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATGATGCGGGGAAATTCCTAAGACTG 1980
DB 1921 GAAAAAGACATCTTGCATGAAAAATGATGCGGGGAAATTCCTAAGACTG 1980
QY 1981 GAGCTAGACACATGAAATGAAATGAGCCAGCTAAAAATTCCTAAGACTG 2040
DB 1981 GAGCTAGACACATGAAATGAAATGAGCCAGCTAAAAATTCCTAAGACTG 2040

RESULT 14
ADG26241
ID ADG26241 standard; cDNA; 2040 BP.
AC ADG26241;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human prostate-specific CDNA #360.
XX
XX Human; prostate-specific polypeptide; gene; ss; prostate cancer;
XX cytosolic.
XX
XX Homo sapiens.
XX
XX US2003157089-A1.
XX
XX 21-AUG-2003.
XX
XX 09-MAY-2002; 2002US-00144678.
XX
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 29-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.

(CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kales MW, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
XX McNeill PD, Houghton RL, Vinals Y De Baesolc, Foy TM, Matanabe Y;
XX Meagher MJ, Deng T;
XX
XX WPI; 2003-777973/73.
XX
XX P-PSDB; ADG26246.
```

```
XX
XX New polynucleotides encoding prostate specific polypeptides isolated from
XX a human prostate tumor cDNA library are useful to diagnose and treat
XX cancer particularly prostate cancer.
XX
XX Example 11; SEQ ID NO 375; 99p; English.
XX
XX The invention relates to human prostate-specific polypeptides and the
XX polynucleotides encoding them. The invention also relates to an isolated
XX antibody or its antigen-binding fragment that specifically binds a
XX polypeptide of the invention, a method of detecting cancer in a patient
XX comprising contacting a biological sample of the patient with an agent
XX that binds a prostate-specific polypeptide and comparing the amount of
XX bound polypeptide compared to a predetermined cut-off value and a fusion
XX protein comprising a prostate-specific polypeptide. The sequences of the
XX invention are used to diagnose and treat cancer, particularly prostate
XX cancer. This sequence represents cDNA encoding a human prostate-specific
XX polypeptide of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification but was obtained in electronic
XX format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2040; DB 10; Length 2040;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 ATGGTGTGTTGAGATTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
XX
XX 61 AGGAGCAAGATGGGCAAGTGTGTCGCCGTTCTCCCTGTGCGAGGAGCGGCAAG 120
XX 61 AGGAGCAAGATGGGCAAGTGTGTCGCCGTTCTCCCTGTGCGAGGAGCGGCAAG 120
XX
XX 121 AGCAACGTGGGCACTTTGTGAGACCAAGCAACTGTCTATGAAGCACTCAGAGCAAG 180
XX 121 AGCAACGTGGGCACTTTGTGAGACCAAGCAACTGTCTATGAAGCACTCAGAGCAAG 180
XX
XX 181 ATGGGCAAGTGTGTCGCCGTTCTCCCTGTGCGAGGAGCGGCAAGTGTGCGAG 240
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XX
XX 241 GGGCGTTCTGAGACCAAGCAACTGTCTATGAAGCACTCAGAGCAAGTGTGCGAG 300
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XX
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XX 301 TGGTCTGCACTGCTTCCCTGTGCGAGGAGCGGCAAGTGTGCGAGTGGCGCTTGG 360
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XX 361 GGAAGCTAGATGACAGTGCCTTCAATGAGCCAGGTACCACTGCTGCTGAGAAATCTG 420
XX 361 GGAAGCTAGATGAGTGCCTTCAATGAGCCAGGTACCACTGCTGCTGAGAAATCTG 420
XX
XX 421 GACAAGCTTCAAGAGCTGCTGTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
XX 421 GACAAGCTTCAAGAGCTGCTGTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
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XX 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTCAATCTGAGCC 540
XX 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTCAATCTGAGCC 540
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XX 541 TCTGCCAATGGGAATTCAGAAATGATTAATCTCTGCTGAGACAGACAGATGCTCAATTA 600
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XX 601 GTCTTGAACAACAAAAGAGGACAGCTGATTAAGGCGGTCAATGCGAGGAAGATGA 660
XX 601 GTCTTGAACAACAAAAGAGGACAGCTGATTAAGGCGGTCAATGCGAGGAAGATGA 660
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XX 661 TGTGCTTAATGTTCTGGAACATGGCACTGATCCAAATATTCAGATGATGATGAAT 720
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Db 661 TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCOAGATGATAGAAAT 720
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Db 721 ACCACTCTGACATACGCTATCTTAATGAAGATTAATTAATGCGCAAGACATGCTCTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAAACAAGATGCGCTCACACACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAAGATGCGCTCACACACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTTAAATGCA 900
Qy 901 CTGAGATGATATGGAAGAGATGCTCTCATATCTTGATATGTTGTGATGACGAAATGA 960
Db 901 CTGAGATGATATGGAAGAGATGCTCTCATATCTTGATATGTTGTGATGACGAAATGA 960
Qy 961 GTGAGCCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGACG 1020
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Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCAGAAACAAGCTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCAGAAACAAGCTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGATGACAAAGGTTCAAAAGGCTGAATTAATGCGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATGACAAAGGTTCAAAAGGCTGAATTAATGCGCCAGAGAAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATGAAGATGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATGAAGATGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATGTTGGATTAATGAAAACTGATAGTGTCACTGCTGCGC 1320
Db 1261 AAGCATGAAGATTAATGTTGGATTAATGAAAACTGATAGTGTCACTGCTGCGC 1320
Qy 1321 AATGATGATATGATTAATTTCTCTCAAGAGAAAGACCACTGAAATTCGCAATTT 1380
Db 1321 AATGATGATATGATTAATTTCTCTCAAGAGAAAGACCACTGAAATTCGCAATTT 1380
Qy 1381 CCTGACAAAGAGATGATCAGAAATTTGCAATTAATTTCTGCTAAGAA 1440
Db 1381 CCTGACAAAGAGATGATGAGATATCAGAAATTTGCAATTAATTTCTGCTAAGAA 1440
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Db 1441 AAAAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGAC 1500
Qy 1501 TCAGAGAGAGATGACAAAGGCTTGAAGGAGATGAAAAATGCGCAGCCAGAAAAATCT 1560
Db 1501 TCAGAGAGAGATGACAAAGGCTTGAAGGAGATGAAAAATGCGCAGCCAGAAAAATCT 1560
Qy 1561 CAAGAAGCAAAATTAATGAATGATGATAGAGATGAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAAGCAAAATTAATGAATGATGATGATGATGAGAAATTTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAGACGAAAGTACTATGTCGATTTCCCAAAAACTGACTAAATGCTGAC 1680
Db 1621 GAAATGAAGAGACGAAAGTACTATGTCGATTTCCCAAAAACTGACTAAATGCTGAC 1680
Qy 1681 ACTGCTGGCAATGCTGATGATTAATTTCTTCAAGAGAGCAAGAACCTGAAAGC 1740
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Qy 1741 CAGCAATTTCTGACATGAGATGAAGATATCAGAGTACGAAACAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACATGAGATGAAGATATCAGAGTACGAAACAATGATCTCAG 1800

Qy 1801 AAGCAATTTTGTGAAGAAAGAAACACTGCAATTTACAGATGATGATTTGATTCATGAA 1860
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Qy 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTGAGCTTCTCTTGTGTGAAGAA 1920
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Qy 1921 GAAAAAGACATCTTGACATGAAAAATAGTACGTTGCGGAGAAATTCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGACATGAAAAATAGTACGTTGCGGAGAAATTCATGCTAAGACTG 1980
Qy 1981 GAGCTTGACACATGAACATCAGAGCCAGCTTAAAAATTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTTGACACATGAACATCAGAGCCAGCTTAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 15
AA06600
ID AA06600 standard; cDNA; 2040 BP.
XX
AC AA06600;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:375.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker St, Yugiu J, Xu J, Mitcham Jr;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 50; Page 223-224; 263pp; English.
XX

The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumor protein (prp). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AA06241 to AA06691 and CC AA08200 to AA08202 represent sequences used in the exemplification of the present invention

Sequence 2040 BP; 716 A; 393 C; 500 G; 431 T; 0 U; 0 Other;

Query Match 99.9%; Score 2038.4; DB 3; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ATGGTGGTGAAGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGGTCCCTGCTGCAAGGAGCCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGTGG 240
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QY 241 GGGGCTTCTGGAAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGGAAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 GGAGACTACGATGACAGTGGCTTCAATGAGGCCAGGTACCACTCCGTGGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGGCTTCAATGAGGCCAGGTACCACTCCGTGGAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGGGCTAAAGTCCCGAGAAAGATCTCATCTGCTGAG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGGGCTAAAGTCCCGAGAAAGATCTCATCTGCTGAG 480
QY 481 CTCAGGAGCACTGACGTGAACAAGAGACAAAGCAAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CTCAGGAGCACTGACGTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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DB 601 GTCTTGAACAACAAAAGAGAGACGCTCTGATTAAGCCGTACAAATGCCAGAGAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATAATGAAGATTAATTAATGAGCAAGAGCACTGCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATAATGAAGATTAATTAATGAGCAAGAGCACTGCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAACAGCATGGCTCAACACCTGTTACTTGGTGA 840
DB 781 TATGCTGCTGATATCGAATCAAAAACAGCATGGCTCAACACCTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAACGAAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAACGAAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGCTGCTCATCTTCTGCTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGAGCTGCTCATCTTCTGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTATTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTGAGCTTCTATTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020

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QY 1021 GCCAGAGATATGCTGTTCTTAGTCATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTTAGTCATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGCAATCCAGAACAGACTTAAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGCTTCAAAAGCAGTGAATAATCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCAAAAAGCTTCAAAAGCAGTGAATAATCCAGCAGAGAAA 1200
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QY 1261 AAGCATGAAAGTAAATATGTTGGAAATTAATGAAAACTTGAATATGTTGCTCACTGCTG 1320
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DB 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGACAGAAACCTGAAATACAGCAATTT 1380
QY 1381 CCTGACAAAGAGTGAAGAGATATCAAGAAATTTGGAAATTTAGTTTCTGACTACAAAGAA 1440
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QY 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAGAACTTAAAGCTGACA 1500
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DB 1621 GAAATGAAGAACACGAAAGTACTGATGCGAATTCAGAAAAACCTGACTAATGGTGC 1680
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DB 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTTCAAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGAGATCAAGTGAAGAGCAAAATGATACTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAGAGATCAAGTGAAGAGCAAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTAATCAAGATGAGATTTCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTAATCAAGATGAGATTTCTGATTCATGAA 1860
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DB 1981 GAGCTAGACACATGAAATCATGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 2040

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OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 15:52:49 ; Search time 360.535 Seconds
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Title: US-09-924-400-303

Perfect score: 2040
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Scoring table: IDENTITY NUC
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2040	100.0	2040	3	US-09-352-616A-375
3	2040	100.0	2040	3	US-09-289-198-303
4	2040	100.0	2040	3	US-09-636-215-375
5	2040	100.0	2040	3	US-09-685-166A-375
6	2040	100.0	2040	3	US-09-429-755-303
7	2040	100.0	2040	3	US-09-679-426-375
8	2040	100.0	2040	3	US-09-759-143-375
9	2040	100.0	2040	3	US-09-651-236-375
10	2040	100.0	2040	3	US-09-699-295-303
11	2040	100.0	2040	3	US-09-534-825A-303
12	2040	100.0	2040	3	US-09-657-279-375
13	2040	100.0	2040	3	US-10-012-896-375
14	1940	95.1	2000	3	US-09-439-313-374
15	1940	95.1	2000	3	US-09-352-616A-374
16	1940	95.1	2000	3	US-09-289-198-302
17	1940	95.1	2000	3	US-09-636-215-374
18	1940	95.1	2000	3	US-09-685-166A-374
19	1940	95.1	2000	3	US-09-429-755-302
20	1940	95.1	2000	3	US-09-679-426-374
21	1940	95.1	2000	3	US-09-759-143-374
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24	1940	95.1	2000	3	US-09-534-825A-302

25	1940	95.1	2000	3	US-09-657-279-374	Sequence 374, App
26	1940	95.1	2000	3	US-10-012-896-374	Sequence 374, App
27	1147.6	56.3	1853	3	US-09-439-313-369	Sequence 369, App
28	1147.6	56.3	1853	3	US-09-062-451-295	Sequence 295, App
29	1147.6	56.3	1853	3	US-09-352-616A-369	Sequence 369, App
30	1147.6	56.3	1853	3	US-09-289-198-295	Sequence 295, App
31	1147.6	56.3	1853	3	US-09-636-215-369	Sequence 369, App
32	1147.6	56.3	1853	3	US-09-685-166A-369	Sequence 369, App
33	1147.6	56.3	1853	3	US-09-429-755-295	Sequence 295, App
34	1147.6	56.3	1853	3	US-09-679-426-369	Sequence 369, App
35	1147.6	56.3	1853	3	US-09-759-143-369	Sequence 369, App
36	1147.6	56.3	1853	3	US-09-651-236-369	Sequence 369, App
37	1147.6	56.3	1853	3	US-09-699-295-295	Sequence 295, App
38	1147.6	56.3	1853	3	US-09-534-825A-295	Sequence 295, App
39	1147.6	56.3	1853	3	US-09-657-279-369	Sequence 369, App
40	1147.6	56.3	1853	3	US-10-012-896-369	Sequence 369, App
41	1131.6	55.5	1155	3	US-09-439-313-373	Sequence 373, App
42	1131.6	55.5	1155	3	US-09-352-616A-373	Sequence 373, App
43	1131.6	55.5	1155	3	US-09-289-198-301	Sequence 301, App
44	1131.6	55.5	1155	3	US-09-636-215-373	Sequence 373, App
45	1131.6	55.5	1155	3	US-09-685-166A-373	Sequence 373, App

ALIGNMENTS

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RESULT 1
US-09-439-313-375
; Sequence 375, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42709
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-375
Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTGCTGAGTGCATTCATGCCGGCTGCTCTTCGTGAAGAAGCAATTTGGTTC 60
1 ATGGCTGCTGAGTGCATTCATGCCGGCTGCTCTTCGTGAAGAAGCAATTTGGTTC 60
Db 1 ATGGCTGCTGAGTGCATTCATGCCGGCTGCTCTTCGTGAAGAAGCAATTTGGTTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCCCTTCCCTGCTGCAGGAGCGGCAAG 120
61 AGAGCAAGATGGGCAAGTGTGCTGCCCTTCCCTGCTGCAGGAGCGGCAAG 120
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121 AGCAAGTGGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGCAATGTGCTCCGCACTGCTTCCCTCTGTGAGGGGAGTGGCAAGCAAGT 240
181 ATGGCAATGTGCTCCGCACTGCTTCCCTCTGTGAGGGGAGTGGCAAGCAAGT 240
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Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGAGATGTCACTTAAT 600
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Db 601 GTCTTTGACAAACAAAAGAGAGACAGCTGATTAAGGCGGTACAAATGCCAGGAAGATGA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
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Db 1741 CAGCAATTTCTGACACTGAGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1800
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Qy 1861 GAAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 1861 GAAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Qy 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAAGAAATGGCATGTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAAGAAATGGCATGTAAGACTG 1980
Qy 1981 GAGCTGACACATGAAACATGAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTGACACATGAAACATGAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040

RESULT 2
US-09-352-616A-375
Sequence 375, Application US/09352616A
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jianshun
TITLE OF INVENTION: MITCHAM, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1981 GAGCTAG 2040
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RESULT 3
US-09-289-198-303
; Sequence 303, Applicant: US-09289198
; Patent No. 6586570
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
EARLIER FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 08/062,451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: PatSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGAATTCATGCGGCTCTCTTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTGAATTCATGCGGCTCTCTTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTCCGTTGCTCCGCTGCAAGGAGACGGCAAG 120
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DB 361 GGAAGCTTAAGTACAGTGTCTTCAATGAGCCCAAGGTACCACTCGTGAAGAGTCTG 420
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DB 721 ACCACTGCACTAGGCTATCTATAATGAAGTAAATTAATGGCCAAAGCACTGCTCTTA 780
QY 781 TATGTGTGATATGGAATCAAAAAACAAGATGCTCACACCACTGTACTTGTGTGA 840
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QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGACATGCTCTCAATCTGCTATGTTGTGATCAGCAAGTATA 960
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QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
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Db	1741	CAGCAATTTCTGCACACTGAGAAATGAGATGATCAGCTGACAGAAACAAATATGATCTCAG	1800
Qy	1801	AAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAGATTTCTGATTCATGAA	1860
Qy	1861	GAAGAAGCAGATAGAGAAGGTGTGAAGAAATGAAATCTGAGCTTGTCTAGTTGTAAGAA	1920
Db	1861	GAAGAAGCAGATAGAGAAGGTGTGAAGAAATGAAATCTGAGCTTGTCTAGTTGTAAGAA	1920
Qy	1921	GAAGAAAGACATCTTGACATGAAATATAGTACGTTGGCGGAGAAATTCGCATGCTAAAGCTG	1980
Db	1921	GAAGAAAGACATCTTGACATGAAATATAGTACGTTGGCGGAGAAATTCGCATGCTAAAGCTG	1980
Qy	1981	GAGCTAGACAAATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACAAATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040

RESULT 4

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US-09-636-215-375
? Sequence 375, Application US/09636215
? Patent No. 6620922
? GENERAL INFORMATION:
? APPLICANT: Xu, Jiangchun
? APPLICANT: Dillon, Davin C.
? APPLICANT: Mitcham, Jennifer L.
? APPLICANT: Harlocker, Susan L.
? APPLICANT: Jiang, Yugu
? APPLICANT: Henderson, Robert A.
? APPLICANT: Kaios, Michael D.
? APPLICANT: Fanger, Gary R.
? APPLICANT: Retter, Marc W.
? APPLICANT: Stolk, John A.
? APPLICANT: Day, Craig H.
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Carter, Derrick
? APPLICANT: Li, Samuel
? APPLICANT: Wang, Aijun
? APPLICANT: Skeiky, Yaser A. W.
? APPLICANT: Hepler, William
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? TITL OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
? FILE REFERENCE: 210121.42717C17
? CURRENT APPLICATION NUMBER: US/09/636,215
? NUMBER OF SEQ ID NOS: 852
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 375
? LENGTH: 2040.
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-636-215-375

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Query Match	100.0%	Score 2040;	DB 3;	Length 2040;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTGTGTTGAGGTGATTCCATGCGCGCTGCTTTCTTGAGAGAACCAATTGTC	60	
Db	1	ATGTGTGTTGAGGTGATTCCATGCGCGCTGCTTTCTTGAGAGAACCAATTGTC	60	
QY	61	AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGTGAGGAGAGCGGCAAG	120	
Db	61	AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGTGAGGAGAGCGGCAAG	120	
QY	121	AGCAACGTGGGCACTTCTGAGAGCCAGACGACTTGTCTATGAGACACTGAGGCAAG	180	

Db	121	AGCAAGTGGGCATTCTTGAGACCAGACGACTCTGCTATGAAACACTCAGAGCAAG	180
Qy	181	ATGGGCAAGTGGTGCCTGCACCTGCTCCCTGCTGCAGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAGGGGAGTGGCAAGCAAGCTG	240
Qy	241	GGCGCTTCTGAGACCAAGACGACTCTGCTATGAAACACTCAGGAACAAGTGGCAAG	300
Db	241	GGCGCTTCTGAGACCAAGACGACTCTGCTATGAAACACTCAGGAACAAGTGGCAAG	300
Qy	301	TGGTGTGCCCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGAGTAAGTGGCCCTTG	360
Db	301	TGGTGTGCCCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGAGTAAGTGGCCCTTG	360
Qy	361	GGAAGCTACGATGACAGTGCCTTCATGAGGCCAGGTGCACGTCCTGGAGAAATCTG	420
Db	361	GGAAGCTACGATGACAGTGCCTTCATGAGGCCAGGTGCACGTCCTGGAGAAATCTG	420
Qy	421	GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
Db	421	GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
Qy	481	CTCAGGGACACTGACGTGACAAAGAGACAAAGACAAAGAGACTGCTCTCATCTTGGCC	540
Db	481	CTCAGGGACACTGACGTGACAAAGAGACAAAGACAAAGAGACTGCTCTCATCTTGGCC	540
Qy	541	TCTGCGAATGGGAATTCAGAGTGTGTAATTCCTCGCTGGACAGACATGTCAACTTAAT	600
Db	541	TCTGCGAATGGGAATTCAGAGTGTGTAATTCCTCGCTGGACAGACATGTCAACTTAAT	600
Qy	601	GTCCTTGCAACAACAAAGAGACAGCTCTGATAAAGCCGTACACATGCAAGAAAGTAA	660
Db	601	GTCCTTGCAACAACAAAGAGACAGCTCTGATAAAGCCGTACACATGCAAGAAAGTAA	660
Qy	661	TGTGCGTAAATGTTGCTGGAAATGCGCATATCCAAATATTCAGATGAGATGGAAT	720
Db	661	TGTGCGTAAATGTTGCTGGAAATGCGCATATCCAAATATTCAGATGAGATGGAAT	720
Qy	721	ACCACTGCGACTACGCTATCTATATGAAATTAATGAGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGCGACTACGCTATCTATATGAAATTAATGAGCCAAAGCACTGCTCTTA	780
Qy	781	TATGTCGCTGATTCGAATCAAAAAACAAGCATGGCTCACACGACTGTATCTTGGTGA	840
Db	781	TATGTCGCTGATTCGAATCAAAAAACAAGCATGGCTCACACGACTGTATCTTGGTGA	840
Qy	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTAATCAAGAAAAAGCAATTTAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTAATCAAGAAAAAGCAATTTAATGCA	900
Qy	901	CTGGATGATATGGAAGACTGCTCTCACTTCCTGTATGTTGTGGATCAGCAAGTATA	960
Db	901	CTGGATGATATGGAAGACTGCTCTCACTTCCTGTATGTTGTGGATCAGCAAGTATA	960
Qy	961	GTCAGCCTTCTAATCTGAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG	1020
Db	961	GTCAGCCTTCTAATCTGAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG	1020
Qy	1021	GCCAGAGATATGCTGTTTCTAATCATCATATGTAATTTGCCAGTTATCTTCTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAATCATCATATGTAATTTGCCAGTTATCTTCTGACATAC	1080
Qy	1081	AAAGAAAAACAGATGTCTAAAATCTCTCTGAAAAACAGATCCAGAACAAAGCTTTAAG	1140
Db	1081	AAAGAAAAACAGATGTCTAAAATCTCTCTGAAAAACAGATCCAGAACAAAGCTTTAAG	1140
Qy	1141	CTGACATCAGAGAAAGTCAAAAGTTCAAGGCAAGTGAATAATGCAAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGAAAGTCAAAAGTTCAAGGCAAGTGAATAATGCAAGCCAGAGAAA	1200
Qy	1201	ATGTCCTCAAGAACCAAAATTAATTAAGATGTGATATGAGAGTTTGAAGAAATTAAG	1260
Db	1201	ATGTCCTCAAGAACCAAAATTAATTAAGATGTGATATGAGAGTTTGAAGAAATTAAG	1260

QY	1261	AAGCATGAAAGTAATAAATGTGGATTACTAGAAAACCTGATAAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAAGTAATAAATGTGGATTACTAGAAAACCTGACTAAATGTGTCACTGTGGC	1320
QY	1321	AATGTGTATTAATGTGATTAATTCCTCAAAAGAACAGACACCTGAAATACAGCAATTT	1380
Db	1321	AATGTGTATTAATGTGATTAATTCCTCAAAAGAACAGACACCTGAAATACAGCAATTT	1380
QY	1381	CCTGCAACGAAAGTAGAAGATATCACGAATTTGCGAATTGATTCTGACTACAAAGAA	1440
Db	1381	CCTGCAACGAAAGTAGAAGATATCACGAATTTGCGAATTGATTCTGACTACAAAGAA	1440
QY	1441	AAACGATAGCCAAATATCTCTTCGTAATAACGCAACCCAGAAACAAGACTTAAAGCTGCA	1500
Db	1441	AAACGATAGCCAAATATCTCTTCGTAATAACGCAACCCAGAAACAAGACTTAAAGCTGCA	1500
QY	1501	TCAGAGAGAAAGTCACAAAAGCCTTGAGGCAAGTGAATAATGGCCAGCCAGAGAAAAGTCT	1560
Db	1501	TCAGAGAGAGAGTCACAAAAGCCTTGAGGCAAGTGAATAATGGCCAGCCAGAGAAAAGTCT	1560
QY	1561	CAAGAACAGAAATTAATTAAGATGTGTATAGAGACTAGAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGAACAGAAATTAATTAAGATGTGTATAGAGACTAGAAAATTTTATGGCTATCGAA	1620
QY	1621	GAAATGAAGAAAGACACGAAAGTACTATGTCCGATTTCCAGAAAACCTGATTAATGTGTCC	1680
Db	1621	GAAATGAAGAAAGACACGAAAGTACTATGTCCGATTTCCAGAAAACCTGATTAATGTGTCC	1680
QY	1681	ACTGTGGCAATGTGTGATGATGATGAATTAATTCCTCCAGAGAAAGAGAGAAACCTGAAAGC	1740
Db	1681	ACTGTGGCAATGTGTGATGATGATGAATTAATTCCTCCAGAGAGAGAGAAACCTGAAAGC	1740
QY	1741	CAGCAATTTCTTGACACTGAGATGAAGAGATATCAACATGACGAACAATATGATCTCAG	1800
Db	1741	CAGCAATTTCTTGACACTGAGATGAAGAGATATCAACATGACGAACAATATGATCTCAG	1800
QY	1801	AAGCAATTTTGTGAAGAAACAGAACCTGGAATTTTACAGATGAGATTTCTGATTCATA	1860
Db	1801	AAGCAATTTTGTGAAGAAACAGAACCTGGAATTTTACAGATGAGATTTCTGATTCATA	1860
QY	1861	GAAAAGCAGATGAGATGTGGTGAATAATGAAATTTGAGCTTCTCTTAGTTGTAGAAA	1920
Db	1861	GAAAAGCAGATGAGATGTGGTGAATAATGAAATTTGAGCTTCTCTTAGTTGTAGAAA	1920
QY	1921	GAAAAAGACATCTTGACATGAAAATATGATCGTTGCGGAGAAATTTGCCATGCTAAGACTG	1980
Db	1921	GAAAAAGACATCTTGACATGAAAATATGATCGTTGCGGAGAAATTTGCCATGCTAAGACTG	1980
QY	1981	GAGCTAGACACATGAAACATTAAGGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTAGACACATGAAACATTAAGGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 5
US-09-685-166A-375

GENERAL INFORMATION:

APPLICANT: Xu, Jingshun

APPLICANT: Dillon, Davin C.

APPLICANT: Hartchem, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel

```

1  APPLICANT:  Mang, Aijun
2  APPLICANT:  Skeiky, Kasir A.W.
3  APPLICANT:  Hepler, William
4  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
5  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
6  FILE REFERENCE:  210121.427C21
7  CURRENT APPLICATION NUMBER:  US/09/685,166A
8  CURRENT FILING DATE:  2000-10-10
9  NUMBER OF SEQ ID NOS:  898
10 SOFTWARE:  FastSeq for Windows Version 3.0
11 SEQ ID NO 375
12 LENGTH:  2040
13 TYPE:  DNA
14 ORGANISM:  Homo sapien
15 US-09-685-166A-375

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Query Match	100.0%;	Score 2040;	DB 3;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	1	ATGGTGGTTGAGTTGATTTCCATGCGGGCTGCGCTTCTGTGGAACAACGATTTGGTCTC	60
Db	1	ATGGTGGTTGAGTTGATTTCCATGCGGGCTGCGCTTCTGTGGAACAACGATTTGGTCTC	60
OY	61	AGAGCAAGATGGGCAAGTGGTCTGCGGTTGCTTCCCTGCTGCAAGGAGAGCGGCAAG	120
Db	61	AGAGCAAGATGGGCAAGTGGGCAAGTGGGCTGCGGTTGCTTCCCTGCTGCAAGGAGAGCGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTTGAGAGCCAGACGACTTGTCTATGAGAACACTCAGAGGCAAG	180
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OY	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG	240
Db	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG	240
OY	241	GGCGCTTCTGAGAACCAAGACGACTTGTCTATGAAACACTCAGAGCAAGATGGGCAAG	300
Db	241	GGCGCTTCTGAGAACCAAGACGACTTGTCTATGAAACACTCAGAGCAAGATGGGCAAG	300
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OY	361	GGAGACTACAGTGCAGTGGCTCTTCAATGAGCCAGAGTACCAAGTCCGTGGAGAAATCTG	420
Db	361	GGAGACTACAGTGCAGTGGCTCTTCAATGAGCCAGAGTACCAAGTCCGTGGAGAAATCTG	420
OY	421	GACAACTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCAAGAAAGATCTCATCTGTATG	480
Db	421	GACAACTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCAAGAAAGATCTCATCTGTATG	480
OY	481	CTCAGGGACACTGACGTGACAGAGAGCAAGCAAAAGAGACTGTCTTACATCTTGGCC	540
Db	481	CTCAGGGACACTGACGTGACAGAGAGCAAGCAAAAGAGACTGTCTTACATCTTGGCC	540
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Db	541	TCTGCGAATGGGAATTGCAAGTGTGTAATATCTCCGTGCTGGAACAGACGATGTCAACTAAT	600
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Db 841 CATGACAAAAACAGCAAGTCGTGAATTTTATATAGAAAAAGCGAATTTAAATGCA 900
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Db 901 CTGGATAGATATGGAAGGACTGCTCATCTGTGTATGTTGTGGATCAGCAATATAT 960
Qy 961 GTGACGCTTCTACTTGTAGCAAAATATTTGATGTATCTTCTCAAGATCTATCTGACAG 1020
Db 961 GTGACGCTTCTACTTGTAGCAAAATATTTGATGTATCTTCTCAAGATCTATCTGACAG 1020
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Db 1321 AATGTGATATATGATTTAATTTCTCAAGAGAGAGAGAACCTGAAATATCAGCAATT 1380
Qy 1381 CCTGACAAAGAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTACAAAGAA 1440
Qy 1441 AAAACAGATGCCAAATATCTTTCTGAAAAACAGCAATCCAGAACAGACTTAAAGCTGAC 1500
Db 1441 AAAACAGATGCCAAATATCTTTCTGAAAAACAGCAATCCAGAACAGACTTAAAGCTGAC 1500
Qy 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATGGCCAGCAGAGAAAGATCT 1560
Qy 1561 CAAGAACCAAGAAATTAATAGATGTGTAGAGAGCTAGAAAAATTTATGTGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATAGATGTGTAGAGAGCTAGAAAAATTTATGTGCTATCGAA 1620
Qy 1621 GAAATGAGAGAGCAGGAAGTACTCATGTGGAATTTCCAGAAAACCTGACTAATGGTGC 1680
Db 1621 GAAATGAGAGAGCAGGAAGTACTCATGTGGAATTTCCAGAAAACCTGACTAATGGTGC 1680
Qy 1681 ACTGCTGGCAATGTGATATGATTTAATTTCTCCAGAGAGAGAGAGCACTGTAAGAC 1740
Db 1681 ACTGCTGGCAATGTGATATGATTTAATTTCTCCAGAGAGAGAGAGCACTGTAAGAC 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTGAAGCAAAATGATATCTGAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTGAAGCAAAATGATATCTGAG 1800
Qy 1801 AAGCAATTTTGTGAAGACAGAACTGTGAATTTACAGATGAAGATTTCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGACAGAACTGTGAATTTACAGATGAAGATTTCTGATTCATGAA 1860
Qy 1861 GAAAGCAGATGAATGTGTAAGAAAAATGAAATTTCTGAGCTTTCTTTAGTTGTAGAAA 1920
Db 1861 GAAAGCAGATGAATGTGTAAGAAAAATGAAATTTCTGAGCTTTCTTTAGTTGTAGAAA 1920

Db 1861 GAAAGCAGATGAAGTGTGTAAGAAAAATGAAATTTCTGAGCTTTCTTTAGTTGTAGAAA 1920
Qy 1921 GAAAAAGACATCTTGTGATGAAAAATGATACGTTGCGGAGAGAAATTCCTAGTGAAGCTG 1980
Db 1921 GAAAAAGACATCTTGTGATGAAAAATGATACGTTGCGGAGAGAAATTCCTAGTGAAGCTG 1980
Qy 1981 GAGCTAGACACAAATGAAACATGAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTAGACACAAATGAAACATGAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040

RESULT 6
US-09-429-755-303
Sequence 303, Application US/09429755A
Patent No. 6656480
GENERAL INFORMATION:
APPLICANT: Prudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda G.
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
NUMBER OF FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTTGATGATGATTCATGCGGCTGCTCTTGTGTAAGAGCCATTTGCTTC 60
Db 1 ATGTGTTGATGATGATTCATGCGGCTGCTCTTGTGTAAGAGCCATTTGCTTC 60
Qy 61 AGAGCAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
Db 61 AGAGCAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
Qy 121 AGCAACGTGGGCACTTGTGAGACCAAGCAAGCTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTGTGAGACCAAGCAAGCTGCTATGAAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGAGCTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGAGCTG 240
Qy 241 GCGGCTTGTGAGACCAAGCAAGCTTGTGTAAGAACTCAGAGAAAGATGGCAAG 300
Db 241 GCGGCTTGTGAGACCAAGCAAGCTTGTGTAAGAACTCAGAGAAAGATGGCAAG 300
Qy 301 TGGTCTGCAATGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Db 301 TGGTCTGCAATGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Qy 361 GGAGACTAGATGACAGTGCCTTCAATGAGAGCCAGATACAGTCCGTGGAAGATCTG 420
Db 361 GGAGACTAGATGACAGTGCCTTCAATGAGAGCCAGATACAGTCCGTGGAAGATCTG 420
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Db 1201 ATGCTCAAGAACAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATGTTGGAATTAATAGAAAACCTGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAGTAAATGTTGGAATTAATAGAAAACCTGATGATGATGATGATGATG 1320
QY 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGAGAGAACTGAAATACGAAATTT 1380
Db 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGAGAGAACTGAAATACGAAATTT 1380
QY 1381 CCTGACAGAGAGAGAGATGATCAGAGATTTGGCAATTTGATTTCTGATCAAGAAA 1440
Db 1381 CCTGACAGAGAGAGAGATGATCAGAGATTTGGCAATTTGATTTCTGATCAAGAAA 1440
QY 1441 AAACAGATGCCAAATATCTCTCTGAAAAACAGCAACCCAGAACTTAAGCTGAGAC 1500
Db 1441 AAACAGATGCCAAATATCTCTCTGAAAAACAGCAACCCAGAACTTAAGCTGAGAC 1500
QY 1501 TCAGAGAGAGAGATCACAAGAGCTTGAAGGAGAGAGAAATGCGCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGAGATCACAAGAGCTTGAAGGAGAGAGAAATGCGCAGCAGAGAAAGATCT 1560
QY 1561 CAAAGAACAGAAATTAATAGATGATGATGAGAGCTGAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAAGAACAGAAATTAATAGATGATGATGAGAGCTGAGAAATTTTATGCTATCGAA 1620

QY 1621 GAAATGAAGAGACAGGAAGTACTCATGTCGATTTCCAGAAAACCTGATATGATGCC 1680
Db 1621 GAAATGAAGAGACAGGAAGTACTCATGTCGATTTCCAGAAAACCTGATATGATGCC 1680
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Db 1681 ACTGCTGGCAATGATGATGATGATTAATCTCTCAAGAGAGAGAGAGAAACCTGAAAC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAGATGAGAGAAACAAATGATCTCAG 1800
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QY 1861 GAAAAGCAGATGAGAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTAGAAA 1920
Db 1861 GAAAAGCAGATGAGAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTAGAAA 1920
QY 1921 GAAAAAGCATTTGATGATGAAAAATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 GAAAAAGCATTTGATGATGAAAAATGATGATGATGATGATGATGATGATGATGATG 1980
QY 1981 GAGCTAGACACAAATGAAATCATGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAA 2040
Db 1981 GAGCTAGACACAAATGAAATCATGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAA 2040

RESULT 7
US-09-679-426-375
Sequence 375, Application US/09679426
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCTTGAAGATGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGATCTC 60
Db 1 ATGCTGCTTGAAGATGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGATCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTCCCTGCTGAGGAGAGCGGCAAG 120
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Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACAAGAGACTGTCTATGAAACACTCAGAGCAAG 180
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Db 121 AGCAACGTGGGCACTTCTGAGACAAGAGACTGTCTATGAAACACTCAGAGCAAG 180
QY 181 ATGGGCAATGTGTGCGGCGCACTGCTTCCTGCTGAGGAGGAGTGGCAAGAGCACTG 240
| | | | |
Db 181 ATGGGCAATGTGTGCGGCGCACTGCTTCCTGCTGAGGAGGAGTGGCAAGAGCACTG 240
QY 241 GGGGCTTCTGAGACAAGAGACTGTCTATGAAACACTCAGAGCAAGATGGGCAAG 300
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Db 241 GGGGCTTCTGAGACAAGAGACTGTCTATGAAACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCTGCTGAGGAGGAGGAGGAGCAAGAGTGGGCGCTTGG 360
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Db 301 TGGTGTGCACTGCTTCCTGCTGAGGAGGAGGAGGAGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGACTAGATGACAGTGTCTATGAGAGCCAGGTAACAAGTCCGTGAGAAATCTG 420
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Db 361 GGAAGACTAGATGACAGTGTCTATGAGAGCCAGGTAACAAGTCCGTGAGAAATCTG 420
QY 421 GACAAGCTCAAGAGCTGCTGAGGAGGAGTAAAGTCCAGAAAGAGTCTACGTCATG 480
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Db 421 GACAAGCTCAAGAGCTGCTGAGGAGGAGTAAAGTCCAGAAAGAGTCTACGTCATG 480
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Db 481 CTCAGGAGCACTGACCTGAGACAAGAGACAAGCAAAAGAGAGCTCTCTACATCTGGCC 540
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Db 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGAGCAGAGATGTCAACTTAAT 600
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Db 721 ACCACTCTGCACTAGCTATCTATTAATGAAGATTAATGAGCAAGAGACTGCTTAA 780
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QY 841 CATGAGCAAAAAACAGAGAGCTGTAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
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Db 841 CATGAGCAAAAAACAGAGAGCTGTAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
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Db 901 CTGAGATGATGATGAAGAGAGCTGCTCATATCTTGTGATGTTGTGATCAGCAATATA 960
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Db 961 GTACAGCTTCTACTTGAAGAAAAATTTGATGTATCTTTCAGAGTCTATCTGAGCAGAG 1020
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Db 1021 GCCAGAGAGATGCTGTTTCTAGTCAATCATGATTAATTTGACAGTTACTTCTGACTAC 1080
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Db 1201 ATGTCTCAAGAAACAGAAATTAATAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
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Db 1441 AAAACAGTCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
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Db 1501 TCAGAGAAAGAGTCAAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGATCT 1560
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Db 1561 CAAGAACAGAAATTAATTAAGATGTGATGAGAGCTGAGAAATTTTATGCTATCGAA 1620
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Db 1921 GAAAAAGAGATGAGATGAGATGAGTGTGCGGAGAGAAATTTGCAATGCAAGACTG 1980
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Db 1981 GAGCTAGACACATGAAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040

RESULT 8
US-09-759-143-375
; Sequence 375, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaser A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGTGGTGAAGTATTCATGCGGCTGCTCTTGTGAAGAAGCATTTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCGGCTTCCCTGCTGCAAGGAGCGCAAG 120
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DB 601 GTCTTGAACAACAAAAGAGAGAGAGTAAAGCGGTAAAGTCCAGAGAGAGTAA 660
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DB 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720

QY 721 ACCACTGCACTAGCTATCTATATGAAGATAATTAAATGGCCAAAGCACTGCTTAA 780
DB 721 ACCACTGCACTAGCTATCTATATGAAGATAATTAAATGGCCAAAGCACTGCTTAA 780
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DB 781 TATGGTGTGATATGGAATCAAAAAACAGATGGCTCACACACTGTTACTTGGTGA 840
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DB 841 CATGAGCAAAAAACAGAGTCTGAAATTTTATCAAGAAAAAAGCGAATTTAAATGA 900
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DB 1081 AAAGAAAAACAGATGCTAAATCTCTGAAAAACAGCAATCCGAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGTCAACAAAGCTTCAAGGCAAGTAAATAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGTCAACAAAGCTTCAAGGCAAGTAAATAGCCAGCAGAGAAA 1200
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DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGGTATAGAGAGTTGAGAAAGAAATGAG 1260
QY 1261 AAGCATGAAAGTAATATGTTGGATTACTAGAAAACTGCACTAATGGTGTCACTGTGGC 1320
DB 1261 AAGCATGAAAGTAATATGTTGGATTACTAGAAAACTGCACTAATGGTGTCACTGTGGC 1320
QY 1321 AATGGTATATGATTAATTTCTCAAGGAAGACAGAACACTGAAATAGCAATTT 1380
DB 1321 AATGGTATATGATTAATTTCTCAAGGAAGACAGAACACTGAAATAGCAATTT 1380
QY 1381 CCTGACAAAGGAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGGAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATTAATCTCTGAAAAACAGCAACCCGAACAAAGCTTAAAGCTGACA 1500
DB 1441 AAACAGATGCAAAATTAATCTCTGAAAAACAGCAACCCGAACAAAGCTTAAAGCTGACA 1500
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DB 1501 TCAGAGGAAGATGACAAAGGCTTGAAGGCAAGTGAATAGGCAAGCAGAGAAAAAGTCT 1560
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DB 1561 CAAAGAACCAAGAAATTAATAGATGGTATAGAGACTAGAAAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAACAGGAAGTACTGATGCGAATTTCCCAAGAAACCTGACTAATGGTGGC 1680
DB 1621 GAAATGAAGAACAGGAAGTACTGATGCGAATTTCCCAAGAAACCTGACTAATGGTGGC 1680
QY 1681 ACTGCTGCAATGATGATGATTAATTTCTCAAGGAAGAGAGAACACTGTAAGC 1740
DB 1681 ACTGCTGCAATGATGATGATTAATTTCTCAAGGAAGAGAGAACACTGTAAGC 1740
QY 1741 CAGCAATTTCTGACATGAGATGAAGATATCAAGTGAAGAACAAATGATATCTCAG 1800
DB 1741 CAGCAATTTCTGACATGAGATGAAGATATCAAGTGAAGAACAAATGATATCTCAG 1800


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Db      1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGACCACTGTAATAATCAGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAAGTTCTGATCAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAAGTTCTGATCAAGAA 1440
Qy      1441 AAACAGATGCCAAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCAATGAAAAATGCGCAAGCAAGAAAGATCT 1560
Db      1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCAATGAAAAATGCGCAAGCAAGAAAGATCT 1560
Qy      1561 CAAGAACCAGAAATTAATAAGATGGTATAGAGACTAGAAATTTTATGCTATCGAA 1620
Db      1561 CAAGAACCAGAAATTAATAAGATGGTATAGAGACTAGAAATTTTATGCTATCGAA 1620
Qy      1621 GAAATGAAAGACGCGAAGTACTCATGTCCGAAATTCGCAAAAACCTGACTATGCTGCC 1680
Db      1621 GAAATGAAAGACGCGAAGTACTCATGTCCGAAATTCGCAAAAACCTGACTATGCTGCC 1680
Qy      1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAAAGCAACCTGAAAC 1740
Db      1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAAAGCAACCTGAAAC 1740
Qy      1741 CAGCAATTTCTCTGACATGAGATGAAGAGTATCAGAGTGAAGCAAAATGATCTGAC 1800
Db      1741 CAGCAATTTCTCTGACATGAGATGAAGAGTATCAGAGTGAAGCAAAATGATCTGAC 1800
Qy      1801 AAGCAATTTTGTGAAGAACGAACTGTGAATTTACAGATGAGATTTGATTCATGAA 1860
Db      1801 AAGCAATTTTGTGAAGAACGAACTGTGAATTTACAGATGAGATTTGATTCATGAA 1860
Qy      1861 GAAACACATAGAAAGTGTGAAAAAATGAATTTCTGAGCTTTCTTGTGTAAAGAA 1920
Db      1861 GAAACACATAGAAAGTGTGAAAAAATGAATTTCTGAGCTTTCTTGTGTAAAGAA 1920
Qy      1921 GAAAAAGACATCTGTGATGAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGCTG 1980
Db      1921 GAAAAAGACATCTGTGATGAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGCTG 1980
Qy      1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2040
Db      1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2040

RESULT 10
US-09-699-295-303
/ Sequence 303, Application US/09699295
/ Patent No. 6828431
/ GENERAL INFORMATION:
/ APPLICANT: Prudakie, Tony N.
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Smith, John M.
/ APPLICANT: Misner, Linda E.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ FILE REFERENCE: 210121.419C10
/ CURRENT APPLICATION NUMBER: US/09/699,295
/ NUMBER OF SEQ ID NOS: 326
/ SOFTWARE: FaSTSeq for Windows Version 3.0
/ SEQ ID NO 303
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-699-295-303
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Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGTGTGTTAGAGTTGATTCATGCGCGCTGCTCTTGTGTAAGAAAGCAATTTGCTTC 60
Db      1 ATGTGTGTTAGAGTTGATTCATGCGCGCTGCTCTTGTGTAAGAAAGCAATTTGCTTC 60
Qy      61 AGAGACAGATGGGCAATGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
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Qy      121 AGCAACGTGGGCACTTCTGAGAACCAAGCACTGTGCTATGAAGCACTCAGAGCAAG 180
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Db      661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy      721 ACCACTCTGACCTACGCTATCTATATAGAAATTAATTAAGGCAAGCACTGCTCTTA 780
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Qy      781 TATGTGTGATGATGAAATCAAAAGCAAGCATGCTTCAACCACTGTACTTGTGTGTA 840
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Db      841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGCAATTTAAATGCA 900
Qy      901 CTGATATGATGAGAGAGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db      901 CTGATATGATGAGAGAGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy      961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db      961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
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QY 1021 GCCAGAGATGCTGTTCTAGTCATCATGTAATTTGCCAGTACTTTCTGATAC 1080
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| | | | |
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| | | | |
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGGCTGTAATAATAGCCAGAGAAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATTAAGATGTAATGAGAGGTTGAAGAAATGAG 1260
| | | | |
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGTAATGAGAGGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGAATTAAGAAAACCTGACTAATGCTGCTGCG 1320
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Db 1261 AAGCATGAAAGTAAATATGTTGGAATTAAGAAAACCTGACTAATGCTGCTGCG 1320
QY 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
| | | | |
Db 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
QY 1381 CCTGACACAGAAAGTGAAGATCAAGAAATTTGGAATTTAGTTCTGACTCAAGAA 1440
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Db 1381 CCTGACACAGAAAGTGAAGATCAAGAAATTTGGAATTTAGTTCTGACTCAAGAA 1440
QY 1441 AAAAGATGCAAAATCTCTTGAAAACGCAACCCAGAACAGATTAAAGCTGACA 1500
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Db 1441 AAAAGATGCAAAATCTCTTGAAAACGCAACCCAGAACAGATTAAAGCTGACA 1500
QY 1501 TCGAGAGAGATGCAAAAGGCTTGAGGGCAAGTGAATAATGCGCAAGCAAGAAAGATCT 1560
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Db 1501 TCGAGAGAGATGCAAAAGGCTTGAGGGCAAGTGAATAATGCGCAAGCAAGAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATTAAGATGTAATGAGAGCTAGAAATTTAAGGCTATCGAA 1620
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Db 1561 CAAGAACAGAAATTAATTAAGATGTAATGAGAGCTAGAAATTTAAGGCTATCGAA 1620
QY 1621 GAAATGAAAGAGCAGGAAGTCAATGTCGATTTCCCAAGAAAACCTGAAATGTCG 1680
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QY 1681 ACTGCTGGCAATGTAATGTAATTAATCTTCCAGAAAGAGCAGAACCTGAAAGC 1740
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Db 1681 ACTGCTGGCAATGTAATGTAATTAATCTTCCAGAAAGAGCAGAACCTGAAAGC 1740
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QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
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Db 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAGTGTGAAAAAATGAATTTCTGAGCTTTCTCTTACTGTAAGAAA 1920
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Db 1861 GAAAGCAGATAGAGTGTGAAAAAATGAATTTCTGAGCTTTCTCTTACTGTAAGAAA 1920
QY 1921 GAAAAAGATCTTTGCAATGAAAAATGTAATTTGCGGGAAGAAATTTGCAATGTAAGCTG 1980
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Db 1921 GAAAAAGATCTTTGCAATGAAAAATGTAATTTGCGGGAAGAAATTTGCAATGTAAGCTG 1980
QY 1981 GAGCTAGACACATGAAACATCAAGAGCAGCTTAAAAAATAAAAAATAAAAAATAAAAA 2040
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Db 1981 GAGCTAGACACATGAAACATCAAGAGCAGCTTAAAAAATAAAAAATAAAAAATAAAAA 2040

RESULT 11
US-09-534-825A-303
; Sequence 303, Application US/09534825A
; Patent No. 6861506

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C7
CURRENT APPLICATION NUMBER: US/09/534,825A
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 317
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-534-825A-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACGATTTGCTTC 60
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Db 1 ATGCTGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACGATTTGCTTC 60
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| | | | |
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 AGCAAGTGGGCACTTTCTGAGACAGACGACTGCTGTAATGAAGACCTCAGAGCAAG 180
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Db 121 AGCAAGTGGGCACTTTCTGAGACAGACGACTGCTGTAATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCCGCACTGCTTCCCTGCTGAGAGGGGAGTGGCAAGAACCTG 240
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QY 301 TGGTGTGCACTGCTTCCCTGCTGAGAGGGGAGGCGGCAAGAGTGGGCGCTTGG 360
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Db 301 TGGTGTGCACTGCTTCCCTGCTGAGAGGGGAGGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGATTAAGATGACAGTGTCTTCAATGAGCCAGGTACAGTCCGTGAGAAAGATCTG 420
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| | | | |
Db 661 TGTGCTTAATGTTGTGTAAGATGCACTGATCCAAATTAATTCAGATGATGAAAT 720
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Db      721  ACCACTCTGCAGTACCTATCTATATGAAGATTAATGAGCAAGACAGCTGCTTAA 780
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Db      781  TATGTCGTGATATGCAATCAAAAACAGATGCGCTCACACACTGTTACTTGGTGA 840
Qy      841  CATGACCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAATGCA 900
Db      841  CATGACCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAATGCA 900
Qy      901  CTGGATAGATATGAAGAGACTGCTCATATCTTCTCAAGATCTATCTGACAGAG 960
Db      901  CTGGATAGATATGAAGAGACTGCTCATATCTTCTCAAGATCTATCTGACAGAG 960
Qy      961  GTCAGGCTTCTATCTGAGCAAAATATGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
Db      961  GTCAGGCTTCTATCTGAGCAAAATATGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
Qy      1021  GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db      1021  GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy      1081  AAGAAAAACAGATGCTAAAAATCTCTTCAAAAACAGCAATCCAGAACAGATTAAAG 1140
Db      1081  AAGAAAAACAGATGCTAAAAATCTCTTCAAAAACAGCAATCCAGAACAGATTAAAG 1140
Qy      1141  CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1200
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Db      1201  ATGTCTCAAGAACAGAAATTAATTAAGATGATGATAGAGAGTTGAAGAAATGAAG 1260
Qy      1261  AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db      1261  AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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Db      1321  AATGTGATTAATGATTAATTTCTCTCAAGAAAGAGAGAAACCTTAATTCAGCAATTT 1380
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Db      1501  TCGAGAGAAAGTCAAAAAGCTTGAAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560
Qy      1561  CAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATG 1620
Db      1561  CAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy      1621  GAAATGAAGAGACGGAAGTACTGATGATGATGATGATGATGATGATGATGATGATG 1680
Db      1621  GAAATGAAGAGACGGAAGTACTGATGATGATGATGATGATGATGATGATGATGATG 1680
Qy      1681  ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db      1681  ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Qy      1741  CAGCAATTTCTGACATGAGATGAAGATGATGATGATGATGATGATGATGATGATG 1800
Db      1741  CAGCAATTTCTGACATGAGATGAAGATGATGATGATGATGATGATGATGATGATG 1800
Qy      1801  AAGCAATTTTGTGAAGACAGAACTGGAATTAATTAAGATGATGATGATGATGATG 1860

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Db      1861  GAAAAAGCATGATGAAGTGTGTAATAATTAATTAATTAATTAATTAATTAATTAAT 1920
Qy      1921  GAAAAAGCATGATGATGAAGTGTGTAATAATTAATTAATTAATTAATTAATTAAT 1980
Db      1921  GAAAAAGCATGATGATGAAGTGTGTAATAATTAATTAATTAATTAATTAATTAAT 1980
Qy      1981  GAGCTAGACACATGAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2040
Db      1981  GAGCTAGACACATGAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2040

RESULT 12
US-09-657-279-375
; Sequence 375, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
Db      1  ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
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Db      61  AGGAGCAAGATGAGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy      121  AGCAACGTGGGCACTTCTGAGACACAGCACTGCTGATGAAGACATCAGAGCAAG 180
Db      121  AGCAACGTGGGCACTTCTGAGACACAGCACTGCTGATGAAGACATCAGAGCAAG 180
Qy      181  ATGGGCAAGTGTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db      181  ATGGGCAAGTGTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy      241  GGCCTTCTGAGACACAGCACTGCTGATGAAGACATCAGAGAAAGATGAGCAAG 300
Db      241  GGCCTTCTGAGACACAGCACTGCTGATGAAGACATCAGAGAAAGATGAGCAAG 300

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/ APPLICANT: Meagher, Madeleine Joy
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C27
/ CURRENT APPLICATION NUMBER: US/10/012.896
/ NUMBER OF SEQ ID NOS: 1011
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-012-896-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAAGCCATTGTGCTC 60

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DB 61 AGAAGCAAAATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120

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DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGCTATGAAACACTCAGAGCAAG 180

QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAACGTG 240

QY 241 GGGGCTTCTGAGACACACAGACACTCTGCTATGAAACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGACACACAGACACTCTGCTATGAAACACTCAGAGCAAGTGGCAAG 300

QY 301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAAGTGGGCGCTTGG 360

QY 361 GGAAGTACGATGACAGTGTCTTCAATGAGCCCAAGTACCACTGCTGAGAGAGATCTG 420
DB 361 GGAAGTACGATGACAGTGTCTTCAATGAGCCCAAGTACCACTGCTGAGAGAGATCTG 420

QY 421 GAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

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DB 481 CTCAGGGAACACTGACGTGAAACAAGAGAGACAAAGAGAGAGCTGCTTACATCTGGCC 540

QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAAACTCTGCTGAGACAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGTAATAAACTCTGCTGAGACAGATGTCAACTTAAT 600

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DB 601 GTCTTGAACAACAAAAAGAGAGACAGCTCTGATTAAGCCGTACAAATGCCAGGAAGTGA 660

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DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATTTCTCAGATGATGGAAT 720

QY 721 ACCACTCTGCACTACGTATCTATTAATGAGATTAATTAATGAGCAAGCACTGCTCTTA 780
DB 721 ACCACTCTGCACTACGTATCTATTAATGAGATTAATTAATGAGCAAGCACTGCTCTTA 780

QY 781 TATGTGTCTGATATCGAATTAACAAAAACAGACAGCTCTCAGACACTGTTACTTGTGTA 840
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DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGGATGATGATGAGAGGTTGAAGAAATGAAG 1260

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QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGACAGAACCTGAAATATGAGCAATTT 1380
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DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440

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DB 1441 AAAAGATGCCAAAAATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA 1500

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DB 1681 ACTGCTGGCAATGTGTATGATTAATTTCTTCCAAAGGAAGAGCAAGCACTGAAAGAC 1740

QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATGATCAAGTGAAGAACAAATGATCTGAG 1800
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DB 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAGATTTCTGATTAAGAA 1860

QY 1861 GAAAGACGATGAAAGTGTGTAATAAATGAAATTTCTGAGCTTTCTTATGTTGTAAGAAA 1920
DB 1861 GAAAGACGATGAAAGTGTGTAATAAATGAAATTTCTGAGCTTTCTTATGTTGTAAGAAA 1920
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Oy	1	ATGGTGGTTGAGTTGATTTCCATGCGCGGCTGCTCTTCTGTGAGAAACCATTTGGTCTC	60
Db	1	ATGGTGGTTGAGTTGATTTCCATGCGCGGCTGCTCTTCTGTGAGAAACCATTTGGTCTC	60
Oy	61	AGGAGCAAGATGGGCAAGTGTGTGCTGCGGTTGCTTCCCCTGCTGCAAGGAGAGCGCGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGTGTGCTGCGGTTGCTTCCCCTGCTGCAAGGAGAGCGCGCAAG	120
Oy	121	AGCAACGTGGGCACTTTCGTGAGACCAAGACGACTGTGTATGAAAGACCTGAGAGGCAAG	180
Db	121	AGCAACGTGGGCACTTTCGTGAGACCAAGACGACTGTGTATGAAAGACCTGAGAGGCAAG	180
Oy	181	ATGGGCAAGTGTGTGCGGCACTGCTTCCCCTGTGTCAGGGGAGAGTGGCAAGACGACGTG	240
Db	181	ATGGGCAAGTGTGTGCGGCACTGCTTCCCCTGTGTCAGGGGAGAGTGGCAAGACGACGTG	240
Oy	241	GGCGCTTCTGAGACACGACGACTGTCTATGAAACACTCAGGAAACAAGATGGGCAAG	300
Db	241	GGCGCTTCTGAGACACGACGACTGTCTATGAAACACTCAGGAAACAAGATGGGCAAG	300
Oy	301	TGGTGTCTGCCACTGCTTCCCCTGTGTGACGAGGGGAGCGGCAAGACGAGTGGGCGCTTGG	360
Db	301	TGGTGTCTGCCACTGCTTCCCCTGTGTGACGAGGGGAGCGGCAAGACGAGTGGGCGCTTGG	360
Oy	361	GGAGCTACGATGACGTGCGCTTCACTGAGGCCAGGATACACGTCCTGGAGAAAGATCTG	420
Db	361	GGAGCTACGATGACGTGCGCTTCACTGAGGCCAGGATACACGTCCTGGAGAAAGATCTG	420
Oy	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCCAGAAAGATCTCATCGTCAAG	480
Db	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCCAGAAAGATCTCATCGTCAAG	480

QY	481	CTCAGGGACATCGACGTGTAACAAGAGGACAGCAAAAAGAGACATCGCTCTACATCTGGCC	540
Db	481	CTCAGGGACATCGACGTGTAACAAGAGGACAGCAAAAAGAGACATCGCTCTACATCTGGCC	540
QY	541	TCCTGCCAATGGGAATTCAGAAGTAGTAAATCTCTGCTGAGCAGACGATGTCAACTTAT	600
Db	541	TCCTGCCAATGGGAATTCAGAAGTAGTAAATCTCTGCTGAGCAGACGATGTCAACTTAT	600
QY	601	GTCCTTGACAACAAAAAGAGCAGCTCTGATTAAGGCCGTACATGCCAGAGATGTA	660
Db	601	GTCCTTGACAACAAAAAGAGCAGCTCTGATTAAGGCCGTACATGCCAGAGATGTA	660
QY	661	TGTGGCTTAATGTTGCTGTGAACATGGCACGTATCCAAATATTTCCAGATGATGTAAT	720
Db	661	TGTGGCTTAATGTTGCTGTGAACATGGCACGTATCCAAATATTTCCAGATGATGTAAT	720
QY	721	ACCACTCTGCATCAGCTATCTAATATGAGATAAATTAATGCCCAAGCCTGCTCTTA	780
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QY	781	TATGCTGTGATATTCGAATCAAAAAACAGCATGGCCCTCACACCACTGTACTTGTGT	840
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QY	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGGACTGCTCTCATCTTCTGTATGTTGTGATCAGCAGATTA	960
Db	901	CTGATATGATATGGAAGGACTGCTCTCATCTTCTGTATGTTGTGATCAGCAGATTA	960
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Db	961	GTCAGCCTTCTACCTTGAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGACG	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTTCGACTAC	1080
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Db	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGCTTAAAG	1140
QY	1141	CTGACATCAGAGGAAGGTCACAAAAGTTCAAAAGCATGAAATTAAGCAGCCAGAGAAA	1200
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QY	1201	ATGTCCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAGAAATGAG	1260
Db	1201	ATGTCCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAGAAATGAG	1260
QY	1261	AAGCATGAATTAATATGTTGGGATTAATCTGAAAAACCTGATTAATGTTGTCTACCTGGC	1320
Db	1261	AAGCATGAATTAATATGTTGGGATTAATCTGAAAAACCTGATTAATGTTGTCTACCTGGC	1320
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Db	1321	AATGGTGTAATATGATTAATCTCTCAAGGAAGAGCAGAACACTGGAATAATCACCAATTT	1380
QY	1381	CCTGACAAAGAAAGTGAAGAGTATCACGAATTTGGCAATTAAGTTTCTGACTAACAAAGAA	1440
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QY	1501	TCAGAGGAAGTCACAAAAGCTTGTAGGGCATGTAATAATGGCCAGCCAGAGAAAAAGATCT	1560
Db	1501	TCAGAGGAAGTCACAAAAGCTTGTAGGGCATGTAATAATGGCCAGCCAGAGAAAAAGATCT	1560

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DB 1548 -----AGAGTAGAAAAATTTATGCTATCGAA 1575
QY 1621 GAAATGAGAGACGAGAGTACTCATGTCGATTTCCAGAAAACTGACTAATGCTGCC 1680
DB 1576 GAAATGAGAGACGAGAGTACTCATGTCGATTTCCAGAAAACTGACTAATGCTGCC 1635
QY 1681 ACTGCTGAGCAATGATGATGATTAATTCCTCCAGAGAGAGAGACACTGAAAGC 1740
DB 1636 ACTGCTGAGCAATGATGATGATTAATTCCTCCAGAGAGAGAGACACTGAAAGC 1695
QY 1741 CAGCAATTTCTCTGACACTGAGAAATGAAAGTATCAGAGTCCAGAAAAATGATCTCAG 1800
DB 1696 CAGCAATTTCTCTGACACTGAGAAATGAAAGTATCAGAGTCCAGAAAAATGATCTCAG 1755
QY 1801 AAGCAATTTTGTGAGAGACGAAACCTGGAATTTACAGATGAGATTTGATTCATGAA 1860
DB 1756 AAGCAATTTTGTGAGAGACGAAACCTGGAATTTACAGATGAGATTTGATTCATGAA 1815
QY 1861 GAAAGAGATAGAGTGTGTAAGAAAAATGAATTTCTGAGCTTCTCTTGGTTGTAAGAA 1920
DB 1816 GAAAGAGATAGAGTGTGTAAGAAAAATGAATTTCTGAGCTTCTCTTGGTTGTAAGAA 1875
QY 1921 GAAAAAGACATCTTGACATGAAAAATGATGCTGCGGAGAAATGCTCATGTAAGACTG 1980
DB 1876 GAAAAAGACATCTTGACATGAAAAATGATGCTGCGGAGAAATGCTCATGTAAGACTG 1935
QY 1981 GAGCTGACACATGAAACATCAGAGCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
DB 1936 GAGCTGACACATGAAACATCAGAGCAGCTTAAAAAATTTAAAAAATTTAAAAA 1995

RESULT 15

US-09-352-616A-374
/ Sequence 374, Application US/09352616A
/ Patent No. 6395278
/ GENERAL INFORMATION:
/ APPLICANT: Dillion, Davin C.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Jiang, Yugu
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
/ FILE REFERENCE: 210121.427C8
/ CURRENT APPLICATION NUMBER: US/09/352.616A
/ NUMBER OF SEQ ID NOS: 472
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-352-616A-374

Query Match 95.1%; Score 1940; DB 3; Length 2000;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

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DB 61 AGAGAGCAAGTGGCAAGTGTGCTGCTGTTCTTCCCTGCTGCAAGGAGAGCGCAAG 120
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DB 121 AGGACGTGGGCACTTCTGAGACACAGACACTGCTATGAAAGACACTCAGAGCAAG 180
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DB 241 GGGCGCTTCTGAGACCAAGACACTCTGCTATGAAAGACACTCAGGAAACAATGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGAGCGCAAGAGGATGGGCGCTTGG 360
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QY 361 GGAAGCTACAGATGACAGTCTTCAATGAGCCAGGTAACAGTCCGTGGAAGATCTG 420
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Db 1321 AATGGTAAATAGATTAATTTCTCAAGAGAGAGACACCTGAAATCGCAATTT 1380
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QY 1561 CAAGAACCAAGAAATAATAGATGGTGAATAGAGCTAGAAAAATTTATGGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATAATAGATGGTGAATAGAGCTAGAAAAATTTATGGCTATCGAA 1620
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QY 1681 ACTGCTGCGAATGTGTATGATGATTAATTTCTCCAGAGAGAGCAAAACCTGGAAGC 1740
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OM nucleic - nucleic search, using sw model

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Perfect score: 2040

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Scoring table: IDENTITY_NUC
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Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	2040	100.0	2040	US-09-780-669-375	Sequence 375, App
4	2040	100.0	2040	US-09-810-936-303	Sequence 303, App
5	2040	100.0	2040	US-09-822-827-375	Sequence 375, App
6	2040	100.0	2040	US-09-429-755-303	Sequence 303, App
7	2040	100.0	2040	US-09-924-400-303	Sequence 303, App
8	2040	100.0	2040	US-09-895-793-375	Sequence 375, App
9	2040	100.0	2040	US-09-895-814-375	Sequence 375, App
10	2040	100.0	2040	US-10-012-896-375	Sequence 375, App
11	2040	100.0	2040	US-10-010-940-375	Sequence 375, App
12	2040	100.0	2040	US-10-212-678A-375	Sequence 375, App
13	2040	100.0	2040	US-10-144-678A-375	Sequence 375, App
14	2040	100.0	2040	US-10-033-527-7	Sequence 7, App11
15	2040	100.0	2040	US-10-294-025-375	Sequence 375, App
16	2040	100.0	2040	US-10-079-137B-303	Sequence 303, App
17	1940	95.1	2000	US-09-825-301-6	Sequence 6, App11
18	1940	95.1	2000	US-09-759-143-374	Sequence 374, App
19	1940	95.1	2000	US-09-780-669-374	Sequence 374, App
20	1940	95.1	2000	US-09-810-936-302	Sequence 302, App
21	1940	95.1	2000	US-09-822-827-374	Sequence 374, App
22	1940	95.1	2000	US-09-429-755-302	Sequence 302, App
23	1940	95.1	2000	US-09-924-400-302	Sequence 302, App

24	1940	95.1	2000	3	US-09-895-793-374	Sequence 374, App
25	1940	95.1	2000	3	US-09-895-814-374	Sequence 374, App
26	1940	95.1	2000	5	US-10-012-896-374	Sequence 374, App
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29	1940	95.1	2000	6	US-10-144-678A-374	Sequence 374, App
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34	1147.6	56.3	1853	3	US-09-759-143-369	Sequence 369, App
35	1147.6	56.3	1853	3	US-09-780-669-369	Sequence 369, App
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37	1147.6	56.3	1853	3	US-09-822-827-369	Sequence 369, App
38	1147.6	56.3	1853	3	US-09-429-755-295	Sequence 295, App
39	1147.6	56.3	1853	3	US-09-924-400-295	Sequence 295, App
40	1147.6	56.3	1853	3	US-09-895-793-369	Sequence 369, App
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42	1147.6	56.3	1853	5	US-10-012-896-369	Sequence 369, App
43	1147.6	56.3	1853	5	US-10-010-940-369	Sequence 369, App
44	1147.6	56.3	1853	6	US-10-212-679-295	Sequence 295, App
45	1147.6	56.3	1853	6	US-10-144-678A-369	Sequence 369, App

ALIGNMENTS

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US-09-825-301-7
; Sequence 7, Application US/09825301
; Patent No. US20020009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesch, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS OF REAGENTS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-7

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGGTGTGAGCTTGAATTCATGCGGCTGCTTCTGTGAAGAGCAATTGGTTC 60

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QY      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAGAGGAGTGGCAAGCAAGCTG 240
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RESULT 2
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Sequence 375, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTATTCATGCGGCTCTTCTGTGAAGAGCATTTGGTCTC 60
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RESULT 3
US-09-780-669-375
Sequence 375, Application US/09780669
Patent No. US2002005197A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTTTCCATGCGCGCTGCTCTTCTGTGAAGACCATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTTTCCATGCGCGCTGCTCTTCTGTGAAGACCATTTGGTCTC 60

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RESULT 4
US-09-810-936-303
Sequence 303, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda B.
APPLICANT: Dillon, Davin C.
APPLICANT: Rietter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT FILING DATE: US/09/810,936
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTGAAGTATTCATGCGCGCTCTCTTGTGGAAGAGCCATTTGCTTC 60
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RESULT 5
US-09-822-827-375
; Sequence 375, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
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; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-375
Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGAAAGCATTTGGTCTC 60
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Qy 301 TGTGTCTGCACTGTCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
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Qy 361 GGAAGACTAGATGACAGTGTCTTCAATGAGAGCCAGTACAGTCCGTGTGAAGATCTG 420
Db 361 GGAAGACTAGATGACAGTGTCTTCAATGAGAGCCAGTACAGTCCGTGTGAAGATCTG 420
Qy 421 GACAAAGCTCACAAGAGCTGCGGTGTGGGTTAAAGTCCCGAAGAAAGATCTACGATG 480
Db 421 GACAAAGCTCACAAGAGCTGCGGTGTGGGTTAAAGTCCCGAAGAAAGATCTACGATG 480
Qy 481 CTCAAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
Db 481 CTCAAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGTGAGACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGTGAGACAGAGATGCACTTAAT 600
Qy 601 GTCTTGAACAACAAAAGAGAGCAGCTGTGATTAAGGCGGTACAATGCGCAGAGATGAA 660
Db 601 GTCTTGAACAACAAAAGAGAGCAGCTGTGATTAAGGCGGTACAATGCGCAGAGATGAA 660
Qy 661 TGTGCTTAATGTGTCTGAGACATGCACTGATCCAAATATTCAGATGAGTATGAAAT 720
Db 661 TGTGCTTAATGTGTCTGAGACATGCACTGATCCAAATATTCAGATGAGTATGAAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAGATTAATTAATGCGCAAGACATGCTCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAGATTAATTAATGCGCAAGACATGCTCTTA 780
Qy 781 TATGTGTGATATGAAATCAAAAAACAAGATGAGCTTCAACCACTGTTACTGGTGTGA 840
Db 781 TATGTGTGATATGAAATCAAAAAACAAGATGAGCTTCAACCACTGTTACTGGTGTGA 840
Qy 841 CATGACAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGACAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATATGATATGAGAGAGCTCTCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
Db 901 CTGATATGATATGAGAGAGCTCTCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
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QY 961 GTGAGCTTCTACTTGAGCAAAATATGATCTTCTCAAGATCTATCGAGACAG 1020
DB 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGTGTCTAAAATCTCTTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
DB 1081 AAAAGAAAACAGTGTCTAAAATCTCTTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATAGCCAGCCAGAGATA 1200
DB 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATAGCCAGCCAGAGATA 1200
QY 1201 ATGTCTCAAGAACAGAAAATAAATAGATGTGATAGAGAGTTAGAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAAATAAATAGATGTGATAGAGAGTTAGAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTATATGTGGGATTAAGAAAACCTGACTATGTGTCACTGCTGCG 1320
DB 1261 AAGCATGAAAGTATATGTGGGATTAAGAAAACCTGACTATGTGTCACTGCTGCG 1320
QY 1321 AATGTGATATATGATTAATCTCTCAAGGAGAGAGAACCTGAAAATCGCAATTT 1380
DB 1321 AATGTGATATATGATTAATCTCTCAAGGAGAGAGAACCTGAAAATCGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATGATCAGAAATTTGGAATTTGATCTGACCTCAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATGATCAGAAATTTGGAATTTGATCTGACCTCAAGAA 1440
QY 1441 AAAAGATGCCAAATATCTCTTCTGAAAACAGCAATCCAGAACAGCTTAAGCTGAC 1500
DB 1441 AAAAGATGCCAAATATCTCTTCTGAAAACAGCAATCCAGAACAGCTTAAGCTGAC 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGTGAAGAAATGGCCAGGAGAGAAATGCT 1560
DB 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGTGAAGAAATGGCCAGGAGAGAAATGCT 1560
QY 1561 CAAGAACAGAAATATATAGATGTGATAGAGCTGAGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACAGAAATATATAGATGTGATAGAGCTGAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAGAGAGACGGAAGTACTATGTGGAATCTCCAGAAAACCTGATATGTGCTC 1680
DB 1621 GAAATGAGAGAGACGGAAGTACTATGTGGAATCTCCAGAAAACCTGATATGTGCTC 1680
QY 1681 ACTGCTGGAATGTGATATGATTAATTTCTCCAGAGAGAGAGCACTGTAAGC 1740
DB 1681 ACTGCTGGAATGTGATATGATTAATTTCTCCAGAGAGAGAGCACTGTAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAGAGTATCAAGTGAAGCAAAATGATCTGAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAGAGTATCAAGTGAAGCAAAATGATCTGAG 1800
QY 1801 AAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGAGATTTGATTCATGA 1860
DB 1801 AAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGAGATTTGATTCATGA 1860
QY 1861 GAAAGCAATGAGATGTGTTGAAAAATGAAATTCGAGCTTCTCTGTGTGAAGAA 1920
DB 1861 GAAAGCAATGAGATGTGTTGAAAAATGAAATTCGAGCTTCTCTGTGTGAAGAA 1920
QY 1921 GAAAAAGATCTGATGAAAAATAGATGTTGCGGAGAAATTTGCCATGCTAAGCTG 1980
DB 1921 GAAAAAGATCTGATGAAAAATAGATGTTGCGGAGAAATTTGCCATGCTAAGCTG 1980
QY 1981 GAGCTGAGACAAATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
DB 1981 GAGCTGAGACAAATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 6
US-09-429-755-303
Sequence 303, Application US/09429755A
Patent No. US20020111467A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-303
Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGATGATTCATGTCGAGCTGCTCTTCTGTGAAGAACATTTGGTCTC 60
DB 1 ATGTGTGTTGAGATGATTCATGTCGAGCTGCTCTTCTGTGAAGAACATTTGGTCTC 60
QY 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 ACCAATGTTGAGCACTTCTGAGAACCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
DB 121 ACCAATGTTGAGCACTTCTGAGAACCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGTCGAGCACTGCTTCCCTCTCTCAAGGAGAGTGGCAAGCAAGT 240
DB 181 ATGGCAAGTGTGTCGAGCACTGCTTCCCTCTCTCAAGGAGAGTGGCAAGCAAGT 240
QY 241 GGCCTTCTGAGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GGCCTTCTGAGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGTGCTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAGGAGTGGCGCTTGG 360
DB 301 TGTGCTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAGGAGTGGCGCTTGG 360
QY 361 GGAAGCTAGAGACAGTGCCTTCAATGAGAGCCAGGTACAGGTGCGTGAAGATCTG 420
DB 361 GGAAGCTAGAGACAGTGCCTTCAATGAGAGCCAGGTACAGGTGCGTGAAGATCTG 420
QY 421 GACAAAGCTCAGAGAGTGCCTTCAATGAGAGCCAGGTACAGGTGCGTGAAGATCTG 480
DB 421 GACAAAGCTCAGAGAGTGCCTTCAATGAGAGCCAGGTACAGGTGCGTGAAGATCTG 480
QY 481 CTCAGAGACACTGAGCTGAAACAAGAGCAAGCAAGAGAGATCTTCACTTGGCC 540
DB 481 CTCAGAGACACTGAGCTGAAACAAGAGCAAGCAAGAGAGATCTTCACTTGGCC 540
QY 541 TGTGCAATGGGAATTCGAAGTATGAATCCCTGCTGAGAGAGAGTCACTTAAT 600
DB 541 TGTGCAATGGGAATTCGAAGTATGAATCCCTGCTGAGAGAGAGTCACTTAAT 600
QY 601 GTCTTGAACAACAAAGAGAGCAAGCTGTATGAAGCGCTTCAATGCGAGAGATGA 660
DB 601 GTCTTGAACAACAAAGAGAGCAAGCTGTATGAAGCGCTTCAATGCGAGAGATGA 660
QY 661 TGTGCTTATGTGTGCTGGAACATGGCACTGATCCAAATATTTCCAGATGATGAAT 720

Db	661	TTGGGTTTAAATGTTCTCTGGAACTGGCACTGATCCAAATATTTCCAGATGAGTATGGAAT	720
QY	721	ACCACCTTGCACCTAGCCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTTGCACTAGCCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA	780
QY	781	TATGGTGGTGAATATGGAATCAAAAAACAAGCTGGCTTCAACCACTGTTACTGGTGA	840
Db	781	TATGGTGGTGAATATGGAATCAAAAAACAAGCTGGCTTCAACCACTGTTACTGGTGA	840
QY	841	CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
QY	901	CTGGATTAATATGGAAGCACTGCTCTACTACTGCTGATGTTGGATTCAGCAAGTATA	960
Db	901	CTGGATTAATATGGAAGCACTGCTCTACTACTGCTGATGTTGGATTCAGCAAGTATA	960
QY	961	GTCAGCCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG	1020
QY	1021	GCCAGAGATATGCTGTTCTAAGCATATCATATTTGGCCAGTTACTTTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTCTAAGCATATCATATTTGGCCAGTTACTTTGACATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCGAAACAAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCGAAACAAGACTTAAAG	1140
QY	1141	CTGACATCAAGAGAAAGCTCACAAAGGTTCAAAGGCACTGAAATATGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAAGAGAGCTCACAAAGGTTCAAAGGCACTGAAATATGCCAGCCAGAGAA	1200
QY	1201	ATGCTCAAGAAACCAAAATTAATTAAGATGGTGAATAAGAGCTTGAAGAAATATGAG	1260
Db	1201	ATGCTCAAGAAACCAAAATTAATTAAGATGGTGAATAAGAGCTTGAAGAAATATGAG	1260
QY	1261	AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACTGCTAATGGTGCACCTGGTGC	1320
Db	1261	AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACTGCTAATGGTGCACCTGGTGC	1320
QY	1321	AATGGTGAATATGATTAATTTCTTCAAGAAAGACAGACAACCTGAAATCAGCAATTT	1380
Db	1321	AATGGTGAATATGATTAATTTCTTCAAGAAAGACAGACAACCTGAAATCAGCAATTT	1380
QY	1381	CCTGACAAACGAAAGTGAAGATATCAAGAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAAGTGAAGATATCAAGAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440
QY	1441	AAAAGATGSCCAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGGTGCA	1500
Db	1441	AAAAGATGSCCAAATATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGGTGCA	1500
QY	1501	TCAGAGGAAGTCACAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
Db	1501	TCAGAGGAAGTCACAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
QY	1561	CAGAAACCAAGAAATTAATTAAGATGGTGAATAGAGCTTAGAAAAATTTTATGGCTATGCAA	1620
Db	1561	CAGAAACCAAGAAATTAATTAAGATGGTGAATAGAGCTTAGAAAAATTTTATGGCTATGCAA	1620
QY	1621	GAAATGAAGAAACAGGAAGTCTCATGTCGGAATCCAGAAAACTGATCTAATGGTGC	1680
Db	1621	GAAATGAAGAAACAGGAAGTCTCATGTCGGAATCCAGAAAACTGATCTAATGGTGC	1680
QY	1681	ACTGCTGGCAATGATGATGATGATTAATTTCTTCCAGAGAAAGAGCAACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGATGATGATGATTAATTTCTTCCAGAGAAAGAGCAACCTGAAAGC	1740
QY	1741	CAGCAATTTCTGACACTGAGATGAAGATATCAAGTGAAGAACCAATATGATCTCAG	1800

Db	1741	CAGCAATTTCTCTGACACTGAGAAATGAAAGATATCACAGTACGCAACAAATATGATCTCAG	1800
Qy	1801	AAGCAATTTTGTGGAAGAACAGAACTCGAATATTAACAGATGAGATTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGGAAGAACAGAACTCGAATATTAACAGATGAGATTCTGATTCATGAA	1860
Qy	1861	GAAAGCAGATAGAAAGTGTTGAAATAAATTCGAGCTTCTCTTAATGTGAAGAA	1920
Db	1861	GAAAGCAGATAGAAAGTGTTGAAATAAATTCGAGCTTCTCTTAATGTGAAGAA	1920
Qy	1921	GAATAAGCATCTTCGATGAAAATATGATCGTTGGGAGAAATAATGGCATGCTAAGACTG	1980
Db	1921	GAATAAGCATCTTCGATGAAAATATGATCGTTGGGAGAAATAATGGCATGCTAAGACTG	1980
Qy	1981	GAGCTAGACACATGAATAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTAGACACATGAATAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA	2040

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RESULT 7
US-09-924-400-303
; Sequence 303, Application US/09924400
; Patent No. US20020165371A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misner, Lynda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
APPLICANT: Li, Samuel X.
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C12
CURRENT APPLICATION NUMBER: US/09/924,400
CURRENT FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
US-09-924-400-303

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGTGTTGAGTTGATTCCATCCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
DB      1 ATGTGTGTTGAGTTGATTCCATCCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60

QY      61 AGAGACAAAGATGGGCAAGTGTGCTGCCGTGCTTCCCTGCTGACAGGAGCGGCAAG 120
DB      61 AGAGACAAAGATGGGCAAGTGTGCTGCCGTGCTTCCCTGCTGACAGGAGCGGCAAG 120

QY      121 AGCAACGTGGGCACTTCTGTGAAGACCAAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
DB      121 AGCAACGTGGGCACTTCTGTGAAGACCAAGACGACTCTGTATGAAGACACTCAGAGCAAG 180

QY      181 ATGGGCAAGTGGTGGCGGCACCTGCTTCCCGCTGCGACGGGGGAGTGGCAAGACGTCG 240
DB      181 ATGGGCAAGTGGTGGCGGCACCTGCTTCCCGCTGCGACGGGGGAGTGGCAAGACGTCG 240

QY      241 GGCGCTTCTGGAGACCAAGACGACTCTGTATGAAGACACTCAGGAACAAGATGGCAAG 300
DB      241 GGCGCTTCTGGAGACCAAGACGACTCTGTATGAAGACACTCAGGAACAAGATGGCAAG 300

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QY	301	TGTCCTGCTCCACCTGCTTCCCTCCCTGCTGCAAGGGGAGCCGCAAGAGCAAGTGGGCGCTTGG	360
DB	301	TGTCCTGCTCCACCTGCTTCCCTCTCTGCAAGGGGAGCCGCAAGAGCAAGTGGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGCCTCTCATGAGAGCCACAGTACCACTGTCCTGGAGAAAGATCTG	420
DB	361	GGAGACTACGATGACAGTGCCTCTCATGAGAGCCACAGTACCACTGTCCTGGAGAAAGATCTG	420
QY	421	GACAAAGCTTCACAGAGCTGCCTGGTGGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
DB	421	GACAAAGCTTCACAGAGCTGCCTGGTGGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
QY	481	CTCAGAGGACACTGAGCTGTAACAAGAAAGCAACAGCAAAAGAGACTGCTCTCATGCTGGCC	540
DB	481	CTCAGAGGACACTGAGCTGTAACAAGAAAGCAACAGCAAAAGAGACTGCTCTCATGCTGGCC	540
QY	541	TCTGCGCAATGGGAATTCAGAAAGTAGTAATAAATCTCGCTGAGACAGACGATGTCACCTTAAT	600
DB	541	TCTGCGCAATGGGAATTCAGAAAGTAGTAATAAATCTCGCTGAGACAGACGATGTCACCTTAAT	600
QY	601	GTCTCTTGACAAACAAAAGAGAGCAGCTCTGATTAAGGCCGTACAAATGCCAGAAAGATGAA	660
DB	601	GTCTCTTGACAAACAAAAGAGAGCAGCTCTGATTAAGGCCGTACAAATGCCAGAAAGATGAA	660
QY	661	TGTGCGTTAATCTTGGCTGGAACATGAGCACTGATCCAAATATTCAGATGAGATGGAAT	720
DB	661	TGTGCGTTAATCTTGGCTGGAACATGAGCACTGATCCAAATATTCAGATGAGATGGAAT	720
QY	721	ACCACTCTGCACACTAGCTATCTATATATGAAAGTAATTAATGAGCCAAAGCACTGCTCTTA	780
DB	721	ACCACTCTGCACACTAGCTATCTATATGAAAGTAATTAATTAATGAGCCAAAGCACTGCTCTTA	780
QY	781	TATGCTGCTGATATATGAATCAAAAAACAAGCATGAGCTTCACACCACTGTATCTTGGTGTGA	840
DB	781	TATGCTGCTGATATATGAATCAAAAAACAAGCATGAGCTTCACACCACTGTATCTTGGTGTGA	840
QY	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAAGCAATTTAATATGCA	900
DB	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAAGCAATTTAATATGCA	900
QY	901	CTGGATAGATATGGAAGAGCTGCTCATATCTGGCTGATATGTTGGATCAGCAAGTATA	960
DB	901	CTGGATAGATATGGAAGAGCTGCTCATATCTGGCTGATATGTTGGATCAGCAAGTATA	960
QY	961	GTTCAGCCTTCTACTTGAAGCAAAATTTATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
DB	961	GTTCAGCCTTCTACTTGAAGCAAAATTTATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
QY	1021	GCCAGAGAGTATGCTGTTTCTATGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC	1080
DB	1021	GCCAGAGAGTATGCTGTTTCTATGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC	1080
QY	1081	AAAGAAAAACAGATCCTAAAAATCTCTCTGAAAACAGCAATCCAGAACAAAGACTTAAAG	1140
DB	1081	AAAGAAAAACAGATCCTAAAAATCTCTCTGAAAACAGCAATCCAGAACAAAGACTTAAAG	1140
QY	1141	CTGACATCAGAGAGAGTGTCAAAAGTTTCAAAGGCACTGAAATAATGCGACCCAGAGAAA	1200
DB	1141	CTGACATCAGAGAGAGTGTCAAAAGTTTCAAAGGCACTGAAATAATGCGACCCAGAGAAA	1200
QY	1201	ATGTCCTCAAGAACCCAGAAATTAATATAGATGCTGATAGAGAGTTGAAGAAATGAG	1260
DB	1201	ATGTCCTCAAGAACCCAGAAATTAATATAGATGCTGATAGAGAGTTGAAGAAATGAG	1260
QY	1261	AAGCATGAAAGTAATTAATGTTGGGATTTACTAGAAAACTGACCTAAATGCTGTCACTGCTGGC	1320
DB	1261	AAGCATGAAAGTAATTAATGTTGGGATTTACTAGAAAACTGACCTAAATGCTGTCACTGCTGGC	1320
QY	1321	AATGCTGATTAATGATTTAATTCCTCAAGAGAAAGCAACACTGAAATTCAGCAATTT	1380
DB	1321	AATGCTGATTAATGATTTAATTCCTCAAGAGAAAGCAACACTGAAATTCAGCAATTT	1380
QY	1381	CCTGACAAACGAAAGTAAAGATATCACAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440

Db	1381	CTCAGACACGAAAGTGAAGATACAGAAATTTGGAAATTAGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCGAAATACTCTTCTGAAACAGCAACCAGAACAGACTTAAAGCTACA	1500
Db	1441	AAACAGATGCGAAATACTCTTCTGAAACAGCAACCAGAACAGACTTAAAGCTACA	1500
Qy	1501	TCAGAGGAAGATCACAAAGCTTGAAGGCGAGTGAATAATGCGCAGCAGAGAAAGATCT	1560
Db	1501	TCAGAGGAAGATCACAAAGCTTGAAGGCGAGTGAATAATGCGCAGCAGAGAAAGATCT	1560
Qy	1561	CAAGAACCAAGAAATTAATAGATGATGATAGAGAGCTAAGAAATTTTATGCGTATGAA	1620
Db	1561	CAAGAACCAAGAAATTAATAGATGATGATAGAGAGCTAAGAAATTTTATGCGTATGAA	1620
Qy	1621	GAAATGAAGAAAGCAGGAGTACTCATGTGSGATTTCCAGAAAACTGACTAATGTGACC	1680
Db	1621	GAAATGAAGAAAGCAGGAGTACTCATGTGSGATTTCCAGAAAACTGACTAATGTGACC	1680
Qy	1681	ACTGCTGGCAATGSGTATGATGATTAATTTCTTCAGAGAAAGCAGAACACCTGAAGC	1740
Db	1681	ACTGCTGGCAATGSGTATGATGATTAATTTCTTCAGAGAAAGCAGAACACCTGAAGC	1740
Qy	1741	CAGCAATTTTCTGACACTGAGAATGAAAGATATCAAGTACGACAAACAAATGATATCTCAG	1800
Db	1741	CAGCAATTTTCTGACACTGAGAATGAAAGATATCAAGTACGACAAACAAATGATATCTCAG	1800
Qy	1801	AAGCAATTTTGTGAAGAAACAGAAACCTGGAATATTAACAGATGAGATTCTGATTCATGA	1860
Db	1801	AAGCAATTTTGTGAAGAAACAGAAACCTGGAATATTAACAGATGAGATTCTGATTCATGA	1860
Qy	1861	GAAAAAGAGATAGAAAGTGTGTAATAATGAAATTTCTGAGCTTCTCTTAGTTGTAAGAA	1920
Db	1861	GAAAAAGAGATAGAAAGTGTGTAATAATGAAATTTCTGAGCTTCTCTTAGTTGTAAGAA	1920
Qy	1921	GAAAAAGACATCTTGACATGAAATATGATGCTTGCGGGAAGAAATTTGCCATGCTAAGCTG	1980
Db	1921	GAAAAAGACATCTTGACATGAAATATGATGCTTGCGGGAAGAAATTTGCCATGCTAAGCTG	1980
Qy	1981	GAGCTAGACACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTAGACACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 8
 US-09-895-793-375
 ; Sequence 375, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hegler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinalde de Basols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITL OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

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FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895.793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; P-adj. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTGCTCTTCTGTGAAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTGCTCTTCTGTGAAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACACTGTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTGTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTCTTCTGTGAGAGGAGTGGCAAGCAAGCGT 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTCTTCTGTGAGAGGAGTGGCAAGCAAGCGT 240
QY 241 GGGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 TGGTGTGCTGCTGCTCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 GGAAGATGAGTACAGTGTGCTCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 361 GGAAGATGAGTACAGTGTGCTCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 GACAACTCCACAGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
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QY 481 CTCAGGAGCACTGACGCTGAAACAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
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QY 541 TCTGCCAATGGGAATTCAGAGAGTAAATCTCTGCTGAGACAGAGTCAACTTAAT 600
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QY 601 GTCTTGAACAACAAAAGAGAGCAGCTGTGATTAAGGCGCTTAAATGCCAGAGATGA 660
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QY 661 TGTGCGTTAATGTTGTGGAACATGGCACTGATCAAAATATTCAGATGATGAAT 720
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QY 781 TATGTGCTGATATTCGATCAAAACAAAGCATGGCTCACACACTGTTACTGGTGA 840
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DB 901 CTGATATGATATGAAAGACCTCTCATACTTGTGCTGATATGTTGGATCAGCAAGTAA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAGC 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAGC 1020
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DB 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAATTTAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATGAAGATGATGAGAGTGAAGAGAGAGAGAGAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATGAAGATGATGAGAGTGAAGAGAGAGAGAGAG 1260
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DB 1621 GAAATGAAGAGAGAGAGTATCTATGTCGAGATTTCCAGAGAAACCTGACTAATG 1680
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DB 1681 ACTGTGCAATGATGATGATTAATTTCTTCAAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACATGAGATGAAGAGTATCAAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 CAGCAATTTCTGACATGAGATGAAGAGTATCAAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 AAGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1801 AAGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 GAAAGAGAGATGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 GAAAGAGAGATGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATGATAGTGTGCGGAGAGAGAGAGAGAGAGAG 1980
DB 1921 GAAAAAGACATCTTGCATGAAAAATGATAGTGTGCGGAGAGAGAGAGAGAGAGAG 1980
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QY 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
DB 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 9
US-09-895-814-375
Sequence 375, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Roy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: PASTESEQ for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGGCCATTGGTCTC 60

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DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGCAAGGAGTGGCAAG 120

QY 121 AGCAAGTGTGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGTGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180

QY 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGTGGCAAGCAAG 240
DB 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGTGGCAAGCAAG 240

QY 241 GGGGCTTCTGGAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGGAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300

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DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGTGGCAAGCAAGTGGCAAGTGG 360

QY 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCCAAGGTACCAAGTCCGCTGGAAGATCTG 420
DB 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCCAAGGTACCAAGTCCGCTGGAAGATCTG 420

QY 421 GACAACTCCACAGAGCTGCTGCTGGAAGTCCCGCAAGAAAGATCTCATGCTGATG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGGAAGTCCCGCAAGAAAGATCTCATGCTGATG 480

QY 481 CTCAGGAGCACTGACCTGAAAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
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QY 721 ACCACTCTGCACTACCTCTATTAATGAAGATTAATGAGCAAGCAAGCAAGCAAG 780
DB 721 ACCACTCTGCACTACCTCTATTAATGAAGATTAATGAGCAAGCAAGCAAGCAAG 780

QY 781 TATGCTGATGATGGAATCAAAAACAAAGCAAGCTGCAAGCAAGCTGATCTGATG 840
DB 781 TATGCTGATGATGGAATCAAAAACAAAGCAAGCTGCAAGCAAGCTGATCTGATG 840

QY 841 CATGACAAAACAGCAAGCTGGAATTTTAAATCAAGAAAACAGCAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGCTGGAATTTTAAATCAAGAAAACAGCAATTTAAATGCA 900

QY 901 CTGATGATGATGGAAGCACTGCTCATATCTGCTGATGTTGTTGATGCAAGATTA 960
DB 901 CTGATGATGATGGAAGCACTGCTCATATCTGCTGATGTTGTTGATGCAAGATTA 960

QY 961 GTGAGCTCTAATTGAGCAAAATATGATGATCTTCAAGATCTAATCTGAGCAAG 1020
DB 961 GTGAGCTCTAATTGAGCAAAATATGATGATCTTCAAGATCTAATCTGAGCAAG 1020

QY 1021 GCCAGAGATGCTGTTCTAGTCATCATGATTAATTTGCAAGTCTTCTGATG 1080
DB 1021 GCCAGAGATGCTGTTCTAGTCATCATGATTAATTTGCAAGTCTTCTGATG 1080

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QY 1141 CTGACATCAGAGAGATCAAAAGTTCAAAGCAAGCAAGCAAGCAAGCAAGCAAG 1200
DB 1141 CTGACATCAGAGAGATCAAAAGTTCAAAGCAAGCAAGCAAGCAAGCAAGCAAG 1200

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DB 1201 ATGCTCAAGAACAGAAATTAATGAAGTGTGATGAAGAGTGAAGAAATGAAG 1260

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QY 1321 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380

QY 1381 CCTGCAACGAAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1440
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Qy 1441 AACAGATGCCAAATATCTTCTGTGAAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500
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Qy 1921 GAAAAAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 GAAAAAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
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RESULT 10

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US-10-012-896-375
; Sequence 375, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepker, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Manteabe, Yoshihiro
; APPLICANT: Mesgher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27

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; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-375

Query Match 100.0%; Score 2040; DB 5; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATGTTGAGTTGATTCATAGCGGCTGCTCTTCGTGTAAGACATTTGCTTC 60
Db 1 ATGGATGTTGAGTTGATTCATAGCGGCTGCTCTTCGTGTAAGACATTTGCTTC 60
Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCGTTGCTTCCCTGCTGAGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGTTGCTTCCCTGCTGAGAGAGCGGCAAG 120
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Qy 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGAGAGTGGCAAGCGTG 240
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Db 301 TGGTCTGCTGCACTGCTTCCCTGCTGAGAGAGAGAGTGGGCAAGCGCTTGG 360
Qy 361 GGAAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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QY 841 CATGAGCAAAAAACAGAAAGTCTGGAATTTTATCAAGAAAAAAGCGAATTTAAATGCA 900
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QY 1021 GCCAGAGATTAAGCTTCTTCTAGTCAATCAATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAAAGGAGTGAATATAGCCAGCCAGAGAAA 1200
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QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
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Db 1441 AAAACAGATGCAAAATATCTCTTCTGAAAAACAGCAACCAAGAAACAAACTTAAGCTGACA 1500
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Db 1501 TCAGAGAGAGAGTCAAAAAGCTTTGAGGGCAGTGAATGCGCAGGCAAGAGAAAGATCT 1560
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RESULT 12
US-10-212-679-303
; Sequence 303, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, David
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-303

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGTGTGTGAGGTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCAATTTGTTCTC 60
QY 61 AGGAGCAGATGGGCAAGTGTGCTGCGCTTCTCTCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAGATGGGCAAGTGTGCTGCGCTTCTCTCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTTGAGAGACACAGAGCACTGCTGATGAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTTGAGAGACACAGAGCACTGCTGATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGAGCAACTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGAGCAACTG 240
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QY 241 GGGCTTTGGAGACCAAGCACTCTGTATGAAACACTCAAGAAAGATGGGCAAG 300
 DB 241 GGGCTTTGGAGACCAAGCACTCTGTATGAAACACTCAAGAAAGATGGGCAAG 300
 QY 301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGGGGAGCGGCAAGAGATGGGCGCTGG 360
 DB 301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGGGGAGCGGCAAGAGATGGGCGCTGG 360
 QY 361 GGAAGCTACGATGACAGTGCCTTCATGAGCCAGGATCCAGTCCGTGAGAAAGATCTG 420
 DB 361 GGAAGCTACGATGACAGTGCCTTCATGAGCCAGGATCCAGTCCGTGAGAAAGATCTG 420
 QY 421 GACAAGCTCCAGAGAGTGCCTGCTGGGGGTAAGTCCCGCAAAAGATCTCATGCTCATG 480
 DB 421 GACAAGCTCCAGAGAGTGCCTGCTGGGGGTAAGTCCCGCAAAAGATCTCATGCTCATG 480
 QY 481 CTCAGGGAACACTGACGTAAGCAAGAAAGGAACAAGCAAAAGAGACTGCTCATCTGGCC 540
 DB 481 CTCAGGGAACACTGACGTAAGCAAGAAAGGAACAAGCAAAAGAGACTGCTCATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGTGACAGACGATGCTCACTTAAT 600
 DB 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGTGACAGACGATGCTCACTTAAT 600
 QY 601 GTCTCTTGAACAACAAAAGAGAGCACTCTGATTAAGGCGCTCAATGCCAGAAAGATGAA 660
 DB 601 GTCTCTTGAACAACAAAAGAGAGCACTCTGATTAAGGCGCTCAATGCCAGAAAGATGAA 660
 QY 661 TGTGGCTTAATGTTGCTGGAACAGTGCATGATCCAAATTTCCAGATGATGATGAAAT 720
 DB 661 TGTGGCTTAATGTTGCTGGAACAGTGCATGATCCAAATTTCCAGATGATGATGAAAT 720
 QY 721 ACCACTCTGCACTACGCTATCTTAATGAAATGAAATTAATGAGCAAGCACTGCTTGA 780
 DB 721 ACCACTCTGCACTACGCTATCTTAATGAAATGAAATTAATGAGCAAGCACTGCTTGA 780
 QY 781 TATGTGCTGATATCGAATCAAAAACAGCATGCGCTCACACACTGTTACTTGGTGA 840
 DB 781 TATGTGCTGATATCGAATCAAAAACAGCATGCGCTCACACACTGTTACTTGGTGA 840
 QY 841 CATGACCAAAAACAGCAAGTGTGAAATTTTAATCAAGAAAGAAAGCGAATTTAAATGCA 900
 DB 841 CATGACCAAAAACAGCAAGTGTGAAATTTTAATCAAGAAAGAAAGCGAATTTAAATGCA 900
 QY 901 CTGGATAGATGAGAGAGACTGCTCATATCTGCTGATGTTGTGATGACGAAATTA 960
 DB 901 CTGGATAGATGAGAGAGACTGCTCATATCTGCTGATGTTGTGATGACGAAATTA 960
 QY 961 GTGACGCTTCTACTTGAAGCAAAATTTGATGATCTTTCAGAGATCTATCTGACAGAG 1020
 DB 961 GTGACGCTTCTACTTGAAGCAAAATTTGATGATCTTTCAGAGATCTATCTGACAGAG 1020
 QY 1021 GCCAGAGATGAGTCTGTTCTACTCATCATGATTAATTTGCGAATTACTTTCTGACTAC 1080
 DB 1021 GCCAGAGATGAGTCTGTTCTACTCATCATGATTAATTTGCGAATTACTTTCTGACTAC 1080
 QY 1081 AAAAGAAAAAGATGCTAAATAATCTCTTCTGAAAAAGCAATCCAGAAACAAGACTTAAG 1140
 DB 1081 AAAAGAAAAAGATGCTAAATAATCTCTTCTGAAAAAGCAATCCAGAAACAAGACTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGAGCTGAAATAATGCGACGAGAGAAA 1200
 DB 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGAGCTGAAATAATGCGACGAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAAGAAAGAG 1260
 DB 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAAGAAAGAG 1260
 QY 1261 AAGCATGAAAGATATATGAGATTACTGAAAACTGACTAATGATGCTGAGC 1320
 DB 1261 AAGCATGAAAGATATATGAGATTACTGAAAACTGACTAATGATGCTGAGC 1320

QY 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAAAATCGCAATTT 1380
 DB 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAAAATCGCAATTT 1380
 QY 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 DB 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 QY 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCAAGAACAGACTTAAGCTGACA 1500
 DB 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCAAGAACAGACTTAAGCTGACA 1500
 QY 1501 TCGAGAGAAAGATCAAAAAGCTTGAAGGCACTGAAATATGCGCAGCAAGAAAGATCT 1560
 DB 1501 TCGAGAGAAAGATCAAAAAGCTTGAAGGCACTGAAATATGCGCAGCAAGAAAGATCT 1560
 QY 1561 CAAGAACCAAGAAATTAATGAGTGTGATGAGAGCTGAAATTTATGCTATCGAA 1620
 DB 1561 CAAGAACCAAGAAATTAATGAGTGTGATGAGAGCTGAAATTTATGCTATCGAA 1620
 QY 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCAATTCAGAAAACTGACTAAATGGTGCC 1680
 DB 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCAATTCAGAAAACTGACTAAATGGTGCC 1680
 QY 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGCAACACTGAAAGC 1740
 DB 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGCAACACTGAAAGC 1740
 QY 1741 CAGCAATTTCTGACACTGAGAAATGAAAGTATCAAGTGAAGCAACAAATATGATCTGAG 1800
 DB 1741 CAGCAATTTCTGACACTGAGAAATGAAAGTATCAAGTGAAGCAACAAATATGATCTGAG 1800
 QY 1801 AAGCAATTTTGTGAGAGAGAGCAACACTGGAATATTAACAGATGAGATTCGATTCAGAA 1860
 DB 1801 AAGCAATTTTGTGAGAGAGAGCAACACTGGAATATTAACAGATGAGATTCGATTCAGAA 1860
 QY 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTTCTTATGTTGTAAGAA 1920
 DB 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTTCTTATGTTGTAAGAA 1920
 QY 1921 GAAAAAGACATCTGATGAAAAATGATGATGCTGGGGAAGAAATTCGATGAAAGCTG 1980
 DB 1921 GAAAAAGACATCTGATGAAAAATGATGATGCTGGGGAAGAAATTCGATGAAAGCTG 1980
 QY 1981 GAGCTGACACATGAGAAACATGAGAGCCAGCTTAAGAAAAATGAAAAATGAAAAA 2040
 DB 1981 GAGCTGACACATGAGAAACATGAGAGCCAGCTTAAGAAAAATGAAAAATGAAAAA 2040

RESULT 13
 US-10-144-678A-375
 ; Sequence 375, Application US/10144678A
 ; Publication No. US20030157089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darlick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yael A. W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.

```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassole, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-375

Query Match      100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGTTGATGAGTTGATTCATGCGCGCTGCTCTTTCTGTGAAGACCATTTGGTCTC 60
DB      1 ATGTGTTGATGAGTTGATTCATGCGCGCTGCTCTTTCTGTGAAGACCATTTGGTCTC 60

QY      61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB      61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120

QY      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGTAATGAAGACACTCAGAGCAAG 180
DB      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGTAATGAAGACACTCAGAGCAAG 180

QY      181 ATGGGCAAGTGGGCGCGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
DB      181 ATGGGCAAGTGGGCGCGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240

QY      241 GGGCTTCTGAGAGCAAGCAAGCACTGCTGTAATGAAGACACTCAGAGCAAGGAGTGGCAAG 300
DB      241 GGGCTTCTGAGAGCAAGCAAGCACTGCTGTAATGAAGACACTCAGAGCAAGGAGTGGCAAG 300

QY      301 TGGTGTGCCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGAGTGGCGCTTGG 360
DB      301 TGGTGTGCCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGAGTGGCGCTTGG 360

QY      361 GGAAGCTACGATGACAGTGTCTTCATGAGCCCAAGGTACCAAGTGTGGAGAAAGATCTG 420
DB      361 GGAAGCTACGATGACAGTGTCTTCATGAGCCCAAGGTACCAAGTGTGGAGAAAGATCTG 420

QY      421 GACAAGCTCCACAGAGTGTGCTGTGGGGGTAAAGTCCCGCAAGAAAGATCTCATGTCTATG 480
DB      421 GACAAGCTCCACAGAGTGTGCTGTGGGGGTAAAGTCCCGCAAGAAAGATCTCATGTCTATG 480

QY      481 CTCAGGAGCACTGACGTGAACAAGAAAGCAAGCAAAAGAGACTGCTCTACATCTGGCC 540
DB      481 CTCAGGAGCACTGACGTGAACAAGAAAGCAAGCAAAAGAGACTGCTCTACATCTGGCC 540

QY      541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGCTGCAAGAGATGTAATTAAT 600
DB      541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGCTGCAAGAGATGTAATTAAT 600

QY      601 GTCCTTGAACAACAAAAGAGAGAGCTGTGTAAGGCGGTACAATGCGCAGAAAGATGA 660
DB      601 GTCCTTGAACAACAAAAGAGAGAGCTGTGTAAGGCGGTACAATGCGCAGAAAGATGA 660

QY      661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAATATTCAGATGATGAAGAT 720
DB      661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAATATTCAGATGATGAAGAT 720

QY      721 ACCACTCTGACATACGCTATCTAATGAAGATTAATGAGCACTGCTCTTA 780
DB      721 ACCACTCTGACATACGCTATCTAATGAAGATTAATGAGCACTGCTCTTA 780
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QY      781 TATGGTCTGATATGGAATCAAAAAACAAGATGGGCTCACACCACTGTACTGTGTGA 840
DB      781 TATGGTCTGATATGGAATCAAAAAACAAGATGGGCTCACACCACTGTACTGTGTGA 840

QY      841 CATGAGCAAAAAACAGAGTGTGAAATTTTATCAGAAAAAAGCGAATTTAATGCA 900
DB      841 CATGAGCAAAAAACAGAGTGTGAAATTTTATCAGAAAAAAGCGAATTTAATGCA 900

QY      901 CTGGATAGATATGAAAGAGCTGCTCATCTTGTGTATGTTGGATCAGCAAGTATA 960
DB      901 CTGGATAGATATGAAAGAGCTGCTCATCTTGTGTATGTTGGATCAGCAAGTATA 960

QY      961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCCAGAGCTATCTGAGCAGAG 1020
DB      961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCCAGAGCTATCTGAGCAGAG 1020

QY      1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTAATTTGCGAGTTACTTTCTGACTAC 1080
DB      1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTAATTTGCGAGTTACTTTCTGACTAC 1080

QY      1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAG 1140
DB      1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAG 1140

QY      1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGGCAAGTAAATAGCCAGCAGAGAA 1200
DB      1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGGCAAGTAAATAGCCAGCAGAGAA 1200

QY      1201 ATGTCTCAAGAAACAGAAAAATAAAGATGATGATAGAGGTTGAAGAAATGAAG 1260
DB      1201 ATGTCTCAAGAAACAGAAAAATAAAGATGATGATAGAGGTTGAAGAAATGAAG 1260

QY      1261 AAGCATGAAAGTAAATATGAGGATTTACTAGAAAACTGACTAATGATGTCCTGTGCG 1320
DB      1261 AAGCATGAAAGTAAATATGAGGATTTACTAGAAAACTGACTAATGATGTCCTGTGCG 1320

QY      1321 AATGGTATATGATTAATTTCTCAAGAGGAGAGAGAACACTGAAAAATCAGCAATTT 1380
DB      1321 AATGGTATATGATTAATTTCTCAAGAGGAGAGAGAACACTGAAAAATCAGCAATTT 1380

QY      1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
DB      1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440

QY      1441 AAAAGATGCCAAAATATCTTCTGAAAAACAGAACCCAGAACCAAGACTTAAGCTGACA 1500
DB      1441 AAAAGATGCCAAAATATCTTCTGAAAAACAGAACCCAGAACCAAGACTTAAGCTGACA 1500

QY      1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCACTGAAAAATGGCCAGCAGAGAAAAAGATCT 1560
DB      1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCACTGAAAAATGGCCAGCAGAGAAAAAGATCT 1560

QY      1561 CAAGAACCGAATTAATTAAGATGATGATAGAGAGTGAAGAAATTTATGCTATCGAA 1620
DB      1561 CAAGAACCGAATTAATTAAGATGATGATAGAGAGTGAAGAAATTTATGCTATCGAA 1620

QY      1621 GAAATGAAGAACACAGGAAGTACTCATGTGCGATTTCCAGAAAACTGACTAATGATGCG 1680
DB      1621 GAAATGAAGAACACAGGAAGTACTCATGTGCGATTTCCAGAAAACTGACTAATGATGCG 1680

QY      1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGGAAGC 1740
DB      1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGGAAGC 1740

QY      1741 CAGCAATTTCTGACACTGAGATGAAGATGATCAAGTGAAGAAACAAATGATATCTCAG 1800
DB      1741 CAGCAATTTCTGACACTGAGATGAAGATGATCAAGTGAAGAAACAAATGATATCTCAG 1800

QY      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTGATTCATGAA 1860
DB      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTGATTCATGAA 1860
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QY 1861 GAAAAAGATAGATGATGTTGAAAAATGATTTCTGAGCTTCTCTAGTTGTAGAAA 1920
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Db 1861 GAAAAAGATAGATGATGTTGAAAAATGATTTCTGAGCTTCTCTAGTTGTAGAAA 1920
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|
|
QY 1921 GAAAAAGATCTTGTGATGAAAAATGTAAGTTGCGGGAGAAAAATTCATGCTAGACTG 1980
|
|
|
Db 1921 GAAAAAGATCTTGTGATGAAAAATGTAAGTTGCGGGAGAAAAATTCATGCTAGACTG 1980
|
|
|
QY 1981 GAGCTGACATGATGAAACATGAGAGCTGAAAAATTCATGCTAGACTGAAAAATTCATG 2040
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|
|
Db 1981 GAGCTGACATGATGAAACATGAGAGCTGAAAAATTCATGCTAGACTGAAAAATTCATG 2040
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|
|
RESULT 14
US-10-033-527-7
; Sequence 7, Application US/10033527
; Publication No. US20030170631A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; TITLE OF INVENTION: AND MONITORING OF BREAST CANCER
; FILE REFERENCE: 210121.513C1
; CURRENT APPLICATION NUMBER: US/10/033.527
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-033-527-7

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 CTCAGGGAACATGACGTGAAACAAAGAGCAAGCAAAAAGAGCTGCTACATCTGGCC 540
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|
Db 481 CTCAGGGAACATGACGTGAAACAAAGAGCAAGCAAAAAGAGCTGCTACATCTGGCC 540
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|
QY 541 TCTGCAATGGGAATTCAGAAATGATGAAATCTGCTGGAAGAGAGATGCAATTAAT 600
|
|
|
Db 541 TCTGCAATGGGAATTCAGAAATGATGAAATCTGCTGGAAGAGAGATGCAATTAAT 600
|
|
|
QY 601 GTCTTGAACAACAAAAAGAGACAGCTGATGAAAGCCGTACATGCCAGAAATGAA 660
|
|
|
Db 601 GTCTTGAACAACAAAAAGAGACAGCTGATGAAAGCCGTACATGCCAGAAATGAA 660
|
|
|
QY 661 TGTGGTTAATGTTGCTGGAACATGCAATGCAATTAATTCAGATGTAAGAAAT 720
|
|
|
Db 661 TGTGGTTAATGTTGCTGGAACATGCAATGCAATTAATTCAGATGTAAGAAAT 720
|
|
|
QY 721 ACCACTGCTACATGCTATCTATATGAAATTAATTAATGAGCCAAAGCACTGCTTA 780
|
|
|
Db 721 ACCACTGCTACATGCTATCTATATGAAATTAATTAATGAGCCAAAGCACTGCTTA 780
|
|
|
QY 781 TATGCTGATATGATCAATCAAAAAACAAAGATGCTCAACCACTGTTACTGGTGA 840
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|
|
Db 781 TATGCTGATATGATCAATCAAAAAACAAAGATGCTCAACCACTGTTACTGGTGA 840
|
|
|
QY 841 CATGAGCAAAAAACAGAAATGCTGAAATTTTAAATCAAAAAAGCAATTTAAATGCA 900
|
|
|
Db 841 CATGAGCAAAAAACAGAAATGCTGAAATTTTAAATCAAAAAAGCAATTTAAATGCA 900
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|
|
QY 901 CTGATATGATGAAAGAGACTGCTCATACTGCTGATATGTTGTTGATCAGCAATATA 960
|
|
|
Db 901 CTGATATGATGAAAGAGACTGCTCATACTGCTGATATGTTGTTGATCAGCAATATA 960
|
|
|
QY 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAGC 1020
|
|
|
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAGC 1020
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|
|
QY 1021 GCCAGAGATATGCTGTTCTGATCATCATGATATTTGCAAGTACTTCTGACTAC 1080
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|
|
Db 1021 GCCAGAGATATGCTGTTCTGATCATCATGATATTTGCAAGTACTTCTGACTAC 1080
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|
QY 1081 AAAAGAAAAACAGATGCTAAATAATCTCTGAAAAACAGAAATCCAGAAACAGCTTAAG 1140
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|
|
Db 1081 AAAAGAAAAACAGATGCTAAATAATCTCTGAAAAACAGAAATCCAGAAACAGCTTAAG 1140
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|
|
QY 1141 CTGACATCAGAGAAAGATCACAAAGTTCAAAAGCATGAAATATGCCAGCAGAGAAA 1200
|
|
|
Db 1141 CTGACATCAGAGAAAGATCACAAAGTTCAAAAGCATGAAATATGCCAGCAGAGAAA 1200
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|
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|
|
Db 1201 ATGTCTCAAGAAACAGAAATTAATAGATGATGATGAGAGTTGAAGAAATGAAAG 1260
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|
QY 1261 AAGCATGAAAGTAAATGTTGGATTAATAGAAAACTGAACTAATGTTGCTGCTGAG 1320
|
|
|
Db 1261 AAGCATGAAAGTAAATGTTGGATTAATAGAAAACTGAACTAATGTTGCTGCTGAG 1320
|
|
|
QY 1321 AATGTTGATTAATGATTAATTCCTCAAAAGAAAGAGAGCAACCTGAAATACGCAATTT 1380
|
|
|
Db 1321 AATGTTGATTAATGATTAATTCCTCAAAAGAAAGAGAGCAACCTGAAATACGCAATTT 1380
|
|
|
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATTTCTGATCAAAAGAA 1440
|
|
|
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATTTCTGATCAAAAGAA 1440
|
|
|
QY 1441 AAAAGATGCAAAATATCTCTGAAAAACAGAAATCCAGAAACAGAACTTAAGCTGACA 1500
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|
|
Db 1441 AAAAGATGCAAAATATCTCTGAAAAACAGAAATCCAGAAACAGAACTTAAGCTGACA 1500
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|
|
QY 1501 TCAAGAGAAAGATCAAAAGGCTTGAAGGCACTGAAATATGCTCAGCCAGAGAAAGATCT 1560
|
|
|
Db 1501 TCAAGAGAAAGATCAAAAGGCTTGAAGGCACTGAAATATGCTCAGCCAGAGAAAGATCT 1560
|
|
|
QY 1561 CAAGAAACCAAAATTAATAGATGATGATAGAGCTAGAAAAATTTTATGCTATCGAA 1620
|
|
|

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|||||
Db 1561 CAGAGACCAAGAAATAAATAGATGTGATAGAGACTAGAAAAATTTTATGGCTATCGAA 1620
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Qy 1621 GAAATGAAGAAGACGGAAGTACTCATATGCCGATTTCCCAAGAAAACTGTACTAATGGTGGC 1680
|||
Db 1621 GAATATGAAGAAGACGGAAGTACTCATATGCCGATTTCCCAAGAAAACTGTACTAATGGTGGC 1680
|||
Qy 1681 ACTGTGCGAATGTGTATGATGATTAATTCCTCAAGGAAGACAGAAACACTGTAAAGC 1740
|||
Db 1681 ACTGTGCGAATGTGTATGATGATTAATTCCTCAAGGAAGACAGAAACACTGTAAAGC 1740
|||
Qy 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGACGACAAATGATTAATCTGAG 1800
|||
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGACGACGACAAATGATTAATCTGAG 1800
|||
Qy 1801 AAGCAATTTTGAAGAAGACGAACTGTGAATTTACAGATGAGATTTCTGATTCATGAA 1860
|||
Db 1801 AAGCAATTTTGAAGAAGACGAACTGTGAATTTACAGATGAGATTTCTGATTCATGAA 1860
|||
Qy 1861 GAAAAACAGATAGAAAGTGTGAAAAAATGAATTTCTGAGCTTTCTCTTAGTTGTAAGAA 1920
|||
Db 1861 GAAAAACAGATAGAAAGTGTGAAAAAATGAATTTCTGAGCTTTCTCTTAGTTGTAAGAA 1920
|||
Qy 1921 GAAAAAGACATCTTGACATGAAAAATAGTACGTTGCGGGAAGAAATTCGCAATGCTAAGACTG 1980
|||
Db 1921 GAAAAAGACATCTTGACATGAAAAATAGTACGTTGCGGGAAGAAATTCGCAATGCTAAGACTG 1980
|||
Qy 1981 GAGCTGACACATGAAACTCGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2040
|||
Db 1981 GAGCTGACACATGAAACTCGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2040
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RESULT 15
US-10-294-025-375

/ Sequence 375, Application US/10294025
/ Publication No. US20030185830A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Stolk, John A.
/ APPLICANT: Kalos, Michael D.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C29
/ CURRENT APPLICATION NUMBER: US/10/294,025
/ NUMBER OF SEQ ID NOS: 1038
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-294-025-375

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
|||
Db 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
|||
Qy 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
|||
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
|||
Qy 121 AGCAAGTGGGCACTTCTGAGACACAGAGCACTGCTATGAAAGCACTCAGAGCAAG 180
|||
Db 121 AGCAAGTGGGCACTTCTGAGACACAGAGCACTGCTATGAAAGCACTCAGAGCAAG 180
|||
Qy 181 ATGGGCAATGTGGCCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
|||
Db 181 ATGGGCAATGTGGCCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
|||

Qy 241 GCGGCTTGTGAGACCAAGCACTGTGCTATGAAGACACTGAGGAACAAGATGGGCAAG 300
|||
Db 241 GCGGCTTGTGAGACCAAGCACTGTGCTATGAAGACACTGAGGAACAAGATGGGCAAG 300
|||
Qy 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGGCGCAAGAGCAAGTGGGCGCTTGG 360
|||
Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGGCGCAAGAGCAAGTGGGCGCTTGG 360
|||
Qy 361 GGAAGCTACAGTACAGAGGCTTCAATGAGGCCAGGTACCAAGTCCGTGGAATAAGCTG 420
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Db 361 GGAAGCTACAGTACAGAGGCTTCAATGAGGCCAGGTACCAAGTCCGTGGAATAAGCTG 420
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Qy 421 GACAAAGCTCAGAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCGCATG 480
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Qy 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
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Db 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
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Qy 541 TCTGCAATGGGAATTCAGAAATGATTAATTCCTGCTGGAACAGAGATGCACTTAAT 600
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Db 541 TCTGCAATGGGAATTCAGAAATGATTAATTCCTGCTGGAACAGAGATGCACTTAAT 600
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Qy 601 GTCTTGAACAACAAAAGAGACAGCTGTATTAAGCCGTAACAATGCCAGGAAGATGA 660
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Db 601 GTCTTGAACAACAAAAGAGACAGCTGTATTAAGCCGTAACAATGCCAGGAAGATGA 660
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Qy 661 TGTGCTTAATGTGTCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
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Db 661 TGTGCTTAATGTGTCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
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Qy 721 ACCACTGCGCACTAGGCTATCTATAAGATAAATTAATTAATGCCAAAGCACTGCTCTTA 780
|||
Db 721 ACCACTGCGCACTAGGCTATCTATAAGATAAATTAATTAATGCCAAAGCACTGCTCTTA 780
|||
Qy 781 TATGTGTGATATGAAATCAAAAAAAGAGTGGCTTCAACCACTGTTACTTGGTGA 840
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Db 781 TATGTGTGATATGAAATCAAAAAAAGAGTGGCTTCAACCACTGTTACTTGGTGA 840
|||
Qy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900
|||
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900
|||
Qy 901 CTGATATGATATGAAAGAGCTGCTCATCTTCTGTAATGTTGGTGAACACCAAGTATA 960
|||
Db 901 CTGATATGATATGAAAGAGCTGCTCATCTTCTGTAATGTTGGTGAACACCAAGTATA 960
|||
Qy 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
|||
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
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Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Qy 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGAAATCCAGAAACCTTAAG 1140
|||
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGAAATCCAGAAACCTTAAG 1140
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Qy 1141 CTGACATCAGAGGAAGTCAAAAGGTTCAAGGCAAGTAATAGCCAGCAGAGAA 1200
|||
Db 1141 CTGACATCAGAGGAAGTCAAAAGGTTCAAGGCAAGTAATAGCCAGCAGAGAA 1200
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Qy 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
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Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
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Qy 1261 AAGCATGAAGATTAATATGAGGATTAATGAAAAAATCTGACTTAATGATGCTGCTGGC 1320
|||
Db 1261 AAGCATGAAGATTAATATGAGGATTAATGAAAAAATCTGACTTAATGATGCTGCTGGC 1320
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Qy 1321 AATGTGATTAATGATTAATTTCTCAAGGAAGAGAGAAACACTGAAAAATCAGCAATTT 1380
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Db 1321 AATGGTATATGATTAATTCTCTCAAGAGAGAGCACTGAAAATCAGCAATTT 1380
QY 1381 CTTGACACACGAAAGTGAAGATATCACGAATTTGCAATTTGATCTGACAAAGAA 1440
Db 1381 CTTGACACACGAAAGTGAAGATATCACGAATTTGCAATTTGATCTGACAAAGAA 1440
QY 1441 AAACAGATGCCAAATCTCTTCTGAAAAGAGAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATCTCTTCTGAAAAGAGAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATCACAAAGCTTGAAGGACAGTAAATGGCCAGAGAAAGATCT 1560
Db 1501 TCAGAGAAAGATCACAAAGCTTGAAGGACAGTAAATGGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCCAGAAATTAATGAAGATGATGATGAGAGCTAGAAAATTTATGGCTATCGAA 1620
Db 1561 CAAGAACCCAGAAATTAATGAAGATGATGATGAGAGCTAGAAAATTTATGGCTATCGAA 1620
QY 1621 GAATGAAAGAACGAGAAATCTCATGTGGAATCCAGAAAACCTGACTAATGGTGCC 1680
Db 1621 GAATGAAAGAACGAGAAATCTCATGTGGAATCCAGAAAACCTGACTAATGGTGCC 1680
QY 1681 ACTGCTGGCAATGGTATGATGATTAATTCCTCCAAAGAAAGACAGACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGGTATGATGATTAATTCCTCCAAAGAAAGACAGACCTGAAAGC 1740
QY 1741 CAGCAATTTCTCTGACACTGAGAAATGAGATATCACAGTACGAAACAAATGATACTCAG 1800
Db 1741 CAGCAATTTCTCTGACACTGAGAAATGAGATATCACAGTACGAAACAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACGAAACATGGAATTTACAGATGAGATTTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACGAAACATGGAATTTACAGATGAGATTTGATTCATGAA 1860
QY 1861 GAAAGAGATAGAGATGTTGAAAAATGAAATTTGAGCTTCTCTTAGTGTGAAGAA 1920
Db 1861 GAAAGAGATAGAGATGTTGAAAAATGAAATTTGAGCTTCTCTTAGTGTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGATGAAAAATGATGCGTGGGAGAGAAATGGCATGTAGACTG 1980
Db 1921 GAAAAAGACATCTTGATGATGAAAAATGATGCGTGGGAGAGAAATGGCATGTAGACTG 1980
QY 1981 GAGCTGACACATGAAACATCAGAGCCAGCTAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 GAGCTGACACATGAAACATCAGAGCCAGCTAAAAAAAAAAAAAAAAAAAAAA 2040
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Search completed: December 18, 2005, 15:26:40
Job time : 1665.77 sec

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:12:24 ; Search time 248.436 Seconds

(without alignments)

4025.047 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040
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Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170.6	8.4	1041	6	US-10-131-826A-21
2	84.6	4.1	14770	6	US-10-821-234-268
3	71.4	3.5	1870	6	US-10-750-185-34429
4	66	3.2	2048	6	US-10-955-054A-16
5	61	3.0	343	7	US-11-108-172-795
6	60.2	3.0	4270	6	US-10-714-781A-54
7	60.2	3.0	5004	6	US-10-714-781A-77
8	58.8	2.9	6928	6	US-10-714-781A-60
9	56	2.7	2505	7	US-11-186-283-9
10	56	2.7	3026	7	US-11-186-283-7
11	52	2.5	6549	7	US-11-186-284-92
12	50.6	2.5	5054	6	US-10-821-234-123
13	50.4	2.5	3025	7	US-11-186-283-3
14	50.4	2.5	1790	7	US-11-000-463-671
15	49.8	2.4	1936	6	US-10-750-185-55958
16	49.4	2.4	2487	6	US-10-689-742-165
17	45	2.2	28524	6	US-10-689-561-13292
18	42.8	2.1	1108	6	US-10-689-742-209
19	42.4	2.1	1454	6	US-10-750-185-57501
20	42	2.0	340000	7	US-11-102-978-3
21	41.8	2.0	201	6	US-10-995-561-32576
22	40.6	2.0	387780	6	US-10-995-561-132559
23	40.6	2.0	387780	6	US-10-995-561-132559

24	40.2	2.0	765	7	US-11-000-463-199	Sequence 199, App
25	40	2.0	2668	6	US-10-131-826A-511	Sequence 511, App
26	39.6	1.9	201	6	US-10-995-561-46034	Sequence 46034, A
27	39.6	1.9	201	6	US-10-995-561-46035	Sequence 46035, A
28	39.6	1.9	201	6	US-10-995-561-46036	Sequence 46036, A
29	39.6	1.9	191091	7	US-11-121-086-60	Sequence 60, App1
30	39.6	1.9	237326	7	US-11-157-389-2	Sequence 2, App1
31	39.4	1.9	3819	6	US-10-131-826A-405	Sequence 405, App
32	39.4	1.9	6189	6	US-10-909-125-825	Sequence 825, App
33	39.2	1.9	103931	7	US-11-117-187-193	Sequence 193, App
34	39.2	1.9	159781	7	US-11-121-086-92	Sequence 92, App1
35	39	1.9	496	6	US-10-131-826A-533	Sequence 533, App
36	39	1.9	187745	7	US-11-121-086-83	Sequence 83, App1
37	38.8	1.9	1332	6	US-10-131-826A-443	Sequence 443, App
38	38.8	1.9	2036	6	US-10-996-217A-8	Sequence 8, App1
39	38.8	1.9	179597	7	US-11-121-086-91	Sequence 91, App1
40	38.8	1.9	268685	6	US-10-933-025-22	Sequence 22, App1
41	38.6	1.9	755	6	US-10-131-826A-153	Sequence 153, App
42	38.6	1.9	75007	6	US-10-995-561-13194	Sequence 13194, A
43	38.4	1.9	1878	6	US-10-750-185-56104	Sequence 56104, A
44	38.4	1.9	2250	6	US-10-955-054A-98	Sequence 98, App1
45	38.2	1.9	201	6	US-10-995-561-32049	Sequence 32049, A

ALIGNMENTS

RESULT 1
US-10-131-826A-21
; Sequence 21, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588

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; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-21

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Query Match	8.4%;	Score 170.6;	DB 6;	Length 1041;
Best Local Similarity	63.7%;	Pred. No. 2.9e-29;		
Matches 276;	Conservative	0;	Mismatches 154;	Indels 3;
				Gaps 1

QY 378 TGGCTTCAATGAGCCAGGTACCAAGTCCGTGGAGAAGATCTGGACAAGCTCCAGAGC 437

Db 300 TGGCTTCGCATTTTCCCAATACCCCATTTAAACCGTATCATCTGAAGAGATCCACAGAGC 359

QY 438 TGGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATGCTCAGGACACTGACGT 497

Db 360 TGTCTTACATGGTAAATCTAGAGAACTGAA---GTACCTTCTGTCTCAACGATTTATGACGC 416

QY 498 GAAACAAGAGGACAAGCAAAAAGAGACTGTCTACATCTGGCTCTGGCCAATGGGAATTC 557

Db 417 CAATTAAGAGAGCAGAGAAAGAAAGACCGCCCTACATTTGGCCTGTGGCCACTGGCCAACC 476

QY 558 AGAAGTAGTAAACTCCTGCTGGACAGAGATGTCAACTTAATGTGCTTGACAACAAAA 617

Db 477 GGAATATGTATCTCTCTGTGTGTCCAGAAAGATGTAGCTTTAACTCTGGACCCTGAGAGA 536

QY 618 GAGGACAGCTGTGATTAAGAGCGGTACATGCCAGAAAGTAAATGTGCGTTAATGTTGCT 677

Db 537 CAGGACACCTCTGATTCAAAGCTGTATCAACTGAGGACAGAGGCTTGTGCAACTCTTGCT 596

QY 678 GGAACATGGCACTGATCCAAATATATCCAGATGAGTATGAAATAACCACTGTGACCTACGC 737

Db 557 GCAAAATGGCGCAATCCAAATATTAAGGATTTCTTTGAAAGGACGTCTGTGACTACGC 656

QY 738 TATCTATATGAAGATTAATTAATGACCAGCACTGCTCTTATATGCTGCTGATATCGA 797

Db 657 TGTGTATATGAAGATACATCCATGTATAAAAAACTTTTTCACATGTTCAAAATATTGA 716

QY 798 ATCAAAAAACAG 810

Db 717 AGAATGCAGCAAG 729

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RESULT 2
US-10-821-234-268
; Sequence 268, Application US/10821234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andarman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 268
; LENGTH: 14770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-268

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Query Match	4.1%	Score 84.6;	DB 6;	Length 14770;
Best Local Similarity	49.9%	Pred. No. 1.9e-09;		
Matches 213; Conservative	0;	Mismatches 214;	Indels 0;	Gaps 0;

OY	511	AAGCAAAAGAGACTGCTCTATCATCTGGCCCTTGGCAATGGGAATTCAGAAAGTAGTAA	570
Db	1879	AAGAAAGATTTACTCTCTTCATGTGGCAGCAAAATATGGAAAGCTTGAAGTGGCAAT	1938
OY	571	CTCTGTGACAGACCATGTCAACTTAATGTCTCTTGACAACAAGAGAGACAGCTGTG	630
Db	1339	CTCTGTCTACGAAAGATGCAATCTCCAGATGCTGCTGGAAAGACGGGCTTAACACACTG	1998
OY	631	ATAAAGCCGTACATGCGCAGGAAGATGATGTGCGTTAATGTTGCTGGAAACATGGCACT	690
Db	1999	CATGTAGTGGACATTCAGATTAACAAAGATGGCCCTTCGTCTTTTGGACCAAGAGCC	2058
OY	691	GATCCAAATATTCAGATGAGTATGAAATACACTCTGGCACTACGGCTATCTTAATGAA	750
Db	2059	TCACCTCAGCAGCGCCGAAAGATGGTTATACGCCACTGCACTGCGCTGCCAAAAGAAC	2118
OY	751	GATTAATTAATGGCCAAAGCACTGCTCTTAATATGATGCTGATATGATCAAAAAACAAG	810
Db	2119	CAGATGACATAGCGACAACCTCTCTGGAAATATGATGCTGATGGCAACGCAATTAACCGG	2178
OY	811	CATGGCCTCACCACTGTACTTGGGTGATCATAGACAAAAACAGCAAGTGTGAAATTT	870
Db	2179	CAAGGAATGTGTTCCGTCCATCTGCGAGCTCAGGAAGGGCACGTGGACATGTGTCTGCTG	2238
OY	871	TTAATCAAGAAAAAGCAATTTAAATGCACTGATAGATTAAGAAAGACTGCTCTCAT	930
Db	2239	CTCCTGGTGAATATGGGAATGTBACTGTAGCAATAAAGCGGCGTGAACCCACTCCAT	2298
OY	931	CTTGCTG 937	
Db	2299	TTGGCTG 2305	

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RESULT 3
US-10-750-185-34429
? Sequence 34429, Application US/10750185
? Publication No. US2005026063A1
? GENERAL INFORMATION:
? APPLICANT: MMI GENOMICS, INC.
? APPLICANT: DENISE, Sue K.
? APPLICANT: KERR, Richard
? APPLICANT: ROSENFELD, David
? APPLICANT: HOLM, Tom
? APPLICANT: BATES, Stephen
? APPLICANT: FANTIN, Denise
? TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
? FILE REFERENCE: MM11100-2
? CURRENT APPLICATION NUMBER: US/10/750,185
? CURRENT FILING DATE: 2003-12-31
? PRIOR APPLICATION NUMBER: US 60/437,482
? PRIOR FILING DATE: 2002-12-31
? NUMBER OF SEQ ID NOS: 64922
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 34429
? LENGTH: 1870
? TYPE: DNA
? ORGANISM: Bovine
US-10-750-185-34429
19866880438718

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Query Match	3.5%	Score 71.4;	DB 6;	Length 1870;
Best Local Similarity	72.1%;	Pred. No. 7.8e-07;		
Matches 93;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;

OY	AGAGCTGCTCAACTGTCGTGATGTTGGACAGCAAGTATAGTCAGCTTCTACT	975
Db	AGAACGCCCTCAACCTTTCGTGTCAGTATGAACTACGAAATTTGTGACACTTCTTG	1634
OY	GAGCAAAATATGATGTATCTTCTCGAAGATCTATCTGGACAGACGGCCAGAGATAGCT	976
Db	CAGCAAGGCTGTGACATCTTTTCTCAAGATGTTTTGGATGACCTGCAGAAATATAGCT	1694
OY	GTTTCTAGT	1044
		1036

Db 1754 GTTATTAGT 1762

RESULT 4

US-10-955-054A-16
Sequence 16, Application US/10955054A
Publication No. US20050266420A1
GENERAL INFORMATION:
APPLICANT: PUSZTAI, LAJOS
APPLICANT: SYMMANS, W. PRASER
APPLICANT: HESS, KENNETH R.
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
FILE REFERENCE: UTXC-880US
CURRENT APPLICATION NUMBER: US/10/955,054A
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 2048
TYPE: DNA
ORGANISM: Homo sapiens
US-10-955-054A-16

Query Match 3.2%; Score 66; DB 6; Length 2048;

Best Local Similarity 56.4%; Pred. No. 1.3e-05; Matches 123; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 523 ACTGCTTACATCTGGCCTCTGCCAATGGAATTCAGAGTAGTAATAAATCTCTGCTGAC 582

Db 1296 AGTCACTGTCGTTGGCTCTAGTAAGCTACACAGATTTGTCAAAATGCTGCTGAT 1355

QY 583 AGACGATGTAATTAATGTCCTTGACAAATAAGGACAGCTGATTAAGCCGTA 642

Db 1356 TGTGAGTTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1415

QY 643 CATGCGAGGAAGATGTAATGCTTAATGCTGSAACATGCACTGATCCAAATAT 702

Db 1416 CATGGAATATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1475

QY 703 CCAGATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 740

Db 1476 GAAACTGACTCTGATATATTTCTATGACTGATGCTGT 1513

RESULT 5

US-11-108-172-795/c
Sequence 795, Application US/11108172
Publication No. US20050260177A1
GENERAL INFORMATION:
APPLICANT: XU, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Yunglong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skelky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121, 471C15
CURRENT APPLICATION NUMBER: US/11/108,172
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 10/025,360

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US 09/922,217

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US 09/833,263

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 09/649,811

PRIOR FILING DATE: 2000-08-28

PRIOR APPLICATION NUMBER: US 09/609,448

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: US 09/575,251

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: US 09/519,444

PRIOR FILING DATE: 2000-03-06

PRIOR APPLICATION NUMBER: US 09/504,629

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: US 09/480,321

PRIOR FILING DATE: 2000-01-10

PRIOR APPLICATION NUMBER: US 09/476,296

PRIOR FILING DATE: 1999-12-30

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1130

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 795

LENGTH: 343

TYPE: DNA

ORGANISM: Homo sapiens

US-11-108-172-795

Query Match 3.0%; Score 61; DB 7; Length 343;

Best Local Similarity 64.5%; Pred. No. 8.7e-05; Matches 91; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 778 TTATATGCTGATATGCAATCAAAAACAGCATGCGCTCACCACTGTTACTTGT 837

Db 342 TCACATGTGTAACAAATATTGGAATCAGCAAGAAATGATATGATGATGATGATGAT 283

QY 838 GTACATGAGCAAAAACAGCAAGCTGCAATTTTATGCAAGAAAAGCAATTTTAA 897

Db 282 GTGAGTCGAAGAAAGTGAAGAAATGTGGAATTTTATTAAGAAAAAGCAATGTAAT 223

QY 898 GCACGTGATGATATGGAAG 918

Db 222 GCCATTGATTATCTTGCAAG 202

RESULT 6

US-10-714-781A-54
Sequence 54, Application US/10714781A
Publication No. US20050255127A1
GENERAL INFORMATION:
APPLICANT: LOOSMORE, SHEENA MAY
APPLICANT: MINKE, JULES MARTEN
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
FILE REFERENCE: 574313-3161.5
CURRENT APPLICATION NUMBER: US/10/714,781A
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: 10/679,520
PRIOR FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: 10/374,953
PRIOR FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 10/116,298
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/281,923
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 10/676,502
PRIOR FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: PCT/FR02/01200
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 54
LENGTH: 4270
TYPE: DNA

ORGANISM: West Nile virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1760)..(3811)
US-10-714-781A-54

Query Match 3.0%; Score 60.2; DB 6; Length 4270;
Best Local Similarity 47.9%; Pred. No. 0.00036;
Matches 173; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 524 CTGCTTACATCTGGCCTCTGCCAATGGGAATTGAGAAGTAAACTCTGCTGGACA 583
DB 977 CTGTCTCATGATGCGGTGTGAGAGACGACTACAAATAGGAAGATCTGTTGAAGA 1036
QY 584 GACGATGCACTTAATGTCTTGAACAAGAGAGCAGCTCGATTAAGGCCGTAC 643
DB 1037 ATAACTATGTAACAAATGTTCTTTACAGCGAGGCTTTACTCTTTGTGTTGGACGCTT 1096
QY 644 AATGCCAGGAAGATGAATGTGCGTTAATGTTCTGGAGACGTGATCCAAATATTC 703
DB 1097 ACCTTAACAAAGTTAATTGGTTAACTCTAATGCTCATTCGGCGGATGATGATATT 1156
QY 704 CAGATGATGATGAATATACCACTCTGCACATGCTATCTAATAAGATTAATTAAATG 763
DB 1157 CAAACACGATCGGTTAACTCTCTACATATAGCCGTATCAATAAATTAACAATG 1216
QY 764 CCAAGCACTGCTCTTAATATGTGCTGATATGGAATCAAAAACAAGCATGGCTCAC 823
DB 1217 TTAACTTCTAATGAACAAGGTGCTGATCTGATCTGCTGATTAACATGGACGTAC 1276
QY 824 CACTGTTACTGCTGATGATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAA 883
DB 1277 CTTTATGATGCTGCTGATGATGAGCAAAAATTTGAATATGACACACTAATTAAAAA 1336
QY 884 A 884
DB 1337 A 1337

RESULT 7
US-10-714-781A-77
; Sequence 77, Application US/10714781A
; Publication No. US20050255127A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: MINK, JULES MARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.5
; CURRENT APPLICATION NUMBER: US/10/714,781A
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/679,520
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 10/676,502
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 77
; LENGTH: 5004
; TYPE: DNA
; ORGANISM: Canarypox virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1864)..(2187)
US-10-714-781A-77

Query Match 3.0%; Score 60.2; DB 6; Length 5004;
Best Local Similarity 47.9%; Pred. No. 0.00039;
Matches 173; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 524 CTGCTTACATCTGGCCTCTGCCAATGGGAATTGAGAAGTAAACTCTGCTGGACA 583
DB 1304 CTGTCTCATGATGCGGTGTGAGAGACGACTACAAATAGGAAGATCTGTTGAAGA 1363
QY 584 GACGATGCACTTAATGTCTTGAACAAGAGAGCAGCTCGATTAAGGCCGTAC 643
DB 1364 ATAACTATGTAACAAATGTTCTTTACAGCGAGGCTTTACTCTTTGTGTTGGACGCTT 1423
QY 644 AATGCCAGGAAGATGAATGTGCGTTAATGTTCTGGAACATGCACTGATCCAAATATTC 703
DB 1424 ACCTTAACAAAGTTAATTGGTTAACTCTAATGCTCATTCGGCGGATGATGATATT 1483
QY 704 CAGATGATGATGAATATACCACTCTGCACATGCTATCTAATAAGATTAATTAAATG 763
DB 1484 CAAACACGATCGGTTAACTCTCTACATATAGCCGTATCAATAAATTAACAATG 1543
QY 764 CCAAGCACTGCTCTTAATATGTGCTGATATGGAATCAAAAACAAGCATGGCTCAC 823
DB 1544 TTAACTTCTAATGAACAAGGTGCTGATCTGATCTGCTGATTAACATGGACGTAC 1603
QY 824 CACTGTTACTGCTGATGATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAA 883
DB 1604 CTTTATGATGCTGCTGATGATGAGCAAAAATTTGAATATGACACACTAATTAAAAA 1663
QY 884 A 884
DB 1664 A 1664

RESULT 8
US-10-714-781A-60
; Sequence 60, Application US/10714781A
; Publication No. US20050255127A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: MINK, JULES MARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.5
; CURRENT APPLICATION NUMBER: US/10/714,781A
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/679,520
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 10/676,502
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 60
; LENGTH: 6928
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2005)..(4059)
US-10-714-781A-60

Query Match 2.9%; Score 58.8; DB 6; Length 6928;
Best Local Similarity 47.0%; Pred. No. 0.00091;
Matches 217; Conservative 0; Mismatches 242; Indels 3; Gaps 1;
QY 524 CTGCTTACATCTGGCCTCTGCCAATGGGAATTGAGAAGTAAACTCTGCTGGACA 583

Db 1128 CTCCTCTTGAAATGCGTGTAAATGTTCAAGAAATACGAGGCTATATAAATCTTGATGAGT 1187
QY 584 GAGAGTCACTTAATATGCTTGAACAACAAAAGAGAGAGCTGTGATAAGCCGTAC 643
Db 1188 ATGAGGCTAAACCTGTAGTACTGAATGACA--ACTTCTGTCTGCATGATGCGGTG 1244
QY 644 AATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAACAATGCGACATGACCAATATTC 703
Db 1245 TGAGAGCGACTACAAATATGTAAGATCTGTGAAGATTAATATGAACAATGTTTC 1304
QY 704 CAATAGATATGAAATATACACTCTGCACTACGCTATCTTAATGAATATAATTAATG 763
Db 1305 TTAAACGCGAGGCTTACTCCCTTGTGTTGGCAGCTTACCTTAACAAGTTAATTTG 1364
QY 764 CCAAGACCTGCTCTTAATATGATGCTGATATGCAATCAAAAACAAGATGCGCTCAC 823
Db 1365 TTAAACTTATATGCTCATCTTCGCGGATGATGATTTTCAACACGAGTGGTTAATC 1424
QY 824 CACTGTACTTGTGTACATGAGCAAAACAGCAAGTCGAAATTTTATCAAGAAA 883
Db 1425 CTCTACATATAGCCGTATCAAAATTAATTAACAATGTTAACTTATATGAACAAAG 1484
QY 884 AAGCAATTTAAATGCACTGATATGATGAAAGACTGCTCATCTGCTGATGTT 943
Db 1485 GTGCTGATCTGACTGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1544
QY 944 GTGATCAGCAAGTATATGTCAGCTTCTTACTTGAACAAATA 985
Db 1545 CTGGAATATTTGAATATGTAGCACACTTAAAAAAATA 1586

RESULT 9
US-11-186-283-9
; Sequence 9, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-9

Query Match 2.7%; Score 56; DB 7; Length 2505;
Best Local Similarity 46.3%; Pred. No. 0.0026;
Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;
QY 524 CTGCTTACATCTGGCTCTGCAATGGAATTCAGAGTATTAATCTCTGTGACA 583
Db 308 CAGCTTCGACCTGCGCGTTTACAAGACAGCCGGAATTAATCACTTCACTGTGACA 367
QY 584 GAGAGTCACTTAATATGCTTGTGACAAACAAAAGAGAGAGCTGTGATTAAGCCGTAC 643

Db 368 GCGAGCAGATGTTTACAGCAAGTGGATAGCGTGCCCTCACAGCCCTCCACATAGCTGCA 427
QY 644 AATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAACAAGCACTGATCCAAATATTC 703
Db 428 TAGCTGACACCCAGAGGCTGCGAAGTGTGCTTACAAATGAGGCGCAATGTGAATGTTCC 487
QY 704 CAGATAGATGGAATATACCATCTGCTGACATGCTTATATATGAAGTAATTAATG 763
Db 488 AAGATCCGCTCTTCTTACCCCACTGCAATGCAACCTTAATGAGGACAGACAGTAA 547
QY 764 CCAAGACCTGCTCTTAATATGATGCTGATATGCAATCAAAAACAAGATGCGCTCAC 823
Db 548 CCAATGCTCTTTGAAGTTTGGTGTGATGTCAATGATGATGATGATGATGATGATGAT 607
QY 824 CACTGTACTTGTGTACATGAGCAAAAACAGCAAGTCGTAATTTTATCA----- 878
Db 608 CTCGTACCTGCGCTCTGCAAAAGGCTCTTCAACATTTGAAACATCTGTGTAAGAAAG 667
QY 879 -GAAAAAGCAATTTAAATGCACTGATATGATGAAAGACTGCTTCACTGCTG 937
Db 668 GAGCAAGCAGATGTAACGCTCAGACAAATGAACCAAGTCCCTGCACTTCTGTT 727
QY 938 TATGTTGATCAGCAAGTATATGTCAGCTTCTTACTTGAACAAATATGATGATGAT 997
Db 728 CTGATTTGACACCAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 787
QY 998 CTCAG 1003
Db 788 CTCAG 793

RESULT 10
US-11-186-283-7
; Sequence 7, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 3026
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(2565)
US-11-186-283-7

Query Match 2.7%; Score 56; DB 7; Length 3026;
Best Local Similarity 46.3%; Pred. No. 0.0028;
Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;
QY 524 CTGCTTACATCTGGCTCTGCAATGGAATTCAGAGTATTAATCTCTGTGACA 583
Db 368 CAGCTTCGACCTGCGCGTTTACAAGACAGCCGGAATTAATCACTTCACTGTGACA 427
QY 584 GAGAGTCACTTAATATGCTTGTGACAAACAAAAGAGAGAGCTGTGATTAAGCCGTAC 643

Db 428 GCGAGCAGATGTTGAGCAAGTGAGATGAGTGGCTTCAAGCCCTCCACATAGTGCAA 487
Qy 644 AATGCCAGAAATGATGATGCTTAATGTTGTTGGAACAATGACATGATCCAAATATTC 703
Db 488 TAGCTGAGACACCCAGAGGCTGCAAGAGTCTGTACAAATGGGCAATGTGAATGTC 547
Qy 704 CAGATGATGGAATTAATGACCTGCTGACATGACCTATCTATAATGAAGTAATTAATG 763
Db 548 AAGATGCCCTCTTCTTCAACCCCACTGCACATTCGACCTCATCTGAGGACGAGATGA 607
Qy 764 CCAGAACACTGCTCTTAATATGTTGCTGATATGATATCAAAAAAAGATGGCTGCAC 823
Db 608 CCAAGTCTCTTTGAAGTTGGTGTGATGTCAATGATTAAGCGTGAAGTTGGGACAGGC 667
Qy 824 CACTGTACTTGTGTATGATGACCAAAAAAGCAATGCTGAATTTTATCA----- 878
Db 668 CTCTGACCTGGCTCTGCAAAAGGCTTCTTCAACATTTGGAACCTCTGTGAAGAA 727
Qy 879 -GAAAAAGCAATTAATGCACTGATATGATGAAGAGACTGCTCATCTACTGCTG 937
Db 728 GAGGCAAGCAGATGTGAAGCTCAGAGACATGAACAACGCTCCTGCACTTCTGTT 787
Qy 938 TATGTTGTGATGACGAAGTATAGTACGCTTCTACTTGAAGCAAAATATGATATCT 997
Db 788 CTCGATTTGGACACCAATATATGAGTACTGCTCCAGAGTGAAGTCCAGC 847
Qy 998 CTCGAG 1003
Db 848 CTCACG 853

RESULT 11
US-11-186-284-92

/ Sequence 92, Application US/11186284
/ Publication No. US2005026493A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Thibodeau, Stephen N.
/ APPLICANT: Burgart, Lawrence J.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF COLON CANCER
/ FILE REFERENCE: MP01-029P2RM
/ CURRENT APPLICATION NUMBER: US/11/186,284
/ PRIOR FILING DATE: 2005-07-21
/ PRIOR APPLICATION NUMBER: US/10/301,822
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 92
/ LENGTH: 6549
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (240)...(4904)
/ US-11-186-284-92

Query Match 2.5%; Score 52; DB 7; Length 6549;
Best Local Similarity 46.8%; Pred. No. 0.03;
Matches 163; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

Qy 491 CTGAGTGAAACAAGAGGCAAGCAAAAGAGGACTGCTTACATGCGCTGCGCAATG 550
Db 2626 CTGCTGTGCGGGCAAAACAGAGAGGGGTTCCACCTTTGTTTGTGACAGCCGACG 2685
Qy 551 GGAATTCAGAAATAGTAAATCTCTGTCGACAGAGATGTCATTAATGCTTGGACA 610
Db 2686 GGCATTGGCAGATTGTTAGACTGCTGTGGAAAGGGGCTGTGATGTGAACCTAAGTACA 2745
Qy 611 ACAAAAAGAGACAGCTGTGATTAAGGCCGTCAATTCAGAGAAATGATGCGTTAA 670
Db 2746 ACCAAGGCCGAGCGCCCTCATGTGTGCTTGAAGGGACCTTGACACCGTGAAT 2805
Qy 671 TGTTCGTGAACATGAGCACTGATCCAAATATTCAGATGATGGAATAATCACTGTC 730
Db 2806 TCTCTCTTCAAAAGGTGACGCCCTTTCTTCTTGAACAAAGGGCTGTGACATTA 2865
Qy 731 ACTAGCTATCTATATGAAGATTAATATGAGCCAAAGCACTGCTTATATGTGCTG 790
Db 2866 GCTGGGCTTGTGTGAAGGTCAAGGGGAGTGTCCAGTATCTGGTTGAAGAGAGCTG 2925
Qy 791 ATATGAATCAAAAAACAAGCATGGCTTCAACCACTGTTACTTGTG 838
Db 2926 CAATGACCAAGACAGACAAAGATGGCCGACACCTTGGACCTGGCTG 2973

RESULT 12
US-10-821-234-123

/ Sequence 123, Application US/10821234
/ Publication No. US2005025114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andermani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 123
/ LENGTH: 5054
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-821-234-123

Query Match 2.5%; Score 50.6; DB 6; Length 5054;
Best Local Similarity 44.4%; Pred. No. 0.056;
Matches 203; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

Qy 526 GCTTACATCTGGCTCTGCAATGGAAATTCAGAGTAGTAAACTCTGCTGACAGA 585
Db 519 GCTTACATCTGCGACCAAGAACGACCATGATGATCAGGAAGCTGCTGACGTCT 578
Qy 586 CGATGCACTTAATGTCCTTTCACACAAAAAGAGACAGCTCTGATTAAGGCCGTACA 645
Db 579 AATGCCAGCCGAAAGGTGACAGCTCTGGAAAAACGCTTTCATTAATGACAGCGCT 638
Qy 646 TGCAGGAAGATGAATGTCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATATTC 705
Db 639 CAGGCTGCTTCAAGCTGTGCAATTTCTGCGAACACAGAGCCCTAACTCAAA 698
Qy 706 GATGATATGAAATACCACTGTCAGTACGCTATCTATATGAAGATTAATTAATGGCC 765
Db 699 GATTTGATGGAATATACCGCTGCTGCTGTGTAACAAAATGTCACAGTGAATCTGT 758
Qy 766 AAGACCTGCTCTTATATGTCCTGATATGCAATCAAAAAACAAGCATGCTCACACA 825
Db 759 CACTTCTCTGATGATGAGCAGATGTCAATTCAGAGAAAGTGAAGAACTGCT 818
Qy 826 CTGTTACTTGTGTATGATGACAAAAACAAGTCGTGAATTTTATCAAGAAAAA 885

Db 819 CTATGCTGCGCTGTGAGTATGGACGCTTAACGCTTGAAGCTTAATTAAGGCT 878
Qy 886 GCGAATTTAAATGACATGATAGATATGAGAGACGCTCTCACTACTTGTGTATGTGT 945
Db 879 GCAGACCTAAACCTTGTAGATTTCTCTTGATATACATCTTACATATTCATAACTCTCA 938
Qy 946 GGATCAGCAAGTATAGTACAGCTTCTTACTTGAGCAA 982
Db 939 GAAATGACAGAAATTCAAAGCTTCTATATCAAAA 975

RESULT 13

US-11-186-283-3
; Sequence 3, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-3

Query Match 2.5%; Score 50.4; DB 7; Length 2505;
Best Local Similarity 44.0%; Pred. No. 0.047;
Matches 213; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

Qy 523 ACTGCTCTACATCTGGCCTTGGCAATGGAAATTCAGAAATAGTAAATCTCTGCTGAC 582
Db 307 ACAGCCTTGATTTAGCAGTTTACAGAGATATGCAAAATGATCACTTCTGCTTAC 366
Qy 583 AGACGATGCACTTAATGCTTGAACAACAAAAGAGACGCTCGATTAAGGCCGTA 642
Db 367 AGTGGAGCTGATATACGACAGGTTTGATATGCGTGGCCCTCACTCCATATTTGACA 426
Qy 643 CAATGCCAGGAAGATGATATGCTTAATGTTGCTGGACATGSCACTGATCCAAATAT 702
Db 427 ATAGTGGCCACTAGAGGCTGCTGATGCTGTTGCAACATGAGATATATGCAATATT 486
Qy 703 CCAGATGAGTATGGAATATCACTGCACTGCACTATCTATATATGAAATTAATTAAT 762
Db 487 CAAGATGCAAGTTTTTTCATCTCATATGCAATGACAGCCGATCATGACATGAACAGGTA 546
Qy 763 GCCAAAGCACTGCTCTTATATGCTGATATGCAATCAAAAACAAGATGGCTCACA 822
Db 547 ACTGCGCTTTTGAATTTGGTGTGATGTAATGTAAGTGAAGTTGAGATAGA 606
Qy 823 CCACTGTTACTTGTGTATACATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAA 882
Db 607 CCCCTCACCTACATCTGCAAAAGATTTCTGAATATTCAAAACCTCTTGAATGAAGAA 666
Qy 883 AAAGCAATTTAAATGACATGATATATGAAAGACGCTCTCATATCTTGTGTATGT 942

Db 667 GCGACAAAGCAGATGTGAATGCTCAAGATATGAAGACCATGTCCACCTTCTGT 726
Qy 943 TGTGATCAGCAGATATAGTACGCTTCTTACTTACGCAAAATATGATATCTTCA 1002
Db 727 TCTGATTTGGAACCATGATATATGATATCTGTGCAAGTATTTGGAAGTTCA 786
Qy 1003 GATC 1006
Db 787 CTC 790

RESULT 14

US-11-186-283-1
; Sequence 1, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (48)..(2552)
US-11-186-283-1

Query Match 2.5%; Score 50.4; DB 7; Length 3025;
Best Local Similarity 44.0%; Pred. No. 0.051;
Matches 213; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

Qy 523 ACTGCTCTACATCTGGCCTTGGCAATGGAAATTCAGAAATAGTAAATCTCTGCTGAC 582
Db 354 ACAGCCTTGATTTAGCAGTTTACAGAGATATGCAAAATGATCACTTCTGCTTAC 413
Qy 583 AGACGATGCACTTAATGCTTGAACAACAAAAGAGACGCTCGATTAAGGCCGTA 642
Db 414 AGTGGAGCTGATATACGACAGGTTTGATATGCGTGGCCCTCACTCCATATTTGACA 473
Qy 643 CAATGCCAGGAAGATGATATGCTTAATGTTGCTGGACATGSCACTGATCCAAATAT 702
Db 474 ATAGTGGCCACTAGAGGCTGCTGATGCTGTTGCAACATGAGATATATGCAATATT 533
Qy 703 CCAGATGAGTATGGAATATCACTGCACTGCACTATCTATATATGAAATTAATTAAT 762
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QY 1003 GATC 1006
Db 834 CCTC 837

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US-11-000-463-671
; Sequence 671, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radolje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIPACN
; CURRENT FILING DATE: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 671
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-671

Query Match 2.4%; Score 49.8; DB 7; Length 1790;
Best Local Similarity 48.4%; Pred. No. 0.056;
Matches 138; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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QY 597 TAATGTCCTTGAACAACAAAAGAGACAGCTGATTAAGCCCGTCAATGCCAGAGA 656
Db 269 CAACCGGACACTAGAGAGGTGAAAGAACTCTTCAATTAGCAGCAGATTGTGGCAGCT 328
QY 657 TGAATGTGCGTTAATGTTGCTGACATGCACTGATCCAAATATTCAGATGATATG 716
Db 329 TGAATCTCGAATTTCTGCTGCTGAAAGAGAGCAGATATTAATGCTCCAGATAACATCA 388
QY 717 AATATCACTCTGCACTAGCTATCTAATAAGATTAATTAAGCCAAAGCACTGCT 776
Db 389 TATTACTCTCTCTCTGCTGCTGTATAGAGGCTCATGTTCTCTGTGTAATTCCTCT 448

QY 777 CTTATATGCTGCTGATATCGAATCAAAAAACAAGCATGGCCCTCAC 821
Db 449 GTCAAGGCTGCTGATTAAGACTGTGAAGGCCCAAGATGGACTGAC 493

Search completed: December 18, 2005, 07:36:42
Job time : 252.436 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:36:50 : Search time 8221.6 Seconds

(without alignments)
11609.127 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

Sequence: 1 atgctggttgaggtgcatc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

12: gb_est12:*

13: gb_est13:*

14: gb_est14:*

15: gb_est15:*

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17: gb_est17:*

18: gb_est18:*

19: gb_est19:*

20: gb_est20:*

21: gb_est21:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	592.4	29.0	633	3	BM763453 K-EST0044
3	581.4	28.5	621	3	BM763942 K-EST0045
4	508	24.9	729	5	BU930826 AGENCOURT
5	478.6	23.5	544	1	AL703938 DKFZp6865
6	472.8	23.2	865	2	BF676987 DKFZp6865
7	376.4	18.5	505	5	BX492731 DKFZp781C
8	357.8	17.5	817	5	BQ441373 AGENCOURT
9	357.2	17.5	910	4	BX437445 BX437445
10	351.2	17.1	2677	4	CR660726 Pongo pyg
11	348.8	17.1	843	1	AU120666
12	345.8	17.0	5130	11	DO053800 Homo sapi
13	343.4	16.8	909	7	CR994478 CR994478
14	324	15.9	5483	4	BM063888 Homo sapi
15	323.2	15.8	1020	3	BM469654 AGENCOURT
16	323	15.8	874	6	CD358418 AGENCOURT
17	316.2	15.5	5130	11	DO053801 Pan trogl
18	305.8	15.0	793	7	CO884999 BovGen 13
19	300.4	14.7	381	7	CR747857 CR747857
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21	289.6	13.9	1079	3	BM548157 AGENCOURT

23	272	13.3	539	1	AA910780
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33	250.8	12.3	582	3	BP280827
34	237.8	11.7	513	11	DO048070
35	235	11.5	423	5	BU584403
36	235	11.5	583	3	BP316828
37	230.4	11.3	289	1	AA53501
38	225.6	11.1	521	8	DN995247
39	223.8	11.0	802	5	BQ432733
40	222.2	10.9	632	7	CV4341500
41	220.8	10.8	956	5	BY717578
42	219.6	10.8	701	8	DR002574
43	217.6	10.7	747	2	BG717440
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45	216.8	10.6	856	3	BI830348

ALIGNMENTS

RESULT 1	HSMB09270	6098 bp	mRNA	linear	HTC 20-JAN-2005
LOCUS	HSMB09270				
DEFINITION	Homo sapiens mRNA, cDNA DKFZp686J0529 (from clone DKFZp686J0529).				
ACCESSION	BX649118				
VERSION	BX649118.1	GI:34368290			
KEYWORDS	HTC.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	Bahr, A., Lauber, J., Mewes, H.W., Well, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and Wiemann, S.				
CONSTRM	The German cDNA Consortium				
JOURNAL	Submitted (20-JAN-2005) MIPs, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY				
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; consortium of the German Genome Project. This clone (DKFZp686J0529) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686J0529 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.				
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	/clone="DKFZp686J0529"				
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	/dev_stage="adult"				
	/note="putative transcript"				
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Best Local Similarity	88.2%	Pred. No. 3.7e-259;			

Matches 1243; Conservative 0; Mismatches 95; Indels 71; Gaps 1;				
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QY	61	AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTTCCCTGTGCAAGGAGAGCGCAAG	120	
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QY	121	AGCAACGTGGGCACTTGTGAGACCAACGACACTTGTGTAAGAACTCAGAGCAAG	180	
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QY	301	TGGTGTCCCACTGCTTCCCTGTGCAAGGAGGAGTGGCAAGCAAGTGGGCTTGG	360	
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ACCESSION				
BM763453				
VERSION				
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
Hominidae; Homo.				
1 (bases 1 to 633)				
REFERENCE				
AUTHORS				
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,				
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and				
Kim, Y.S.				
21C Frontier Korean EST Project 2001				
Unpublished (2002)				
COMMENT				
TITLE				
JOURNAL				
CONTACT				
Genome Research Center				
Korea Research Institute of Bioscience & Biotechnology				
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea				
Tel: +82-42-860-4470				
Fax: +82-42-860-4409				
Email: yongsung@mail.kribb.re.kr				
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High quality sequence stop: 633.				
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phosphatase (BAP) and then deapped intact mRNA was				
ligated with DNA-RNA linker including BcoR I site by				
treatment of T4 RNA ligase and the first strand cDNA was				
synthesized from oligo dT-selected mRNA by priming with				
dT-tailed vector. The dT-tailed vector was adjusted to				
have about 60nt. The cDNA vector was circularized with E.				

coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 29.0%; Score 592.4; DB 3; Length 633;
Best Local Similarity 96.7%; Pred. No. 8.3e-134;
Matches 616; Conservative 0; Mismatches 17; Indels 4; Gaps 1;

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VERSION BM763942.1 GI:19093557
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 621)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

TITLE
JOURNAL
COMMENT

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@email.kribb.re.kr
Plate: 25 row: A column: 11
High quality sequence stop: 621.
Location/Qualifiers

FEATURES
source

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phosphatase (BAP) and then dephosphorylated with tobacco acid
pyrophosphatase (TAP). The dephosphorylated RNA was
ligated with DNA-RNA linker including EcoRI site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E. coli
DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F+ by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."
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ORIGIN

Query Match 28.5%; Score 581.4; DB 3; Length 621;
Best Local Similarity 96.8%; Pred. No. 4.1e-131;
Matches 605; Conservative 0; Mismatches 16; Indels 4; Gaps 1;

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 QY 1050 TCATGTAATTTGGCAGTACTTCTTCTGACTACAAAGAAAAGATGCTATAATCTCTTC 1109
 DB 537 TCATGTAATTTGGCAGTACTTCTTCTGACTACAAAGAAAAGATGTAATAATCTCTTC 596
 QY 1110 TGAACACAGCAATCCAGAACAGAC 1134
 DB 597 TGAACACAGCAATCCAGAACAGAC 621

RESULT 4
 BU930826 729 bp mRNA linear EST 18-OCT-2002
 LOCUS AGNCOURT_10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956
 DEFINITION 5', mRNA sequence.
 ACCESSION BU930826
 VERSION BU930826.1 GI:24119645
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 729)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2943 row: 0 column: 04
 High quality sequence stop: 555.
 Location/Qualifiers
 1..729
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgccgcgcgc); Site 2: SfiI
 (ggccatctggcc); 5' and 3' adaptor were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGCCCATTAAGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN
 Query Match 24.9%; Score 508; DB 5; Length 729;
 Best Local Similarity 94.8%; Pred. No. 4.1e-113;
 Matches 548; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
 QY 579 GGACAGACGATGCTCACTTAATGCTCTTGACAAACAAAGAGACAGCTCTGATAAG-- 636
 DB 3 GGACAGACGATGCTCACTTAATGCTCTTGACAAACAAAGAGAGACAGCTCTGATAAGGT 62

QY 637 -----GCCGTAATGCGCAGGAAGTGAATGCGCTT 668
 DB 63 ATGCATGACCACTATATACAGATGAGGCCGTACAAATGCGAGAAAGATGTCGCTT 122
 QY 669 AATGTTGCTGAAACATGGCAGCTGATCAATATTCAGATGATATGAAATATACACTCT 728
 DB 123 AATGTTGCTGAAACATGGCAGCTGATCAATATTCAGATGATATGAAATATACACTCT 182
 QY 729 GCACCTACGCTATCTATTAATGAAGATTAATGACCAAGCAGCTCTTATATGATGTC 788
 DB 183 GCACCTACGCTATCTATTAATGAAGATTAATGACCAAGCAGCTCTTATATGATGTC 242
 QY 789 TGATATGCAATCAAAAAACAAGCAGGCTCCACACGCTTACTTGGTGATCAGAGCA 848
 DB 243 TGATATGCAATCAAAAAACAAGCAGGCTCCACACGCTTACTTGGTGATCAGAGCA 302
 QY 849 AAAACAGCAAGTCTGAAATTTTATATCAAGAAAAAGCAATTTAAATGCACTGGATAG 908
 DB 303 AAAACAGCAAGTCTGAAATTTTATATCAAGAAAAAGCAATTTAAATGCACTGGATAG 362
 QY 909 ATATGAAGGAGCTGCTTCATATCTTGTGATGTTGTGATGATGACAAATATGTCAGCTT 968
 DB 363 ATATGAAGGAGCTGCTTCATATCTTGTGATGTTGTGATGATGACAAATATGTCAGCTT 422
 QY 969 TCTACTTGAGCAAAATATTTGATGATATCTTCAAGATCTATCTGACAGAGCGCAGAGA 1026
 DB 423 TCTACTTGAGCAAAATATTTGATGATATCTTCAAGATCTATCTGACAGAGCGCAGAGA 482
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 DB 483 GTATGCTGTTTCTAGTCAATCATCATGATATATTTGCCAGTTACTTCTGACAAAGAAA 542
 QY 1089 ACAGATGCTAAATAATCTCTTCTGAAAAACAGCATATCAG 1126
 DB 543 ACAGATGCTAAATAATCTCTTCTGAAAAACAGCATATCAG 580

RESULT 5
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 LOCUS DKFP686B1728_r1 686 (synonym: hicc3) Homo sapiens cDNA clone
 DEFINITION DKFP686B1728 5', mRNA sequence.
 ACCESSION AL703938
 VERSION AL703938.1 GI:19687293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 544)
 Oltensweiler, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
 Wiemann, S.
 EST (Oltensweiler, B., Obermaier, B., Mewes, H.W., Weil, B. and
 Wiemann, S.)
 Unpublished (2001)
 CONTACT: MIPS
 MIPS
 Ingelstaedtler, J., D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,
 Sequenced by MedGenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German genome Project. No sl sequence
 available.
 This clone (DKFP686B1728) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1..544
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 /mol_type="mRNA"

FEATURES
 source

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/dev_string="adult"
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cdna-collection"

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/clone="DKFZp686E1728"
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/lab_host="DH10B"
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/clone_lib="686 (s
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/note="Vector: pTriplEx2; Site_1:
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NOTATION - WNCN

cdna-collection"

ORIGIN

Query Match	23.54;	Score 478.6;	DB 1;	Length 544;
Best Local Similarity	93.64;	Pred. No. 6.1e-106;		
Matches	610	Conserved	6	W. No. 1

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matches 310; conservative 0; mismatches 34

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649 CAGGAGATGAATGTCGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGAT 708

Db	1	CAGGAAAGTGAATGTGTGTTAATGTGCTGGAACTGGCGCCGATGGAAATATTTCAAAAT	60
Qy	709	GAGTATGGAAATACCACTCTGCACATACGCTATCTATAATGAAGATAAATTAATGGCCAAA	768
Db	61	GAGTATGGAAATACCGGCTCTACACTA-TCATCTCAATGAAGATAAATTAATGGCCAAA	119
Qy	769	GCACTGCTCTTATATGTGTGTGATATGCAATCAAAAAACAAGCATGGCGCTCACACACTG	828
Db	120	GCACTGCTCTTATATGTGTGTGATATGCAATCAAAAAACAAGTGGCGCTCACACACTT	179
Qy	829	TTACTGTGTATCATGAGCAAAAAACGCAAGTCGTGAAATTTTATCAAGAAAAACG	888
Db	180	TTGCTGGCGCTGACGAACAAAAAACGAGAGTGTGAAATTTTATCAAAAAAAGCT	239
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Qy	949	TCAGCAAGTATAGTCAGGCTTCTACTTGAGCAAAATATTGATGTATCTTCACAGATCTA	1008
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Qy	1009	TCTGGACAGACGGCGAGAGATGCTGTTCTAGTCATCATATGTAATTTGGCCAGTTA	1068
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Qy	1069	CTTTCTGACATCAAAAGAAAAACAATGCTAAAAATCTTCTGAAAAACGCAATTCAGAA	1128
Db	420	CTTTCTGACATCAAAAGAAAAACAATGCTAAAAATCTTCTGAAAAACGCAATTCAGAA	479
Qy	1129	CAAGACTTAAAGCTGACATCAAGAGAAAGTCAAAAGCTTCAAAAGCATGGAATAATGC	1188
Db	480	CAAGACTTAAAGCTGACATCAAGAGAAAGTCAAAAGCTTAAAGTCAGTGAATAATGC	539
Qy	1189	CAGCC 1193	
Db	540	CAGCC 544	

[illegible]

Db 61 GAGTATGGAATACCGCTCTACACTA-TCTATCTACATGAAGATAATTATGGCCAA 119

[illegible]

829 TTACTTGGTGACATGAGCAAAACAGCAAGTCGTGAATTTTAATCAAGAAAAAGCG 888

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Db 240 AATTAAATGCACCTTGATAGATATGGAAGAACTGCCCTCATACTTGTCTGTATGTTGTGGA 299

1009 TCTGACAGACGGCCAGAGATATGCTGTTTCTAGTCATCATGTAATTGGCCAGTTA 1068

1. *What is the purpose of this study?*

Db 420 CTTTCTGACTATAAGAAACAGATGCTAAAAATCTCTTCTGAACAACAGCAATCCAGAA 479

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QY	1189	CAGCC	1193
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BF676987
LOCIS
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OCE h
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FCE 01 FFC 0000

mRNA sequence,
 accession
 BE676907

KEYWORDS EST.
SCITRICE HCMC sandi'ona (human)

Mammalia: Eutheria: Euarchontiformes: Primates: Catarrhini: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 865)	NIH-MGC	http://mgc.ncbi.nlm.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)	Contact: Robert Strusberg, Ph.D.	
			Email: cgabbs-romail.nih.gov	

FEATURES	Location/Qualifiers
source	1. .865

FEATURES

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/organism="Homo sapiens"
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/clone="IMAGE:4248746"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIM_MGC_83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech) ;
Site 1: 5'fl (ggcgccctcgccc) ; Site 2: 3'fl
(ggcctatcgccc) ; 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCCATTTATGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb) . 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

```

RESULT 7
BX492731

LOCUS BX492731 505 bp mRNA linear EST 04-SRP-2003
DEFINITION DKFZP781C0523 r1 781 (synonym: h1cc4) Homo sapiens cDNA clone
ACCESSION BX492731
VERSION BX492731.1 GI:32004516
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 505)
Bloecker,H., Bloecker,M., Mewes,H.W., Well,B., Amid,C., Oesanger,A.,
Pobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Bloecker,M., Mewes,H.W., Well,B., Amid,C., et al.)
Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@kfz-heidelberg.de;
sequenced by GFP (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 81 sequence available.
This clone (DKFZP781C0523) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubneweg 6, 14059
Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.
Location/Qualifiers
1..505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP781C0523"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1_sfi; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

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Best Local Similarity 92.7%; Pred. No. 6.6e-81;
Matches 395; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 325 TGCAGGGGAGCGGCAAGCAAGTGGCGCTTGGGAGACTACATGAGCTTC 384
DB 80 TGGCTGGGAGCGGCAAGCAAGTGGGCACTTGGGAGACTACAGCAGCGCTTC 139
QY 385 ATGAGCCAGGATACGATCGGTGGAGAAATCTGACAAAGCTCAGAGGCTGCTGG 444
DB 140 ATGAGCCAGGATACGATCGGTGGAGAAATCTGACAAAGCTCAGAGGCTGCTGG 199
QY 445 TGGGATGAAGTCCCGAAGAAAGATCTCATGTCATGCTCAGGAGCACTGAGCAAG 504
DB 200 TGGGATGAAGTCCCGAAGAAAGATCTCATGTCATGCTCAGGAGCACTGAGCAAG 259
QY 505 AAGGACAAAGCAAGAAAGAGACTGCTTACATCTGGCTTGGCCATGGGAATTCAGAA 564
DB 260 AAGGACAAAGCAAGAAAGAGACTGCTTACATCTGGCTTGGCCATGGGAATTCAGAA 319
QY 565 GTTAAATCTGCTGTGAGAGAGATGTCAACTTAATGCTTGGACAAAGAAAGAGAA 624
DB 320 GTTAAATCTGCTGTGAGAGAGATGTCAACTTAATGCTTGGACAAAGAAAGAGAA 379
QY 625 GCTGTGATTAAGGCGGTACATGTCAGAGAGATGAATGTGCTTAATGTTGCTGAAC 684
DB 380 GCTGTGATTAAGGCGGTACATGTCAGAGAGATGAATGTGCTTAATGTTGCTGAAC 439
QY 685 GGCAGTGAATCAAAATTTTCAGATGAGTATGAAATACACTTGGACTACGCTATCT 744
DB 440 GGCAGTGAATCAAAATTTTCAGATGAGTATGAAATACCGCTTACATGCTATCTAC 499

RESULT 8
BQ441373
LOCUS BQ441373
DEFINITION BQ441373 817 bp mRNA linear EST 24-MAY-2002
AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
5', mRNA sequence.
ACCESSION BQ441373
VERSION BQ441373.1 GI:21180449
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 817)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: CLOUTECH
cDNA Library Preparation: CLOUTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2340 row: m column: 08
High quality sequence stop: 516.
Location/Qualifiers
1..817
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/clone="IMAGE:6103855"
/lab_host="DH10B (T1 phase-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccatatacgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 clones contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN
Query Match 17.5%; Score 357.8; DB 5; Length 817;
Best Local Similarity 92.7%; Pred. No. 2.7e-76;
Matches 431; Conservative 0; Mismatches 27; Indels 7; Gaps 5;
QY 1408 AGAATTTGGGAATTAAGTTTCTGACTACAAAGAAACAGATGCCAAATACTCTTCTGAA 1467
DB 319 AGAATTTGGGAATTAAGTTTCTGACTACAAAGAAACAGATGCCAAATACTCTTCTGAA 378
QY 1468 AACACCAACCCGAAACAGACTTAAGTGAATCAAGAGAGAGTCAAGAGCTTGA 1527
DB 379 AACACCAACCCGAAACAGACTTAAGTGAATCAAGAGAGAGTCAAGAGCTTGA 438
QY 1528 GGCAGTGAAGTGGCAGGCAAGAAAGATCTCAAGAACGAAATTAATTAAGATGGT 1587
DB 439 GGCAGTGAAGTGGCAGGCAAGAAAGATCTCAAGAACGAAATTAATTAAGATGGT 498
QY 1588 GATAGAGAGCTGAAGAAATTTTATGCTATCGAAGAAATGAAGAACGGAAGTACTCAT 1647
DB 499 GATAGAGAGCTGAAGAAATTTTATGCTATCGAAGAAATGAAGAACGGAAGTACTCAT 558

QY 1648 GTGGATTCGCCAGAAAACCTGACTAATGTCGCACTGTCGCAATGATGATGATTA 1707
DB 559 GTGGATTCGCCAGAAAACCTGACTAATGTCGCACTGTCGCAATGATGATGATTA 618
QY 1708 ATTCTCTCAAGAGAGAGACCACTGAAAGCCAGCAATTTCTTGAACCTGAG-AATGA 1766
DB 619 ATTCTCTCAAGAGAGAGAGACCACTGAAAGCCAGCAATTTCTTGAACCTGAG-AATGA 678
QY 1767 AGAGTATCAAGT-GACGAACAAAATGATAC-TCAGAGCAATTTTGTGAGAA--CAGA 1822
DB 679 AAGATATCCAGAGAGAGAGACCAAAATGATGATCTTCAAGAACCAATTTTGTGAGAAACAGA 728
QY 1823 AACCTGGAATATATACAGA--TGAGATTCCTGATTCATGAGAGAAA 1865
DB 739 CACCTGGAATTTTACCCGATGAGATCTGATCTCTGAGAGAAA 783

RESULT 9
BX437445 910 bp mRNA linear EST 03-MAY-2004
LOCUS BX437445 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP006Y104
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX437445
VERSION BX437445.2 GI:46959477
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 910)
Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30771569.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5500.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0CAP006Y104&c=5500.r.
FEATURES
source Location/Qualifiers
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP006Y104"
/rissue_type="THYMUS"
/clone_id="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 17.5%; Score 357.2; DB 5; Length 910;
Best Local Similarity 69.6%; Pred. No. 3.9e-76;
Matches 501; Conservative 1; Mismatches 209; Indels 9; Gaps 1;

QY 223 AGTGGCAAGCAACCTGGCGCTTTGAGACACAGACTCTCTTGAAGACATC 282
DB 100 AAGAGCGAAGAGACATGAGTGTCTCTGAAGCCCGCTGCGCCATGAAGAGATT 159
QY 283 AGAACAAGATGGGCAAGTGTGCTGCACTGCTCCCTGCGCAGGGGAGCGGCAAG 342

DB 160 TTTAGTAAGAGGCGAAGTGGCCCTTGCGCCGCGGCGGAGAGACAGC--- 216
QY 343 AGCAAGTGGCGGCTTTGGGGAAGACTAGACATGACATGCTTTCATGAGCCAGATCAC 402
DB 217 -----GCGGAGAGCGGGGCGAGCGGGGAGAGCGCTTACTGACGCCGCTACAC 270
QY 403 GTCCCTGAGAGAAAGATTGGAACAAAGCTTCAAGAGCTGCTGTGGGGGTAAAGTCCACA 462
DB 271 GTCCGAGACCGAGATTCGGCAAGATCCAAAGCTGCCAGCGCGGTATATGTGGGAAA 330
QY 463 AAGATCTCATGCTGATGCTGACAGGACACTGACGTGAACAAGAGAGCAAGAGAG 522
DB 331 GTGACGACATCTTTTGTCTCAGAGAAAGATGCTTGAAGATGAGACAGATGAACAG 350
QY 523 ACTGCTTACATCTGCGCTTGGCAATGGGAAATTCAGAAATGATAAACTCTCTGAGC 582
DB 391 ACGGCTTACATTTGGCTGTGCAATGCTGATCCAGAAATGATATCTCTGCTGTGAC 450
QY 583 AGACGATGTCACCTTAATGCTTTCAGCAACAAAGAGAGACAGCTGTGATTAAGCCGTA 642
DB 451 AGAAATGTCACCTCAATGCTGTGTGACAAAGAAACAGACAGCTGTGATGAAGCTGTA 510
QY 643 CATGCGCAGAGAGATGATGATGCTGATGATGCTGCTGGAACATGCACTGATCCAAATAT 702
DB 511 CATGCGCAGAGAGAGAGATGATGATGCTGATGATGCTGCTGGAACATGCACTGATCCAAAT 570
QY 703 CCAGATGATGATGAAATACCACTGCACTACCTATGCTATATGAGATTAATTAATG 762
DB 571 GGGATGTCATGAGCAACCTGCTTCACTATGCTGTATATGAGACATATACATGTA 630
QY 763 GCCAAGACCTGCTTATATGCTGTGATATGATGATGATGATGATGATGATGATGATGAT 822
DB 631 GCAACCAAGCTCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 690
QY 823 CCAGTGTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 882
DB 691 CCACTTTTACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 750
QY 883 AAGCAATTTTAATGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 942
DB 751 AAGCAATTTTAATGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810

RESULT 10
CR860726 2677 bp mRNA linear HTC 12-NOV-2004
LOCUS CR860726 Pongo pygmaeus mRNA; cDNA DKFZp459F0427 (from clone DKFZp459F0427).
DEFINITION CR860726
ACCESSION CR860726
VERSION CR860726.1 GI:55732274
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pongo.
1 (bases 1 to 2677)
Bloeker, H., Boeher, M., Brandt, P., Mewes, H.W., Well, B., Amid, C.,
Oeinger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GfP (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp459F0427) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459F0427
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

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FEATURES
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                /mol_type="rRNA"
                /db_xref="taxon:9600"
                /clone="DKFZp459F0427"
                /isane_type="cortex"
                /clone_1ib="459 (synonym: pcor1). Vector pSport1_sfl; host
                DH10B; sites SfilA + SfilB"
                /dev_stage="adult"
                /note="hypothetical protein (Homo sapiens), differentially
                spliced"
            1..2677
                /gene="DKFZp459F0427"
            176..973
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            /codon_start=1
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            /protein_id="CAH92841.1"
            /db_xref="GI:55732275"
            /translation="MGVRSFLAACRRBMATRKNRDNDKXGSRVVRKDLGMTHK
            AAIAGDVNLTLSILGLNDVNDROKRTALHLCAHGRPVVADLVARKRLMID
            SNRRLTIAVOCQEAIVCASIIIEHGADPNVDMGTALHAIINENISMGKLLAY
            GADIBRSQGHSTSLIAVNRKEENVAFLLKKKPDLTALDNFGTALITLARNGSTS
            VVYOLHNIHDIYFCODISGMTADYAAASKFOATRLRNDIRARAKA"

ORIGIN
Query Match      17.2%; Score 351.2; DB 4; Length 2677;
Best Local Similarity 53.1%; Pred. No. 1.5e-74;
Matches 887; Conservative 0; Mismatches 748; Indels 37; Gaps 5;

QY 378 TGCCTTCATGAGCCAGGATACACGTCGATGAGAGATCTGACACAGCTCCACAGAC 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 TGGCTTCTCAAAATTCGGGATCCGAGTCCGCGAGAAAGATCTGGGATATCCACAAAGC 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 438 TGCCTGATGAGTAAAGTCCCAAGAAAGATCTCATGTCATGCTCAGGACATGACGT 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 TGCATCGCGGATGATGAACAAGCTGCTGAGAGACATCTTGCTGGGCTGATGACGT 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 498 GAAACAAGAGCAACACAAAGAGACATGCTCTACATCTGGCTCTGCCAATGGGAATTC 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 GAATGACAGGACAAAGAAACAGAGCTGCTTACATTTGGCGTGGCCATGGCCGCTC 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 558 AAGAAGTAGTAAAACTCTGCTGGACAGAGATGTCATTAATGTCTTGAACAACAAA 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 GGGAGTGTGATGCTGATTTGGTGGCCAGAAAATGCCGCTTAACCTACAGACAGTAAA 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 618 GAGGACGCTGTGATTAAGGCGGTACATGCCAGAAAGATGAATGTGCGTTAATGTTGCT 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 490 CAGGACAGCTGTGATCAAGGCTGTACATGTCAAGAAAGCATTTGTGATTCATCTGCT 549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 678 GGAACATGGACATGATCCAAATATTCAGATGATGGAATACACCTCTGACATACGC 737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 550 GGAACATGGCGCGACCCAAATGTTAGATATGTAAGCAACACGCTCTGACATATGC 609
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 738 TATCTATTAAGAAATTAATTAAGCAAGCACTTATATATGATGCTGATATGCA 797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 610 CATGATTAATGAATATATCAATGACAGAAAACTGCTGATATGATGACATATTTGA 669
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 798 ATCAAAAAAACAAGATGCGCTCACACACTGTTACTGTGTAATCATGACAAAAACA 857
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 670 ACGAAGAACCCAGGAGTGACATACATCACTTTACTCGCTGTAATAGAAAAAAGAGA 729
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 858 AGTCGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCACTGATGATGAGAG 917
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 730 AATGGGGAATTTTGTGTAAGAAAAACAATTTACTGCAATGATTAATTTTGAAG 789
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 918 GACTGCTCATPACTTGATGATGTTGTGGATCAGCAAGATATGACGCTTACTTGA 977
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 790 AACAGCCTCATPCTTGCTGCTGTAACGATTAACAAGTGTATGCTTACAGCTTCTTGA 849
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 978 GCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACGCGCAGAGATGCTGT 1037
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 850 GCACATATATGACGCTTTTGGCAAGATATATCTGGATGAGACTGCAAGAACTACGCTGC 909
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1038 TTCTAGTCATATCATATGTAATTTGGCAGTACTTTCTGACTACAAAGAAAAACAATGCT 1097
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 910 TGCCTCTAAGTTTCAAGCA-----CAAGCTTGAAGATGAC 946
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1098 AAAAATCTCTTGTGAAAAACAGCAATCCAGAACAAAGCTTAAAGCTGACATCAGAGAGA 1157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 947 ATCAGAGGAGAGCAAGAAAGCTTGAAGATGTGAAGTACCCAGCCAGCTTGAAGA 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1158 GTCAAAAGTTTCAAAAGCAGTGAATAATGACGCGCAGAGAAAATGTCTCAAGAACAGA 1217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1007 ---AAAAATGAAGAAATCCAGAAATAGAAAAATGGAAGTGTCAAGAAAACGTACATGCTGA 1063
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1218 AATAATTAAGATGATGATAGAGAGTTGAAGAAATGAAGAACATGAAGTAATTA 1277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1064 TGACAGTACAGTTATTAATGATGATGATGATGAATTAATTCACAAATTAAGAACAGAAA 1123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1278 TGTGGGATTTACTAGAAAACTGACTAATGTTGTCACTGCTGGCAATGATGATGATTT 1337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1124 ACCTGATAGTCAATCAATTTCCAGAGAGAGAAATGACAAATTTGATAGCTTGCAGAGA 1183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1338 AATTCCCAAGAGAGAGAGAGAACCTGAAAAATCAGCAATTTCTGACACAGAAAG--T 1395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1184 AACCTCTAATGAAGAAAGAGCAAGTATTAATAAAGTTAAAGCCAAATATATTTCAAGGAT 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1396 GAAAGATATCACAGAAATTTGCAATTTAGTTTCTGCTACAAAGAAAACAGATGCCAAA 1455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1244 GATCTTAATGATATACCTGGGTCATCTGAAAAAACCTCAGAGAGATGATGCTTAAAC 1303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1456 TACTCTTCGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACATCAGAGAGAGATCA 1515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1304 TCTGATGATTAAGATTTTATGTTACTCATGTAACAAAGTGAAGAAAGTGTAAAGATTT 1363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1516 CAAAGCTTAGAGGAGTGAAGAAATGGCCAGACCAAGAAAGATCTCAAGAACCAAGAAATA 1575
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1364 GTTAGCTTATGAATAATCAAGATGCAACAGCTGATGTAAGATGATCAATAGATTA 1423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1576 AATAAGATGATGATAGAGAGCTAGAAAATTTATAGCTATGGAAGAAATGA--AGAAC 1633
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1424 AATGTTTCTGTGAACAATTAAAGTAAATTTCAAAAAATTAATAATATTTTGAATTA 1483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1634 ACGAAGTACTCATGTCGGATTTCCAGAAAACTGACTAATGATGTCCTGCTGCAATG 1693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1484 CTACAAAAGATCTATCTGAAACAAACAAACCAATCAAGTTAGAGATCAGAAATCTT 1543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1694 GTGATGATGATTAATCTCTCAAGAAAGAGCAG-----AACACTGAAAGCAGCAA 1746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1544 GAAAGGAAAAAAGAACTCTGTATTTGAGATTCATCTTACAAACAAGAAAGAAAGAGA 1603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1747 TTTCTGACACTGAGAAATGAAGATATCACATGACGAAACAAATGATATCTCAGAAAGCA 1806
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1604 AATAAGCTGAAGAGATTTGATAGAAAGATACAGAAAGTAAATAATGAGAGAGAG 1663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1807 TTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTCTGATTCATGAAGAAA 1866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1664 TATAGAGACAAACAGAGAGTGAAGAAAAACAATTAACTGACCTCAATCATTTGGAAGTG 1723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1867 CAGATGAAGAGTGTGAAAAAATGAATTCAGCTTTCTCTTAAGTTGAAGAAAGAAAA 1926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1724 GCATTAAGAGACTGTAAAGAGTAACTCAATCAGAAATTCCTCATATCATGTAAGAAAGAGA 1783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1927 GACATCTTGCAAGAAATAGTACGTTGGCGGAGAAATTTGGCCATGCTAAGATGAGCTTA 1986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1784 GACCGGTGACAGAAATTCATCTGATGGGAGTGAATTTGCCAGCTCAGGCTGGAAATA 1843
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1987 GACACAATGAACATCAGAGCAGCTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 2038
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1844 GACACAATTAACATCAGAACAGAACTGAAAAATTAATTAATTTTCAAGATA 1895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 11
AUI20666

LOCUS AUI20666 843 bp mRNA linear EST 01-AUG-2002
 DEFINITION AUI20666 HEMBI Homo sapiens cDNA clone HEMBI001175 5', mRNA
 sequence.
 ACCESSION AUI20666
 VERSION AUI20666.1 GI:10935901
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 843)
 Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
 Yamamoto,J., Makamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isegai,T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isegai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kibarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project: 5', - 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 FEATURES
 source
 1..843
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEMBI001175"
 /isue_type="whole embryo, mainly body"
 /dev_stage="embryo, 10 weeks"
 /clone_1ib="HEMBI1"
 /note="Vector: pME18SFJ3"

ORIGIN
 Query Match 17.1%; Score 348.8; DB 1; Length 843;
 Best Local Similarity 69.2%; Pred. No. 4.4e-74;
 Matches 492; Conservative 0; Mismatches 210; Indels 9; Gaps 1;

QY 223 AGTGCAGAGCAAGCTGGGCGCTTGTGAGACACAGCACTCTGTATGAAGACATC 282
 DB 119 AGAGCCGAGAGACATGAGTGCTCTGAAGCCCGCTGCGGCATGAAGAAGATT 178
 QY 283 AGGAACAAGATGGGCAAGTGTCTGCCACTGTCTCCCTGCTGACGGGGAGCGGCAAG 342
 DB 179 TTATGTAAGAGGCGCAAGTGCCTTGGCTCTCTGCGCGGCGGAGAGCAAGC--- 235
 QY 343 AGCAAGGTGGCGCTTGGGAGACATACATGACAGTGCCTTATGAGGCCAGGTACAC 402
 DB 236 -----GCCGAGAGCGGGGCGAGCGGGGAGGGGCTTACTCGAGCCCGCTACAC 289
 QY 403 GTCCGTGAGGAAGATCTGACAAAGCTCCACAGAGCTCTGTGGGGTAAAGTCCCA 462
 DB 290 GTCCGAGACCGAGATCTCGGCAAGATCCAAAGCTGCCAGCGGGGTATGTGGGAAA 349
 QY 463 AAGGATCTATGCTATGCTCAGGAGACATGACGTGAACAAGAGACAAAGAAAGAG 522
 DB 350 GTGCGAGAGATCTTTTGTCTAGGAAGATGGCTTAAAGATAGAACAAAGTGAACAG 409
 QY 523 ACTGCTCATCTGTGCGCTCTGCGCAATGGAAATTGAGAGTAAACTCTCTGTGAGC 582
 DB 410 AGGCTCTATCATTTGGCTCTGTGCAATGTGTATCCAGAGTAACTCTCTGTGAGC 469
 QY 583 AAGCATGTCAACTTAATGTCTTTCAGCAACAAAAGAGACAGCTGTGTAAGGCGCTGA 642
 DB 470 AGAAATATGCGACGTCAATGTCTGTGCAACGAAAGACAGAGCTGTGTAAGGCGCTGA 529
 QY 643 CAATGCCAAGGAAGATGAATGTGTAAATGTTGCTGGAACATGAGCACTATCAATATT 702

DB 530 CAATGCCAAGGAAGAAATGTGCAATCTTCTGTCTAGAACATGCTCTATCCAAATCTT 589
 QY 703 CCAGATGAGTATGAAATACCACTGTGACACTACCTATCTATATGAAATTAATATG 762
 DB 590 GCGAGATGTCATGCGAACACACTGCTCTTCACTATGTCTGTATATGAGACATATCAGTA 649
 QY 763 GCCAAGACATGCTCTTATATGTGTGTGATATGCAATCAAAAAACAGATGCGCTCACA 822
 DB 650 GCAACAAAGCTGCTTTTGTATATATCAAAATATTTGAAGCAAAAAACAGATGACCTNACA 709
 QY 823 CCATGTTACTTGTGTATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAATCAAGAA 882
 DB 710 CCATCTTTTACTTGTGACTATGAGTAAAAAGCAGCAATGTGTGAATTTTAATTAAGGAA 769
 QY 883 AAGGCAATTTAATGACACTGATATGATATGAGAGCACTCTCTCATCTT 933
 DB 770 AAGCAATGTAAATGCTTAAATAGTTGAGAAAGAGTCAACCACTAATT 820

RESULT 12
 DQ053800
 LOCUS DQ053800
 DEFINITION Homo sapiens KIAA1074 gene, VIRUAL TRANSCRIPT, partial sequence.
 ACCESSION DQ053800
 VERSION DQ053800.1 GI:66899747
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 5130)
 Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
 Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeille,D.,
 White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 A Scan for Positively Selected Genes in the Genomes of Humans and
 Chimpanzees
 (ex) PLOS Biol. 3 (6), E170 (2005)
 JOURNAL 15869325
 PUBMED 2 (bases 1 to 5130)
 REFERENCE Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
 Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeille,D.,
 White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment. Translation starts at the beginning of
 alignment.
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 source
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="10"
 /gene="KIAA1074"
 /locus_tag="HCL4399"

ORIGIN
 Query Match 17.0%; Score 345.8; DB 11; Length 5130;
 Best Local Similarity 71.4%; Pred. No. 3.8e-73;
 Matches 455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 281 TAGAAGAAAGATGGGCAAGTGTCTGCACTGTTCCCTGCTGACAGGGGAGAGCGCA 340
 DB 2 TGAAGAAAGATTTTGTATGAAGAGGCGAGTGCCTTTGGCTCTTTCGCGCGCGGGA 61
 QY 341 AGAGCAAGTGGGCGCTTGGGAGACATGATGACAGTGCCTTCAATGAGCCAGGTACC 400
 DB 62 GGAGCAGCGCGGAGAGCGGGGCGAGCCGGGGAAGGCGCCTTACTGACGCCGCTACC 121

QY 942 T 942
Db 803 T 803

RESULT 14
BC063888
LOCUS
DEFINITION
BC063888 5483 bp mRNA linear HTC 01-Apr-2004
Homo sapiens cDNA clone IMAGE:30389199, with apparent retained intron.

ACCESSION
BC063888
VERSION
BC063888.1 GI:39645658
KEYWORDS
HTC
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schettz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wierley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalys, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED
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2 (bases 1 to 5483)
Strausberg, R.
Direct Submission
Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK
COMMENT
Contact: MGC help desk
Email: cgabds-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Buterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabhu, Parvaneh Seedi, Jr Santos, Angelique Scherch, Ureila Skalska, Duane Smalys, Jeff Scott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRK Plate: 141 Row: O Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein
This clone has the following problem: retained intron.

FEATURES
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DB 1 CAGAAACCTGACTTAATGGTGCACATGCTGCAATGATGATGATTAATTCACAA 60
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DB 61 GGAAGACGACACCTGAAAGCAGCAATTTCTGACACTGGAATGAAGATATCACA 120
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DB 121 GTGATGACAAATGATATCTGACAGCAATTTTGTGAAGACGACCTGGAATTTAC 180
QY 1838 AGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1897
DB 181 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
QY 1898 AGCTTCTCTTACTGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1957
DB 239 AGCTTCTCTTACTGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 298
QY 1958 AAGAAATTCCTGCTTAAGACATGAGCTGACACATGAAATCATGAGCCAGCTAAAA 2017
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QY 2018 AAAAAAAAAA 2027
DB 359 AAAAAAAAAA 368

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ACCESSION
BM469654
VERSION
BM469654.1 GI:18518696
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLNL12351 row: m column: 06
High quality sequence stop: 680.

FEATURES
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1. 1020

1. .1020

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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.

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ORIGIN

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Best Local Similarity	74.6%	Pred. No. 8.6e-68		
Matches 406, Conservative	0	Mismatches 136	Indels 0	Gaps 0

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